

GenCore version 5.1.3  
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OM nucleic - nucleic search, using sw model

Run on: February 1, 2003, 01:06:21 ; Search time 969.74 Seconds  
(without alignments)  
14135.156 Million cell updates/sec

Title: US-09-931-486-111

Perfect score: 471

Sequence: 1 ATCGAAGATCCCGCTTCTT.....CAGATTGCTGGGGTTATAT 471

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 2054640 seqs, 14551402878 residues  
Total number of hits satisfying chosen parameters: 4109280

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :

GenEmbl.\*

- 1: gb\_ba.\*
- 2: gb\_htg.\*
- 3: gb\_in.\*
- 4: gb\_om.\*
- 5: gb\_ov.\*
- 6: gb\_pat.\*
- 7: gb\_ph.\*
- 8: gb\_pl.\*
- 9: gb\_pr.\*
- 10: gb\_ro.\*
- 11: gb\_sts.\*
- 12: gb\_sy.\*
- 13: gb\_un.\*
- 14: gb\_vi.\*
- 15: em\_ba.\*
- 16: em\_fun.\*
- 17: em\_hum.\*
- 18: em\_in.\*
- 19: em\_mu.\*
- 20: em\_om.\*
- 21: em\_or.\*
- 22: em\_ov.\*
- 23: em\_pat.\*
- 24: em\_ph.\*
- 25: em\_pi.\*
- 26: em\_ro.\*
- 27: em\_sts.\*
- 28: em\_un.\*
- 29: em\_vi.\*
- 30: em\_htg\_hum.\*
- 31: em\_htg\_inv.\*
- 32: em\_htg\_other.\*
- 33: em\_htg\_mus.\*
- 34: em\_htg\_pln.\*
- 35: em\_htg\_rod.\*
- 36: em\_htg\_mam.\*
- 37: em\_htg\_vit.\*
- 38: em\_sy.\*
- 39: em\_htgo\_hum.\*
- 40: em\_htgo\_mus.\*
- 41: em\_htgo\_other.\*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB	ID	Description
1	471	100.0	471	6	A48044	A48044 Sequence 11
2	471	100.0	471	6	AR177089	AR177089 Sequence
3	471	100.0	471	6	AX191052	AX191052 Sequence
4	466.2	99.0	528	1	PAE439391	AJ439391 Pseudomon
5	466.2	99.0	11176	1	AE004949	AE004949 Pseudomon
6	466.2	99.0	12065	1	AE004883	AE004883 Pseudomon
7	452.6	96.1	521	1	PAE439389	AJ439389 Pseudomon
8	443.2	94.1	592	1	AF422498	AF422498 Unculture
9	442.2	93.9	531	1	PAE439388	AJ439388 Pseudomon
10	442.2	93.9	660	1	PSEDFC	L28150 Pseudomonas
11	441.2	93.7	498	1	PAE439392	AJ439392 Pseudomon
12	432.2	91.8	490	1	PAE439390	AJ439390 Pseudomon
13	431.8	91.7	659	1	PSEDFB	L28149 Pseudomonas
14	428.6	91.0	659	1	PSEDFB	L28148 Pseudomonas
15	383.2	81.4	10832	1	AE004501	AE004501 Pseudomon
16	382.2	81.4	17712	1	AE004844	AE004844 Pseudomon
17	302.6	64.2	391	1	AF422518	AF422518 Unculture
18	288.8	61.3	477	1	PST390586	AJ390586 Pseudomon
19	285.6	60.6	477	1	PST251909	AJ251909 Pseudomon
20	276.6	58.7	530	1	PST251907	AJ251907 Pseudomon
21	275	58.4	530	1	PST251906	AJ251906 Pseudomon
22	272.6	57.9	499	6	A48047	A48047 Sequence 11
23	272.6	57.9	499	6	AR177092	AR177092 Sequence
24	272.6	57.9	499	6	AX191055	AX191055 Sequence
25	262.8	55.8	486	1	PBA279238	AJ279238 Pseudomon
26	261.2	55.5	485	1	PBA279239	AJ279239 Pseudomon
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33	254.6	54.1	616	1	AF422492	AF422492 Unculture
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35	251.6	53.4	529	1	PST251902	AJ251902 Pseudomon
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37	248.2	52.7	560	1	AF356514	AF356514 Pseudomon
38	244.8	52.0	523	1	PST390581	AJ390581 Pseudomon
39	241.4	51.3	522	1	AF127587	AF127587 Pseudomon
40	236	50.1	527	1	AF127586	AF127586 Pseudomon
41	231	49.0	5679	1	AF134704	AF134704 Pseudomon
42	231	49.0	5785	1	PSU65012	U65012 Pseudomonas
43	228.6	48.5	803	1	AF260010	AF260010 Chlamydia
44	225.8	47.9	504	6	A48046	A48046 Sequence 11
45	225.8	47.9	504	6	AR177091	AR177091 Sequence

ALIGNMENTS

RESULT 1	A48044	Sequence 111 from Patent WO9600298.	471 bp	DNA	linear	PAT 07-MAR-1997
LOCUS	A48044					
DEFINITION	A48044					
ACCESSION	A48044					
VERSION	A48044.1	GI:2301906				
KEYWORDS						
SOURCE		unidentified.				
ORGANISM		unclassified.				
REFERENCE		1 (bases 1 to 471)				
AUTHORS		Jannes,G., Rossau,R. and Van,H.H.				
TITLE		SIMULTANEOUS DETECTION, IDENTIFICATION AND DIFFERENTIATION OF				
JOURNAL		EUBACTERIAL TAXA USING A HYBRIDIZATION ASSAY				
		Patent: WO 9600298-A 111 04-JAN-1996;				

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INNOGENETICS NV (BE)
Other publication AG 2924595 960119.
Location/Qualifiers
1. .471
/db_xref="taxon:32644"
BASE COUNT 116 a 103 c 120 g 132 t
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Best Local Similarity 100.0%; Pred. No. 1e-125;
Matches 471; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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DB 61 GATTGGGCTGTAGCTCAGTTGTTAGAGCGCACCCCTGATAGGCTGAGGTCGGCAGTT 120
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RESULT 3
LOCUS AX191052 471 bp DNA linear PAT 10-AUG-2001
DEFINITION Sequence 111 from Patent EP1091004.
ACCESSION AX191052
VERSION AX191052.1 GI:15149697
KEYWORDS
SOURCE unclassified.
ORGANISM unclassified.
REFERENCE 1 (bases 1 to 471)
AUTHORS James, G., Rossau, R. and Van Heuverswyn, H.
TITLE Simultaneous detection, identification and differentiation of
eubacterial taxa using a hybridization assay
JOURNAL Patent: EP 1091004-A 111 11-APR-2001;
INNOGENETICS N.V. (BE)
FEATURES
Location/Qualifiers
1. .471
BASE COUNT 116 a 103 c 120 g 132 t
ORIGIN
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Best Local Similarity 100.0%; Pred. No. 1e-125;
Matches 471; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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LOCUS AR177089 471 bp DNA linear PAT 17-DEC-2001
DEFINITION Sequence 111 from patent US 6312903.
ACCESSION AR177089
VERSION AR177089.1 GI:17919444
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 471)
AUTHORS James, G., Rossau, R. and Van Heuverswyn, H.
TITLE Simultaneous detection, identification and differentiation of
eubacterial taxa using a hybridization assay
JOURNAL Patent: US 6312903-A 111 06-NOV-2001;
INNOGENETICS N.V. (BE)
FEATURES
Location/Qualifiers
1. .471
BASE COUNT 116 a 103 c 120 g 132 t
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Query Match 100.0%; Score 471; DB 6; Length 471;
Best Local Similarity 100.0%; Pred. No. 1e-125;
Matches 471; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 ATCGAAGATCCCGGCTTCTTCATAAGCTCCACACGAAATGCTTGATTCACCTGGTTAGAC 60
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 DEFINITION  
 ACCESSION  
 VERSION  
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 Best Local Similarity 99.4%; Pred. No. 2.5e-124;  
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 DEFINITION  
 ACCESSION  
 VERSION  
 KEYWORDS  
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 ORGANISM  
 REFERENCE  
 AUTHORS  
 TITLE  
 JOURNAL  
 MEDLINE  
 PUBMED  
 REFERENCE  
 AUTHORS  
 TITLE  
 JOURNAL

AE004949  
 Pseudomonas aeruginosa PA01, section 510 of the complete genome.  
 AE004949 AE004091  
 AE004949.1 GI:9951690  
 Pseudomonas aeruginosa.  
 Pseudomonas aeruginosa.  
 Bacteria; Proteobacteria; gamma subdivision; Pseudomonadaceae;  
 Pseudomonas.  
 1 (bases 1 to 11176)  
 Stover, C.K., Pham, X.Q., Erwin, A.L., Mizoguchi, S.D., Warriner, P., Hickey, M.J., Brinkman, F.S., Hufnagle, W.O., Kowalik, D.J., Lagrou, M., Garber, R.L., Goltry, L., Tolentino, E., Westbrock-Wadman, S., Yuan, Y., Brody, L.L., Coulter, S.N., Folger, K.R., Kas, A., Larbig, K., Lim, R., Smith, K., Spencer, D., Wong, G.K., Wu, Z. and Paulsen, I.T.  
 Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic pathogen  
 Nature 406 (6799), 959-964 (2000)  
 20437337  
 10984043  
 2 (bases 1 to 11176)  
 Stover, C.K., Pham, X.-Q.T., Erwin, A.L., Mizoguchi, S.D., Warriner, P., Hickey, M.J., Brinkman, F.S.L., Hufnagle, W.O., Kowalik, D.J., Lagrou, M., Garber, R.L., Goltry, L., Tolentino, E., Westbrock-Wadman, S., Yuan, Y., Brody, L.L., Coulter, S.N., Folger, K.R., Kas, A., Larbig, K., Lim, R.M., Smith, K.A., Spencer, D.H., Wong, G.K.-S., Wu, Z., Paulsen, I.T., Reizer, J., Sailer, M.H., Hancock, R.E.W., Lory, S. and Olson, M.V.  
 Direct Submission  
 Submitted (16-MAY-2000) Department of Medicine and Genetics,

University of Washington Genome Center, University Of Washington,  
Box 352145, Seattle, WA 98195, USA

## FEATURES

## source

Location/Qualifiers

1. .11176

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BASE COUNT 2242 a 3417 c 3071 g 2446 t

## ORIGIN

Query Match 99.0%; Score 466.2; DB 1; Length 11176;  
Best Local Similarity 99.4%; Pred. No. 3.7e-124;  
Matches 468; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
QY 1 ATCGAAGATCCCGGCTCTTCATAAGCTCCACACGAATTCCTTGATTCACTGTTAGAC 60  
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DB 4818 TTTTGGCGGAATGCTGCTTCACAGTAAACCAGATTCCTTGGGTTATAT 4768

## RESULT 6

AE004883/c

LOCUS

DEFINITION

Pseudomonas aeruginosa PA01, section 444 of the complete

genome.

ACCESSION

AE004883.1

VERSION

AE004883.1

KEYWORDS

Pseudomonas aeruginosa.

SOURCE

Pseudomonas aeruginosa.

ORGANISM

Pseudomonas.

REFERENCE

1 (bases 1 to 12065)

AUTHORS

Stover, C.K., Pham, X.Q., Erwin, A.L., Mizoguchi, S.D., Warrenner, P.,

Hickey, M.J., Brinkman, F.S., Hufnagle, W.O., Kowalik, D.J., Lagrou, M.,

Garber, R.L., Goltry, L., Tolentino, E., Westbrock-Wadman, S., Yuan, Y.,

Brody, L.L., Coulter, S.N., Folger, K.R., Kas, A., Larbig, K., Lim, R.,

Smith, K., Spencer, D., Wong, G.K., Wu, Z. and Paulsen, I.T.

Complete genome sequence of Pseudomonas aeruginosa PA01, an

opportunistic pathogen

Nature 406 (6799), 959-964 (2000)

JOURNAL

MEDLINE

PUBMED

10984043

REFERENCE

2 (bases 1 to 12065)

AUTHORS

Stover, C.K., Pham, X.-Q., Erwin, A.L., Mizoguchi, S.D., Warrenner, P.,



Hickey, M.J., Brinkman, F.S.L., Hufnagle, W.O., Kowalik, D.J.,  
Lagrou, M., Garber, R.L., Goltry, L., Tolentino, E.,  
Westbrook-Wadman, S., Yuan, Y., Brody, L.L., Coulter, S.N.,  
Folger, K.K., Kas, A., Larbig, K., Lim, R.M., Smith, K.A., Spencer, D.H.,  
Wong, G.K.-S., Wu, Z., Paulsen, I.T., Reizer, J., Sailer, M.H.,  
Hancock, R.E.W., Lory, S., and Olson, M.V.  
Direct Submission  
Submitted (16-MAY-2000) Department of Medicine and Genetics,  
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# TITLE JOURNAL

## FEATURES source

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Db 3692 GATTGGGCTGTAGTCACTGTTAGAGCGCACCCCTGATAGGCTGAGGTCGGCAGTT 3633
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Db 3632 CGAATCTGCCAGACCCACCAATTTGTTGCTGCTGCGTATCCGATACGGGCCATAGC 3573
QY 181 TCAGCTGGAGAGCGCTGCTTGCACCGCAGGAGTTCAGATCCTCTCTGGCTC 240
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QY 241 CACCATCTAAACAATCGTCGAAAGCTCAGAAATGAATGCTCGATCAACATGATTT 300
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DEFINITION		23S rRNA gene and ITS1, strain EVA6.	
ACCESSION		AJ439389	
VERSION		1	GI:19682855
KEYWORDS		16S ribosomal RNA; 16S rRNA gene; 23S ribosomal RNA; 23S rRNA gene; internal transcribed spacer 1; ITS1; transfer RNA-Ala; transfer RNA-Ile; trRNA-Ala gene; trRNA-Ile gene.	
SOURCE		Pseudomonas aeruginosa	
ORGANISM		Bacteria; Proteobacteria; gamma subdivision; Pseudomonadaceae; Pseudomonas.	
REFERENCE			
AUTHORS		Han, R., Min, H., Zhang, C. and Cheng, Z.	
TITLE		Comparative analysis of crude oil degrading bacteria on the basis of 16S-23S internal transcribed spacers	
JOURNAL		Unpublished	
REFERENCE		2 (bases 1 to 521)	
AUTHORS		Han, R.	
TITLE		Direct Submission	
JOURNAL		Submitted (17-MAR-2002) Han R., College of Life Science, Zhejiang University, Huajiaochi Campus, Hangzhou, Zhejiang, 310029, CHINA	
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DEFINITION		sequence; 16S-23S ribosomal RNA intergenic spacer, complete	
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VERSION		1	GI:16974703
KEYWORDS		uncultured bacterium.	
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REFERENCE		1 (bases 1 to 592)	
AUTHORS		Lowe, M., Madsen, E.L., Schindler, K., Smith, C., Emrich, S., Robb, F. and Halden, R.U.	
TITLE		Geochemistry and microbial diversity of a trichloroethene-contaminated Superfund site undergoing intrinsic in situ reductive dechlorination	
JOURNAL		FEMS Microbiol. Ecol. 40 (2), 123-134 (2002)	
REFERENCE		2 (bases 1 to 592)	
AUTHORS		Lowe, M.L., Madsen, E.L., Schindler, K., Smith, C., Emrich, S., Robb, F. and Halden, R.U.	
TITLE		Direct Submission	
JOURNAL		Submitted (24-SEP-2001) Physics Department, Loyola College in Maryland, 4501 N. Charles Street, Baltimore, MD 21210, USA	
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LOCUS  
DEFINITION  
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L28150  
ACCESSION  
VERSION  
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16S ribosomal RNA; 23S ribosomal RNA; tRNA; transfer RNA.  
SOURCE  
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ORGANISM  
Pseudomonas aeruginosa  
Bacteria; Proteobacteria; gamma subdivision; Pseudomonadaceae;  
Pseudomonas.

REFERENCE 1 (bases 1 to 660)  
 AUTHORS Tyler, S.D., Strathdee, C.A., Rozee, K.R. and Johnson, W.M.  
 TITLE Oligonucleotide primers designed to differentiate pathogenic  
 pseudomonads on the basis of the sequencing of genes coding for  
 16S-23S rRNA internal transcribed spacers  
 JOURNAL Clin. Diagn. Lab. Immunol. 2 (4), 448-453 (1995)  
 MEDLINE 96082422  
 PUBMED 7583922

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 VERSION AJ439392.1 GI:19682858  
 KEYWORDS 16S ribosomal RNA; 16S rRNA gene; internal transcribed spacer 1;  
 ITS1; transfer RNA-Ala; transfer RNA-Ile; tRNA-Ala gene; tRNA-Ile  
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 SOURCE Pseudomonas aeruginosa.  
 ORGANISM Pseudomonas aeruginosa  
 Bacteria; Proteobacteria; gamma subdivision; Pseudomonadaceae;  
 Pseudomonas.  
 REFERENCE 1  
 AUTHORS Han, R., Min, H., Zhang, C. and Cheng, Z.  
 TITLE Comparative analysis of crude oil degrading bacteria on the basis  
 of 16S-23S internal transcribed spacers  
 JOURNAL Unpublished  
 AUTHORS 2 (bases 1 to 498)  
 TITLE Han, R.  
 JOURNAL Direct Submission  
 Submitted (17-MAR-2002) Han R., College of Life Science, Zhejiang  
 University, Huajiaochi Campus, Hangzhou, Zhejiang, 310029, CHINA  
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Qy	121	CGAATCTGCCAGACCCACCAATTTGTTGGTGTGCTGGTGATCCGATACGGGGCCATAGC	180
Db	174	CGAATCTGCCAGACCCACCAATTTGTTGGTGTGCTGGTGATCCGATACGGGGCCATAGC	233
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PIAIEEFLYPLVQGVDSVALKADVELGGTDOKFNLLMGRELORAYCOEAQVILTWPLL
EGLDGVKMSKSLNIGIOEPAGVWYKLSIPDTLMWRYFELLSFRSLDEIDISFRK
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RITLKAE"
rRNA      8909..10444
/product="16S ribosomal RNA"
tRNA      10509..10585
/product="tRNA-Ile"
tRNA      10614..10689
/product="tRNA-Ala"
BASE COUNT 2112 a 3049 c 3549 g 2122 t
ORIGIN
```

```
Query Match      81.4%; Score 383.2; DB 1; Length 10832;
Best Local Similarity 99.2%; Pred. No. 4.5e-100;
Matches 385; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 ATCGAAGATCCGGCTTCATAGCTCCACACCAATTCCTTGATTCACCTGGTTAGAC 60
Db 10445 ATCGAAGATCTCAGCTCTTCATAGCTCCACACCAATTCCTTGATTCACCTGGTTAGAC 10504

QY 61 GATTGGGCTGTAGCTCAGTTGGTTAGAGCGCACCCCTGATAGGGGTGAGGTCGGCAGTT 120
Db 10505 GATTGGGCTGTAGCTCAGTTGGTTAGAGCGCACCCCTGATAGGGGTGAGGTCGGCAGTT 10564

QY 121 CGAATCTGCCAGACCCACCAATTTGTTGCTGCTGCTGATCCGATACGGGGCCATAGC 180
Db 10565 CGAATCTGCCAGACCCACCAATTTGTTGCTGCTGCTGATCCGATACGGGGCCATAGC 10624

QY 181 TCAGCTGGGAGAGCGCTCTTTCACGAGGAGGTCAGGAGTTCGATCCTCTTGGCTC 240
Db 10625 TCAGCTGGGAGAGCGCTCTTTCACGAGGAGGTCAGGAGTTCGATCCTCTTGGCTC 10684

QY 241 CACCAATCTAAACAATCGTCGAAAGCTCAGAAATGAATGTTGCTGGATGAACATTTGATTT 300
Db 10685 CACCAATCTAAACAATCGTCGAAAGCTCAGAAATGAATGTTGCTGGATGAACATTTGATTT 10744

QY 301 CTGGTCTTTGCCAGAACTGTTCTTTAAATAATTCGGGTATGTGATAGAACTGA 360
Db 10745 CTGGTCTTTGCCAGAACTGTTCTTTAAATAATTCGGGTATGTGATAGAACTGA 10804

QY 361 ATGATCTCTTTTACCTGGTGATCATTCAA 388
Db 10805 ATGATCTCTTTTACCTGGTGATCATTCAA 10832
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Search completed: February 1, 2003, 03:05:03  
Job time : 988.74 secs

GenCore version 5.1.3  
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: January 31, 2003, 19:23:36 ; Search time 111.532 Seconds  
(without alignments)  
9510.154 Million cell updates/sec

Title: US-09-931-486-111

Perfect score: 471

Sequence: 1 ATCGAAGATCCCGGCTTCTT.....CAGATTGCTTGGGGTTATAT 471

Scoring table: IDENTITY\_NUC

Gapop 10.0 , Gapext 1.0

Searched: 2185239 seqs, 1125999159 residues

Total number of hits satisfying chosen parameters: 4370478

Minimum DB seq length: 0

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Fast processing. Minimum Match 0%  
Maximum Match 100%

## Listing first 45 summaries

Database : N\_Geneseq\_101002:\*

1:	/SID2/cgdata/geneseq/geneseq-emb1/NA1980.DAT.*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	471	100.0	471	17	AAT11842 P. aeruginosa UZG
2	272.6	57.9	499	17	AAT11845 P. alcaligenes LMG
3	225.8	47.9	504	17	AAT11844 P. stutzeri LMG 23
4	216	45.9	468	17	AAT11846 P. putida LMG 2232
5	183.8	39.0	588	22	AA169774 16S/23S rRNA spacer
6	174	36.9	520	17	AAT11843 P. pseudoalcaligenes
7	113.4	24.1	470	17	AAT11898 Yersinia enterocol
8	104.4	22.2	400	18	AAV78022 Staphylococcus aur
9	104.4	22.2	400	18	AAV7902 Staphylococcus aur

10	104.4	22.2	1311	18	AAV77852
11	103.8	22.0	249	17	AAH51855
12	103	21.9	1396	22	AAH55089
c 13	103	21.9	2839	22	AAH54998
14	103	21.9	3444	22	AAH54992
15	103	21.9	4429	22	AAH54300
c 16	101.8	21.6	400	18	AAV77984
17	100	21.2	463	17	AAH11870
18	100	21.2	475	17	AAH11869
19	98.4	20.9	496	17	AAH11866
20	98.4	20.9	1265	24	ABO69060
21	98.4	20.9	1409	24	ABO70714
22	98.4	20.8	5015	24	ABO71078
23	98.2	20.8	5097	20	AAH24983
c 24	98.2	20.8	5341	20	AAH24986
c 25	98	20.8	351	18	AAV78405
c 26	95.2	20.2	640681	24	ABA92787
c 27	95.2	20.2	2944528	24	ABA30341
c 28	95	20.2	363	17	AAH11865
c 29	95	20.2	5105	20	AAH24989
c 30	94.4	20.0	243	23	AAH48781
c 31	93.8	19.9	255	23	AAH48800
c 32	93.8	19.9	255	23	AAH48825
c 33	93.8	19.9	255	23	AAH48838
c 34	93.8	19.9	255	23	AAH48846
c 35	93.8	19.9	255	23	AAH48854
c 36	93.8	19.9	255	23	AAH48877
c 37	93.8	19.9	255	23	AAH48882
c 38	93.8	19.9	255	23	AAH48896
c 39	93.8	19.9	255	23	AAH48898
c 40	93.8	19.9	255	23	AAH48967
c 41	93.8	19.9	255	23	AAH49061
c 42	93.6	19.9	684707	24	ABO67196
c 43	93.6	19.9	3011208	24	ABO69245
c 44	93.2	19.8	498	17	AAH11867
c 45	92.6	19.7	582	12	AAQ11404

## ALIGNMENTS

RESULT 1  
AAT11842

AA111842  
ID AAT11842 standard: DNA: 471 BP.

AC AAT11842:

XX 03-SEP-1996 (first entry)

*P. aeruginosa* UZG 5669 16S-23S rRNA spacer region.

AA probe; detection; identification; microorganism; amplify;  
KW 16S-23S rRNA spacer region; respiratory tract; universal;  
KW species-specific; ss.

AA Pseudomonas aeruginosa.

AA PN WO9600298-A1.

04-JAN-1996.

XX 23-JUN-1995: 95WO-EP02452.

XX  
PR 07-APR-1995: 95EP-0870032.

PR 24-JUN-1994; 94EP-0870106;

PA (INNO-) INNOGENETICS NV.

PI Jannes G, Rossau R, Van Heuverswyn H;

XX  
XX

XX Novel hybridisation assay for the detection of eubacteria - esp

PT Mycobacterium, comprises amplifying the 16S-23S rRNA spacer region  
 XX  
 PS Claim 2; Fig 36; 248pp; English.  
 XX  
 CC The sequences given in AAT11791-857 represent the 16S-23S rRNA spacer  
 CC regions derived from various microorganisms. These sequences were  
 CC used in the method of the invention for the detection and identification  
 CC of at least one or more microorganisms. The method comprises amplifying  
 CC the 16S-23S rRNA spacer region and hybridising one or more of the probes  
 CC given in AAT34011-77 to the amplified sequence. These probes were  
 CC specifically used to detect microorganisms in samples originating from  
 CC the respiratory tract. This spacer region is derived from *Pseudomonas*  
 CC *aeruginosa* UZG 5669.  
 XX  
 SQ Sequence 471 BP; 116 A; 103 C; 120 G; 132 T; 0 other;

Query Match 100.0%; Score 471; DB 17; Length 471;  
 Best Local Similarity 100.0%; Pred. No. 2.6e-147;  
 Matches 471; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 ATCGAAGATCCGGCTTCTTATAGCTCCACACCAATGCTTGATTCACCTGGTTAGAC 60  
 Db 1 ATCGAAGATCCGGCTTCTTATAGCTCCACACCAATGCTTGATTCACCTGGTTAGAC 60  
 QY 61 GATTGGGCTGTAGCTCAGTTGGTTAGACCGCCCTCTGATAGGCTGAGGTCGGCAGTT 120  
 Db 61 GATTGGGCTGTAGCTCAGTTGGTTAGACCGCCCTCTGATAGGCTGAGGTCGGCAGTT 120  
 QY 121 CGAATCTGCCAGACCCACCAATGTTGCTGCTGCGATCCGATACGGGCCATAGC 180  
 Db 121 CGAATCTGCCAGACCCACCAATGTTGCTGCTGCGATCCGATACGGGCCATAGC 180  
 QY 181 TCAGCTGGGAGAGCGCCTCTTTCACGACGAGGTCAGGATTCGATCCTCTCTGGCTC 240  
 Db 181 TCAGCTGGGAGAGCGCCTCTTTCACGACGAGGTCAGGATTCGATCCTCTCTGGCTC 240  
 QY 241 CACCATCTAAACAATCTGCGAAGCTCAGAAATGAATGTTCTGGTGAATGAATGATTT 300  
 Db 241 CACCATCTAAACAATCTGCGAAGCTCAGAAATGAATGTTCTGGTGAATGAATGATTT 300  
 QY 301 CTGGCTTTGACACCACTGTTCTTTTAAATTCGGGTATGATAGAAAGTAAAGACTCA 360  
 Db 301 CTGGCTTTGACACCACTGTTCTTTTAAATTCGGGTATGATAGAAAGTAAAGACTCA 360  
 QY 361 ATGATCTCTTTCACCTGGTGAATCAATCAAGTAAATTTGCGAGTTCAAGCGCGAA 420  
 Db 361 ATGATCTCTTTCACCTGGTGAATCAATCAAGTAAATTTGCGAGTTCAAGCGCGAA 420  
 QY 421 TTTTCGGCGAATGCTGCTTTCACAGTATAACAGATTCGTTGGGGTTATAT 471  
 Db 421 TTTTCGGCGAATGCTGCTTTCACAGTATAACAGATTCGTTGGGGTTATAT 471

RESULT 2  
 AAT11845  
 ID AAT11845 standard; DNA; 499 BP.  
 AC AAT11845;  
 XX  
 DT 03-SEP-1996 (first entry)  
 XX  
 DE P. alcaligenes LMG 1224 16S-23S rRNA spacer region.  
 XX  
 KW Probe; detection; identification; microorganism; amplify;  
 KW 16S-23S rRNA spacer region; respiratory tract; universal;  
 KW species-specific; ss.  
 XX  
 OS *Pseudomonas* alcaligenes.  
 XX  
 PN WO9600298-A1.  
 XX  
 PD 04-JAN-1996.  
 XX

PF 23-JUN-1995; 95WO-EP02452.  
 XX  
 PR 07-APR-1995; 95EP-0870032.  
 PR 24-JUN-1994; 94EP-0870106.  
 XX  
 PA (INNO-) INNOGENETICS NV.  
 XX  
 PI Jannes G, Rössau R, Van Heuverswyn H;  
 XX  
 DR WPI; 1996-068882/07.  
 XX  
 CC Novel hybridisation assay for the detection of eubacteria - esp  
 PT Mycobacterium, comprises amplifying the 16S-23S rRNA spacer region  
 XX  
 PS Claim 2; Fig 39; 248pp; English.  
 XX  
 CC The sequences given in AAT11791-857 represent the 16S-23S rRNA spacer  
 CC regions derived from various microorganisms. These sequences were  
 CC used in the method of the invention for the detection and identification  
 CC of at least one or more microorganisms. The method comprises amplifying  
 CC the 16S-23S rRNA spacer region and hybridising one or more of the probes  
 CC given in AAT34011-77 to the amplified sequence. These probes were  
 CC specifically used to detect microorganisms in samples originating from  
 CC the respiratory tract. This spacer region is derived from *Pseudomonas*  
 CC *alcaligenes* LMG 1224.  
 XX  
 SQ Sequence 499 BP; 123 A; 109 C; 130 G; 137 T; 0 other;

Query Match 57.9%; Score 272.6; DB 17; Length 499;  
 Best Local Similarity 80.7%; Pred. No. 7.8e-81;  
 Matches 409; Conservative 0; Mismatches 54; Indels 44; Gaps 6;  
 QY 1 ATCGAAGATCCGGCTTCTTATAGCTCCACACCAATGCTTGATTCACCTGGTTA--- 57  
 Db 1 ATCGAAGATCCGGCTTCTTATAGCTCCACACCAATGCTTGATTCACCTGGTTA--- 57  
 QY 58 -----GACGATGGGCTCTAGCTCAGTGGGAGAGCGCTGCTTTGACGCGCA 93  
 Db 61 GCGATTGGGTTGAGACCGGAGAGTGGGCTCTAGCTCAGTGGTGTAGAGCGCA 120  
 QY 94 CCCCTGATAGGTTGAGTGGGAGTCCGAATCTGCCAGACCCACCAATTTGTTGGTGTG 153  
 Db 121 CCCCTGATAGGTTGAGTGGGAGTCCGAATCTGCCAGACCCACCAATTTGTTGGGATG 180  
 QY 154 CTGCTGTATCCGATACGGGCGCATAGCTCAGCTGGGAGAGCGCTGCTTTGACGCGCA 213  
 Db 181 GCCAGTG---TCAATGGGCGCATAGCTCAGCTGGGAGAGCGCTGCTTTGACGCGCA 237  
 QY 214 GGTGAGGATTCGATCCTCTTGGCTCCACCATCTA-AAACAATCTCGAAGCTCAGAA 272  
 Db 238 GGTGAGGATTCGATCCTCTTGGCTCCACCATCTA-AAACAATCTCGAAGCTCAGAA 297  
 QY 273 ATGAATGTTGTTGATGAACATTTGTTCTGTTTGCACGAGAACTGTTCTTTAAAAA 332  
 Db 298 ATGAACATTTGTTGATGAACATTTGTTCTGTTTGCACGAGAACTGTTCTTTAAAAA 357  
 QY 333 TTCGGGTATGATAGAAGTAAAGTGAATGATCTCTTTTCTGCTGGTGAATCTCAAGTCA 392  
 Db 358 TTTGGGTATGATAGAAGTGA---CTAACAGCGTGTCTTCTGCTGACGCTGTTT---AATCA 412  
 QY 393 AGGTAAATTTGCGAGTTCAACGCGGAATTTTCGGGGAATGTCGCTTCTAC-----A 444  
 Db 413 AGGCAAAATTTGCGAGTTCAACGCGGAATTTTCGGGGAATGTCGCTTCTAC-----A 472  
 QY 445 GTATAACCAAGATTTGCTTGGGGTTATAT 471  
 Db 473 CTATAACCAAGATTTGCTTGGGGTTATAT 499

RESULT 3  
 AAT11844  
 ID AAT11844 standard; DNA; 504 BP.  
 XX

```
AC AAT11844;
XX
XX 03-SEP-1996 (first entry)
XX
XX P. stutzeri LMG 2333 16S-23S rRNA spacer region.
XX
XX Probe; detection; identification; microorganism; amplify;
XX 16S-23S rRNA spacer region; respiratory tract; universal;
XX species-specific; ss.
XX
XX Pseudomonas stutzeri.
XX
XX WO9600298-A1.
XX
XX 04-JAN-1996.
XX
XX 23-JUN-1995; 95WO-EP02452.
XX
XX 07-APR-1995; 95EP-0870032.
XX 24-JUN-1994; 94EP-0870106.
XX
XX (INNO-) INNOGENETICS NV.
XX
XX Jannes G, Rossau R, Van Heuverswyn H;
XX WPI; 1996-068882/07.
XX
XX Novel hybridisation assay for the detection of eubacteria - esp
XX Mycobacterium, comprises amplifying the 16S-23S rRNA spacer region
XX
XX Claim 2; Fig 38; 248pp; English.
XX
XX The sequences given in AAT11791-857 represent the 16S-23S rRNA spacer
XX regions derived from various microorganisms. These sequences were
XX used in the method of the invention for the detection and identification
XX of at least one or more microorganisms. The method comprises amplifying
XX the 16S-23S rRNA spacer region and hybridising one or more of the probes
XX given in AAT34011-77 to the amplified sequence. These probes were
XX specifically used to detect microorganisms in samples originating from
XX the respiratory tract. This spacer region is derived from Pseudomonas
XX stutzeri LMG 2333.
XX
XX Sequence 504 BP; 119 A; 111 C; 137 G; 137 T; 0 other;

Query Match 47.9%; Score 225.8; DB 17; Length 504;
Best Local Similarity 75.1%; Pred. No. 3.7e-65;
Matches 396; Conservative 0; Mismatches 52; Indels 79; Gaps 6;

QY 1 ATCGAAGATCCGGCTTCTTCATAGCTCCACACGAAATGCTTGTATTCACCTGGTTAG-- 58
DB 1 ATCGAAGACACGGGCTTCGTATAGCTCCACACGAAATGCTTGTATTCACCTGGCGAAG 60
QY 59 -----ACGATTGGGCTCTAGCTCAGTCTAGTGGTTAGCGCA 93
DB 61 CGGATTGGGTTTAGACCGGAGAGTAACGATTGGGCTCTAGCTCAGTGGTTAGCGCA 120
QY 94 CCCCTGATAAGGTCGAGTCGCGAGTAACTCCACAGCCCACTTCTTGGTGTG 153
DB 121 CCCCTGATAAGGTCGAGTCGCGAGTAACTCCACAGCCCACTTCTTGGTGTG 172
QY 154 CTGCGTGATCCGATACGGGGCCATAGCTCAGCTGGGAGAGGCGCTTGTGCACGAGA 213
DB 173 -----AAGGGCCATAGCTCAGCTGGGAGAGGCGCTTGTGCACGAGA 218
QY 214 GGTGAGGATTCGATCCCTTCCTGGTCCACCATCTAAACATCTCGTGAAGCTCAGAAA 273
DB 219 GGTGAGGATTCGATCCCTTCCTGGTCCACCATCTAAACATCTCGTGAAGCTCAGAAA 278
QY 274 TGAATGTT-----CGTGGATGAACATGATTTCTGCTCTTCCA 312
DB 279 TGAGTGTTCACGAGTACGAGTTGATTCCTGGGTTGAACATGATTTCTGAGACTTGGC 338
QY 313 CCAGAACTGTTCTTTAAAAATTCGGGTATGTGATAGAAAGTAAGACTGAATGATCTCTTTC 372
```

## RESULT 4

AAT11846

ID AAT11846 standard; DNA; 468 BP.

XX

AC AAT11846;

XX

DT 03-SEP-1996 (first entry)

XX

DE P. putida LMG 2232 16S-23S rRNA spacer region.

XX

KW Probe; detection; identification; microorganism; amplify;

KW 16S-23S rRNA spacer region; respiratory tract; universal;

KW species-specific; ss.

XX

OS Pseudomonas putida.

XX

PN WO9600298-A1.

XX

PD 04-JAN-1996.

XX

PF 23-JUN-1995; 95WO-EP02452.

XX

PR 07-APR-1995; 95EP-0870032.

XX

PR 24-JUN-1994; 94EP-0870106.

XX

PA (INNO-) INNOGENETICS NV.

XX

PI Jannes G, Rossau R, Van Heuverswyn H;

XX WPI; 1996-068882/07.

XX

PT Novel hybridisation assay for the detection of eubacteria - esp

PT Mycobacterium, comprises amplifying the 16S-23S rRNA spacer region

XX

PS Claim 2; Fig 40; 248pp; English.

XX

The sequences given in AAT11791-857 represent the 16S-23S rRNA spacer regions derived from various microorganisms. These sequences were used in the method of the invention for the detection and identification of at least one or more microorganisms. The method comprises amplifying the 16S-23S rRNA spacer region and hybridising one or more of the probes given in AAT34011-77 to the amplified sequence. These probes were specifically used to detect microorganisms in samples originating from the respiratory tract. This spacer region is derived from Pseudomonas putida LMG 2232.

XX Sequence 468 BP; 117 A; 101 C; 117 G; 133 T; 0 other;

SQ

Query Match

Best Local Similarity 45.9%; Score 216; DB 17; Length 468;

Matches 370; Conservative 0; Mismatches 75; Indels 49; Gaps 6;

QY 1 ATCGAAGATCCGGCTTCTTCATAGCTCCACACGAAATGCTTGTATTCACCTGGTTAGA- 59

DB 1 ATCGAGACATCAGCTGCTCATAGCTCCACACGAAATGCTTGTATTCATTTGAAGAAGA 60

QY 60 -----CGATTGGGCTCTAGCTCAGTCTAGTGGTTAGAGCGCACCCCTGA 100

DB 61 CGATTAGGTTAGCAACCTTCGATTGGGCTCTAGCTCAGTCTAGTGGTTAGAGCGCACCCCTGA 120

QY 101 TAAGGTTAGGTCGCGAGTTCGAAATTCGCCACAGCCCACTTGTGTGCTGCTGCTG 160

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Db 121 TAAGGTGAGGTCGGCAGTTCGAATCTGCCAGACCCACCAATT-----164
QY 161 ATCCGATACGGGCGCATAGCTAGCTGAGTGGAGAGCGGCTGCTTGCACGAGGAGTTCAGG 220
Db 165 -----TGTGGGGCCATAGCTAGCTGAGTGGAGAGCGGCTGCTTGCACGAGGAGTTCAGC 219
QY 221 AGTTCGATCCTCTTGGCTCCACCAATC---TAAACAAATCGTGAAGCTCAGAAATGAA 277
Db 220 GGTTCGATCCCGCTTGGCTTCACACCCCGCTTGCAGTTCGCAAGCTTAGAAATGAA 279
QY 278 TGTTCGATGATGAACATGATTCGTGCTTTCGACACGAGAGTTCCTTTAAAAAATTCGG 337
Db 280 TATTCG-CGTCGAATATTGATTTCTGAACCTT--ATCAGAATCGTTCCTTTAAAAAATTCGG 336
QY 338 GTATGATGATGAGTGAAGACTGAATGATCTCTTCACTGCTGATCATTCAGTCAAGGTA 397
Db 337 GTATGATGATGAGTGAAGACTGAAGTGAAGTTCCTTCACTGCTGATCATTCAGTCAAGGTA 396
QY 398 AATTTGCGAGTTCAGCGCGAATTTTCGCGAATTCGCTTCTTCACAGATATACCCAGATT 457
Db 397 AATTTGTCAGT--AATTACAGTTCCTGCGAATTCGCTTCTTCACAGATATACCCAGATT 454
QY 458 GCTTGGGGTTATAT 471
Db 455 GCTTGGGGTTATAT 468

RESULT 5
AAI69774
ID AAI69774 standard; DNA; 588 BP.
XX
AC AAI69774;
DT 13-DEC-2001 (first entry)
XX
DE 16S/23SrRNA spacer region.
XX
KW Bacterium detection; 16S/23SrRNA spacer region; ds.
XX
OS Pseudomonas putida.
XX
PN J02001100020.1
XX
PD 17-08-2001
XX
PF 13-JAN-2000; 2000JP-0004160.
XX
PR 13-JAN-2000; 2000JP-0004160.
XX
PA (MITO ) MITSUBISHI JUKOGYO KK.
XX
WPI; 2001-605311/69.
XX
Detection method of Pseudomonas bacteria -
XX
Claim 6; Page 7; 11pp; Japanese.
XX
The present invention relates to a method for the detection of the
CC present DNA sequence; the 16S/23SrRNA spacer region of Pseudomonas
CC putida. The method can be used to detect Pseudomonas bacteria.
XX
SQ Sequence 588 BP; 147 A; 134 C; 153 G; 149 T; 5 other;

Query Match 39.0%; Score 183.8; DB 22; Length 588;
Best Local Similarity 70.5%; Pred. No. 4.7e-51;
Matches 351; Conservative 0; Mismatches 92; Indels 55; Gaps 6;

QY 1 ATCGAAGATCCCGGCTTCTTCATAAGCTCCACACGAAATTCGCTTGAATTCAGTGGTAGAC 60
Db 63 ATCGACGACATCAGCTGCTGATGAGCTCCACACGAAATTCGCTTGAATTCAGTGGTAGAC 122
QY 61 G-----AATGGGTCTGTAGCTCAGTGTGTTAGAGCGCACCCCTGTATAAGGGT 107

```

```

Db 123 CGATCAAGACCCCTATATAGGCTGTAGCTCAGTTGGTTAGAGCGCACCCCTGTATAANGGT 182
QY 108 GAGGTCCGAGTTCGAATCTGCCAGACCCACCAATTTGTTGGTGTGCTGCGTGCATCCGAT 167
Db 183 GAGGTCCGAGTTCGAATCTGCCAGACCCCTACCAAT-----AT 220
QY 168 AGGGGCCATAGCTCAGCTGGGAGAGCGGCTGCTTTCGACGAGGAGTTCAGGAGTTCGA 227
Db 221 CGGGGCCATAGCTCAGCTGGGAGAGCGGCTGCTTTCGACGAGGAGTTCAGGAGTTCGA 280
QY 228 TCTCTCTGGTCCACCATCTAATAACAATCGTCAAGCTCAAGATGAATGTTTCGTGGA 287
Db 281 TCCCGCTTGGCTCCACCATCTGCTGACCTTGATCAAACTCAAAATGAGCATTCGCGTC 340
QY 288 TGAACATTTGATTTCTGCTTTCGACGAGAACTGTTCTTTAAAAAATTCGGGTATGTGATA 347
Db 341 T-AATGTTGATTTCTGGCTTTTG---TCAGATCGTCTTTAAAAAATTCGGATATGTGATA 396
QY 348 GAAGTAAAGACTGAATGATCTCTTTCACCTGGTGAATTCAGTCAAGGTAAGGTTTCGGA 407
Db 397 GA--TATAGACTCAACACCACTTTCACCTGCTGGTGAATTCAGGCTAAGTAAAAATTCGGA 454
QY 408 GTTC-----RAGCGGAATTTTCGCGAATTCGCTTTCACAGTATACCA 453
Db 455 GTTCTGCTCGAAAGAGCAACTTTCGGAATTTTCGCGAATTCGCTTTCACAGTATACCA 514
QY 454 GATTGCTTGGGTTATAT 471
Db 515 GATTGCTTGGGTTATAT 532

RESULT 6
AAT11843
ID AAT11843 standard; DNA; 520 BP.
XX
AC AAT11843;
XX
DT 03-SEP-1996 (first entry)
XX
DE P. pseudoalcaligenes LMG 1225 16S-23S rRNA spacer region.
XX
KW Probe; detection; identification; microorganism; amplify;
KW 16S-23S rRNA spacer region; respiratory tract; universal;
KW species-specific; ss.
XX
OS Pseudomonas pseudoalcaligenes.
XX
PN W09600298-AL.
XX
PD 04-JAN-1996.
XX
PF 23-JUN-1995; 95WO-EP02452.
XX
PR 07-APR-1995; 95EP-0870032.
XX
PR 24-JUN-1994; 94EP-0870106.
XX
PA (INNO-) INNOGENETICS NV.
XX
PI Jannes G., Rosser R., Van Heuverswyn H.;
XX WPI; 1996-068882/07.
XX
Novel hybridisation assay for the detection of eubacteria - esp
PT Mycobacterium, comprises amplifying the 16S-23S rRNA spacer region
XX
PS Claim 2; Fig 37; 248pp; English.
XX
The sequences given in AAT11791-857 represent the 16S-23S rRNA spacer
CC regions derived from various microorganisms. These sequences were
CC used in the method of the invention for the detection and identification
CC of at least one or more microorganisms. The method comprises amplifying
CC the 16S-23S rRNA spacer region and hybridising one or more of the probes

```

CC given in AAT34011-77 to the amplified sequence. These probes were  
CC specifically used to detect microorganisms in samples originating from  
CC the respiratory tract. This spacer region is derived from *Pseudomonas*  
CC *pseudocataligenes* IMG 1225.

XX Sequence 520 BP; 126 A; 109 C; 134 G; 151 T; 0 other;

Query Match 36.9%; Score 174; DB 17; Length 520;  
Best Local Similarity 70.6%; Pred. No. 8.6e-48;  
Matches 373; Conservative 0; Mismatches 90; Indels 65; Gaps 8;

QY 1 ATCGAAGATCCGGCTTCTTCAATGCTCCACACCAATGCTGATCTACTGTTAGAC 60  
DB 1 ATCGAAGATCCGGCTTCTTCAATGCTCCACACCAATGCTGATCTACTGTTAGAC 60  
QY 61 GAT-----TGGGTCTGTAGCTCAGTTGGTTAGAGCGGACCCCTG 99  
DB 61 AATGCTGTAAACGACCCCGTGTATAGGCTGTAGCTGTTGGTTAGAGCGGACCCCTG 120  
QY 100 ATAAGGGTGAAGTTCGACGCTCGAATCTCCACAGCCACCAATGCTGTTGCTGCTG 159  
DB 121 ATAAGGGTGAAGTTCGACGCTCGAATCTCCACAGCCACCAATGCTGTTGCTGCTG 179  
QY 160 GATCGATACGGGGCCATAGCTCAGCTGGGAGAGCGCCCTGCTTTCACGAGGAGTCTAG 219  
DB 180 -----AATACGGGGCCATAGCTCAGCTGGGAGAGCGCCCTGCTTTCACGAGGAGTCTAG 234  
QY 220 GAGTTCGATCCTCTTGGCTGCACCA-----TCFAAACAATCTCGAAGCTCA 269  
DB 235 CGGTTGATCCGCTTGGCTGCACCACTCTCTGTTGCGGTGAGTGTAAAGAGTTCA 294  
QY 270 GAAATGA-----ATGTCGTTGATGAACATGATGTTCTGCTCTTT-----GCA 312  
DB 295 GAAATGATCCGCTTCAGCTTGTCTGTTGAGTGTGATGTTCTGCTCTTTTTCACCGGTA 354  
QY 313 CCAGAACTGCTTTTAAATAATTCGGGTATGCTGATGAAGTAAAGTGAATGATCTCTTTTC 372  
DB 355 CGAAATATCTTTTAAATAATTCGGGTATGCTGATGAAGT--GACTGATTAATGCTTTTC 412  
QY 373 ACTGTTGATCATCAAGTCAAGTAAATTTG--CGAGTTCAGCGCGAATTTTCGGCGA 430  
DB 413 CTGGCAATGATCTGCTCAAGTAAATTTGTTAGTTCCTCAAGACGCAAAATTTTCGGCGA 472  
QY 431 ATGCTGCTCTAC-----AGTATAACCAAGATTTGCTTGGGTTATAT 471  
DB 473 ATGCTGCTCTACGATTGAGACAGTAAACAGATGCTTGGGTTATAT 520

RESULT 7  
AAT11898  
ID AAT11898 standard; DNA; 470 BP.

XX AC AAT11898;

XX 03-SEP-1996 (first entry)

DE *Yersinia enterocolitica* strain p95 16S-23S rRNA spacer region (#1).

KW Probe; detection; identification; microorganism; amplify;  
KW 16S-23S rRNA spacer region; food; universal;  
KW species-specific; ss.

XX *Yersinia enterocolitica*.

PN W09600298-A1.

XX 04-JAN-1996.

XX 23-JUN-1995; 95WO-EP02452.

PR 07-APR-1995; 95EP-0870032.

PR 24-JUN-1994; 94EP-0870106.

XX

PA

XX (INNO-) INNOGENETICS NV.

PI Jannes G, Rossau R, Van Heuverswyn H;

XX WPI; 1996-068882/07.

DR Novel hybridisation assay for the detection of eubacteria - esp

PT *Mycobacterium*, comprises amplifying the 16S-23S rRNA spacer region

XX Claim 5; Fig 98; 248pp; English.

CC The sequences given in AAT11889-905 represent the 16S-23S rRNA spacer  
CC regions derived from various microorganisms. These sequences were  
CC used in the method of the invention for the detection and identification  
CC of at least one or more microorganisms. The method comprises amplifying  
CC the 16S-23S rRNA spacer region and hybridising one or more probes to  
CC the amplified sequence. These probes were specifically used to detect  
CC microorganisms in samples originating from food. This spacer region is  
CC derived from *Yersinia enterocolitica* strain P95.

XX Sequence 470 BP; 129 A; 101 C; 120 G; 120 T; 0 other;

Query Match 24.1%; Score 113.4; DB 17; Length 470;  
Best Local Similarity 73.1%; Pred. No. 1.6e-27;  
Matches 163; Conservative 0; Mismatches 51; Indels 9; Gaps 1;

QY 64 TGGGCTGTAGCTCAGTTGGTTAGAGCGCACCCCTGATAAGGTTGAGTGGCAGTTTCGA 123

DB 75 TAGGCTGTAGCTCAGTTGGTTAGAGCGCACCCCTGATAAGGTTGAGTGGTGGTTCAA 134

QY 124 ATCTGCCAGACCCACCAATTTGTTGTTG-----CTGCGTGATCCGATACGGGGC 174

DB 135 GTCCACTCAGCCCTACCACTCTCGAAGTGGAAAGGTAAGTCTGACGTTGATGGGGC 194

QY 175 CATAGCTCAGCTGGGAGAGCGCTGCTTTGCACGAGGAGTTCAGGATTCGATCCTCCT 234

DB 195 TATAGCTCAGCTGGGAGAGCGCTGCTTGCACGAGGAGTTCAGGATTCGATCCTCCT 254

QY 235 TGGCTCCACATCTAAACAAATCGTGAAGCTCAGAAATGAA 277

DB 255 TAGCTCCACCATATAGTCTCTGTATTTCATACTTCAGAGTSTA 297

RESULT 8

AAV78022  
ID AAV78022 standard; DNA; 400 BP.

XX AAV78022;

XX 16-MAR-1999 (first entry)

DE *Staphylococcus aureus* contig SEQ ID #3711.

XX

KW Computer readable medium; vaccine; *S. aureus* infection; immunodetection;  
KW cellulitis; eyelid infection; food poisoning; osteomyelitis; therapy;  
KW skin infection; surgical wound infection; scalded skin syndrome;  
KW toxic shock syndrome; ds.

XX *Staphylococcus aureus*.

XX EP786519-A2.

XX 30-JUL-1997.

XX 07-JAN-1997; 97EP-0100117.

XX 05-JAN-1996; 96US-0009861.

XX (HUMA-) HUMAN GENOME SCI INC.

XX Barash SC, Choi GH, Dillon PU, Fannon MR, Kunsch CA;

PI Rosen CA;

XX







XX 03-SEP-2001 (first entry)  
 DT S. epidermidis genomic polynucleotide sequence SEQ ID NO:4453.  
 XX Staphylococcus epidermidis SRI strain; infection; diagnosis;  
 DE vaccination; endocarditis; ds.  
 KW Staphylococcus epidermidis.  
 XX WO200134809-A2.  
 PN 17-MAY-2001.  
 PD 09-NOV-2000; 2000WO-US30782.  
 XX 09-NOV-1999; 99US-0164258.  
 XX (GLAX ) GLAXO GROUP LTD.  
 PA Kimmerly WJ;  
 PI WPI; 2001-316495/33.  
 XX Nucleic acids encoding polypeptides from Staphylococcus epidermidis,  
 DT useful for vaccinating against infections, e.g. endocarditis -  
 XX Claim 8; Page 2187-2188; 2188pp; English.  
 XX AAH52304 to AAH53970 represent nucleic acids (I) encoding polypeptides  
 CC (II), given in AAG81454 to AAG83120, from Staphylococcus epidermidis.  
 CC (I) and (II) can have antibacterial activity and therefore can be used  
 CC in vaccination. The nucleic acids (I) may be used to produce the  
 CC S. epidermidis polypeptides (II) via the production of vectors  
 CC containing them which are used to produce hosts cells which express the  
 CC polypeptides. The polypeptides (II) (and/or nucleic acids) may then be  
 CC used to vaccinate subjects and to raise antibodies against the bacteria.  
 CC The polypeptides may also be used to assay for other inhibitors of their  
 CC activity and therefore identify compounds that may be used for the  
 CC treatment of S. epidermidis infections, e.g. endocarditis. AAH53971 to  
 CC AAH55090 represent specifically claimed S. epidermidis genomic DNA  
 CC polynucleotide sequences from the present invention. AAH55091 to  
 CC AAH55098 represent oligonucleotide sequences and primers which are used  
 CC in the exemplification of the present invention.  
 CC N.B. The present invention specifically claims all the polynucleotide  
 CC sequences given in the sequence listing of the present specification,  
 CC however the sequence listing only goes up to SEQ ID NO:4454 so even  
 CC though sequences are given in the disclosure for SEQ ID NO:4465 to 4472,  
 CC no sequences are present for SEQ ID NO:4455 to 4464.  
 XX Sequence 1396 BP; 410 A; 254 C; 319 G; 413 T; 0 other;

Query Match 21.9%; Score 103; DB 22; Length 1396;  
 Best Local Similarity 76.8%; Pred. No. 8.6e-24;  
 Matches 142; Conservative 0; Mismatches 35; Indels 8; Gaps 1;  
 QY 62 ATTGGGTCTGAGCTCAGTTGGTTAGAGCGCACCCCTGATAGGCTGAGGTGCGGAGTTC 121  
 DB 642 AATGGCCCTATAGCTCAGCTGGTTAGAGCGCAGCGCTGATAGGCTGAGGTGCGTGGTTC 701  
 QY 122 GAATCTGCCAGACCCACCAATTTGGTGTGCTGCGTGATCCGATACGGGGCCATAGCT 181  
 DB 702 GAGTCCACTTAGGGCCACCAATCAATAATTTAAACCTTA-----GGGGGCTTAGCT 753  
 QY 182 CAGCTGGGAGAGCGCTCTGTTGACGAGGAGGTTCAGGAGTTCGATCTCTCTTGGCTCC 241  
 DB 754 CAGCTGGGAGAGCGCTCTGTTGACGAGGAGGTTCAGGAGTTCGATCTCTCTTGGCTCC 813  
 QY 242 ACCAT 246  
 DB 814 ACCAT 818

RESULT 13  
 AAH54998/C  
 ID AAH54998 standard; DNA; 2839 BP.  
 XX AC AAH54998;  
 XX 03-SEP-2001 (first entry)  
 DT S. epidermidis genomic polynucleotide sequence SEQ ID NO:4362.  
 DE Staphylococcus epidermidis SRI strain; infection; diagnosis;  
 KW vaccination; endocarditis; ds.  
 XX Staphylococcus epidermidis.  
 OS WO200134809-A2.  
 PN 17-MAY-2001.  
 PD 09-NOV-2000; 2000WO-US30782.  
 XX 09-NOV-1999; 99US-0164258.  
 XX (GLAX ) GLAXO GROUP LTD.  
 PA Kimmerly WJ;  
 PI WPI; 2001-316495/33.  
 XX Nucleic acids encoding polypeptides from Staphylococcus epidermidis,  
 DT useful for vaccinating against infections, e.g. endocarditis -  
 XX Claim 8; Page 2102; 2188pp; English.  
 XX AAH52304 to AAH53970 represent nucleic acids (I) encoding polypeptides  
 CC (II), given in AAG81454 to AAG83120, from Staphylococcus epidermidis.  
 CC (I) and (II) can have antibacterial activity and therefore can be used  
 CC in vaccination. The nucleic acids (I) may be used to produce the  
 CC S. epidermidis polypeptides (II) via the production of vectors  
 CC containing them which are used to produce hosts cells which express the  
 CC polypeptides. The polypeptides (II) (and/or nucleic acids) may then be  
 CC used to vaccinate subjects and to raise antibodies against the bacteria.  
 CC The polypeptides may also be used to assay for other inhibitors of their  
 CC activity and therefore identify compounds that may be used for the  
 CC treatment of S. epidermidis infections, e.g. endocarditis. AAH53971 to  
 CC AAH55090 represent specifically claimed S. epidermidis genomic DNA  
 CC polynucleotide sequences from the present invention. AAH55091 to  
 CC AAH55098 represent oligonucleotide sequences and primers which are used  
 CC in the exemplification of the present invention.  
 CC N.B. The present invention specifically claims all the polynucleotide  
 CC sequences given in the sequence listing of the present specification,  
 CC however the sequence listing only goes up to SEQ ID NO:4454 so even  
 CC though sequences are given in the disclosure for SEQ ID NO:4465 to 4472,  
 CC no sequences are present for SEQ ID NO:4455 to 4464.  
 XX Sequence 2839 BP; 669 A; 794 C; 562 G; 814 T; 0 other;

Query Match 21.9%; Score 103; DB 22; Length 2839;  
 Best Local Similarity 76.8%; Pred. No. 1.2e-23;  
 Matches 142; Conservative 0; Mismatches 35; Indels 8; Gaps 1;  
 QY 62 ATTGGGTCTGAGCTCAGTTGGTTAGAGCGCACCCCTGATAGGCTGAGGTGCGGAGTTC 121  
 DB 1828 AATGGGCTATAGCTCAGCTGAGTTAGAGCGCAGCGCTGATAGGCTGAGGTGCGTGGTTC 1769  
 QY 122 GAATCTGCCAGACCCACCAATTTGGTGTGCTGCGTGATCCGATACGGGGCCATAGCT 181  
 DB 1768 GAGTCCACTTAGGGCCACCAATCAATAATTTAAACCTTA-----GGGGGCTTAGCT 1717  
 QY 182 CAGCTGGGAGAGCGCTCTGTTGACGAGGAGGTTCAGGAGTTCGATCTCTCTTGGCTCC 241  
 DB 1716 CAGCTGGGAGAGCGCTCTGTTGACGAGGAGGTTCAGGAGTTCGATCTCTCTTGGCTCC 1657

OY 242 ACCAT 246  
Db 1656 ACCAT 1652  
RESULT 14  
AAH54992  
XX AAH54992 standard; DNA; 3444 BP.  
AC AAH54992;  
XX  
DT 03-SEP-2001 (first entry)  
XX  
DE S. epidermidis genomic polynucleotide sequence SEQ ID NO:4356.  
XX  
KW Staphylococcus epidermidis SRI strain; infection; diagnosis;  
KW vaccination; endocarditis; ds.  
XX  
OS Staphylococcus epidermidis.  
XX WO200134809-A2.  
PN  
XX  
PD 17-MAY-2001.  
XX  
PF 09-NOV-2000; 2000WO-US30782.  
XX  
PR 09-NOV-1999; 99US-0164258.  
XX  
PA (GLAX ) GLAXO GROUP LTD.  
XX  
PI Kimmerly WJ;  
XX  
DR WPI; 2001-316495/33.  
XX  
PT Nucleic acids encoding polypeptides from Staphylococcus epidermidis,  
PT useful for vaccinating against infections, e.g. endocarditis -  
XX  
PS Claim 8; Page 2096-2097; 2188pp; English.  
XX  
CC AAH52304 to AAH53970 represent nucleic acids (I) encoding polypeptides  
CC (II), given in AAG81454 to AAG83120, from Staphylococcus epidermidis.  
CC (I) and (II) can have antibacterial activity and therefore can be used  
CC in vaccination. The nucleic acids (I) may be used to produce the  
CC S. epidermidis polypeptides (II) via the production of vectors  
CC containing them which are used to produce hosts cells which express the  
CC polypeptides. The polypeptides (II) (and/or nucleic acids) may then be  
CC used to vaccinate subjects and to raise antibodies against the bacteria.  
CC The polypeptides may also be used to assay for other inhibitors of their  
CC activity and therefore identify compounds that may be used for the  
CC treatment of S. epidermidis infections, e.g. endocarditis. AAH53971 to  
CC AAH5090 represent specifically claimed S. epidermidis genomic DNA  
CC polynucleotide sequences from the present invention. AAH5091 to  
CC AAH5098 represent oligonucleotide sequences and primers which are used  
CC in the exemplification of the present invention.  
CC N.B. The present invention specifically claims all the polynucleotide  
CC sequences given in the sequence listing of the present specification,  
CC however the sequence listing only goes up to SEQ ID NO:4454 so even  
CC though sequences are given in the disclosure for SEQ ID NO:4465 to 4472,  
CC no sequences are present for SEQ ID NO:4455 to 4464.  
XX  
XX Sequence 3444 BP; 1203 A; 597 C; 723 G; 921 T; 0 other;  
Query Match 21.9%; Score 103; DB 22; Length 3444;  
Best Local Similarity 76.8%; Pred. No. 1.4e-23;  
Matches 142; Conservative 0; Mismatches 35; Indels 8; Gaps 1;  
OY 62 ATTGGCTGTAGCTCAGTGTAGAGCGCACCCCTGATAGGTCGAGTCGGCAGTTC 121  
Db 2708 AATGGCCCTAGTCTCAGCTGTGTAGAGCGCACCGCTGATAGCGTGGTGGTTC 2767  
OY 122 GAATGTCCAGACCCACCAATTTGTTGGTGTCTGCGGATCCGATACGGGCCATAGCT 181  
Db 2768 GAGTCCACTTAGGCCACCATCAATATTAARACCTTA-----GGGGCTTAGCT 2819

OY 182 CAGCTGGAGAGCGCTCTTCCACGAGGAGGTTCAGATCTCCTTGGCTCC 241  
Db 2820 CAGCTGGAGAGCGCTCTTTCACGAGGAGGTTCAGATCTCCTTGGCTCC 2879  
OY 242 ACCAT 246  
Db 2880 ACCAT 2884  
RESULT 15  
AAH54300  
ID AAH54300 standard; DNA; 4429 BP.  
XX  
AC AAH54300;  
XX  
DT 03-SEP-2001 (first entry)  
XX  
DE S. epidermidis genomic polynucleotide sequence SEQ ID NO:3664.  
XX  
KW Staphylococcus epidermidis SRI strain; infection; diagnosis;  
KW vaccination; endocarditis; ds.  
XX  
OS Staphylococcus epidermidis.  
XX WO200134809-A2.  
PN  
XX  
PD 17-MAY-2001.  
XX  
PF 09-NOV-2000; 2000WO-US30782.  
XX  
PR 09-NOV-1999; 99US-0164258.  
XX  
PA (GLAX ) GLAXO GROUP LTD.  
XX  
PI Kimmerly WJ;  
XX  
DR WPI; 2001-316495/33.  
XX  
PT Nucleic acids encoding polypeptides from Staphylococcus epidermidis,  
PT useful for vaccinating against infections, e.g. endocarditis -  
XX  
PS Claim 8; Page 1270-1272; 2188pp; English.  
XX  
CC AAH52304 to AAH53970 represent nucleic acids (I) encoding polypeptides  
CC (II), given in AAG81454 to AAG83120, from Staphylococcus epidermidis.  
CC (I) and (II) can have antibacterial activity and therefore can be used  
CC in vaccination. The nucleic acids (I) may be used to produce the  
CC S. epidermidis polypeptides (II) via the production of vectors  
CC containing them which are used to produce hosts cells which express the  
CC polypeptides. The polypeptides (II) (and/or nucleic acids) may then be  
CC used to vaccinate subjects and to raise antibodies against the bacteria.  
CC The polypeptides may also be used to assay for other inhibitors of their  
CC activity and therefore identify compounds that may be used for the  
CC treatment of S. epidermidis infections, e.g. endocarditis. AAH53971 to  
CC AAH5090 represent specifically claimed S. epidermidis genomic DNA  
CC polynucleotide sequences from the present invention. AAH5091 to  
CC AAH5098 represent oligonucleotide sequences and primers which are used  
CC in the exemplification of the present invention.  
CC N.B. The present invention specifically claims all the polynucleotide  
CC sequences given in the sequence listing of the present specification,  
CC however the sequence listing only goes up to SEQ ID NO:4454 so even  
CC though sequences are given in the disclosure for SEQ ID NO:4465 to 4472,  
CC no sequences are present for SEQ ID NO:4455 to 4464.  
XX  
XX Sequence 4429 BP; 1327 A; 928 C; 1004 G; 1170 T; 0 other;  
Query Match 21.9%; Score 103; DB 22; Length 4429;  
Best Local Similarity 76.8%; Pred. No. 1.6e-23;  
Matches 142; Conservative 0; Mismatches 35; Indels 8; Gaps 1;  
OY 62 ATTGGCTGTAGCTCAGTGTGTAGAGCGCACCCCTGATAGGTCGAGTCGGCAGTTC 121

Db 2768 AATGGCCTATAGCTCAGCTGGTTAGAGCGCACGCCCTGATAAGCGTGAGGTCGGTGGTTC 2827  
QY 122 GAATCTGCCAGACCCACCAATGTTGGTCTGCTGGTGATCCGATACGGGGCCATAGCT 181  
Db 2828 GAGTCCACTTAGGCCCCACCATTCAATAATTAAACCTTA-----GGGGGCTTAGCT 2879  
QY 182 CAGCTGGGAGAGCGCCTGCTTTGCACGCAGGAGGTCAGGAGTTTCGATCCTCCTTGGCTCC 241  
Db 2880 CAGCTGGGAGAGCGCCTGCTTTGCACGCAGGAGGTCAGGAGTTTCGATCCTCCTCCTAGTCTCC 2939  
QY 242 ACCAT 246  
Db 2940 ACCAT 2944

Search completed: February 1, 2003, 01:29:11  
Job time : 122.532 secs



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; MOLECULE TYPE: cdna
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
US-08-765-332-111

Query Match      100.0%; Score 471; DB 3; Length 471;
Best Local Similarity 100.0%; Pred. No. 5.5e-156;
Matches 471; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATCGAAGATCCCGGCTCTTCATAAGCTCCACACGAAATGCTTACTGTTAGAC 60
    |||||||
DB 1 ATCGAAGATCCCGGCTCTTCATAAGCTCCACACGAAATGCTTACTGTTAGAC 60
    |||||||

QY 61 GATTGGGTCTGTAGCTCAGTTGGTTAGAGCGCACCCCTGATAAGGGTGAGTTCGGCAGTT 120
    |||||||
DB 61 GATTGGGTCTGTAGCTCAGTTGGTTAGAGCGCACCCCTGATAAGGGTGAGTTCGGCAGTT 120
    |||||||

QY 121 CGAATCTGCCAGACCCACCAATGTTGGTGTGCTGCTGATCCGATACGGGGCCATAGC 180
    |||||||
DB 121 CGAATCTGCCAGACCCACCAATGTTGGTGTGCTGCTGATCCGATACGGGGCCATAGC 180
    |||||||

QY 181 TCAGCTGGGAGAGCGCTGCTTGCACGAGGAGGTTCAGAGTTCGATCCTCTGGCTC 240
    |||||||
DB 181 TCAGCTGGGAGAGCGCTGCTTGCACGAGGAGGTTCAGAGTTCGATCCTCTGGCTC 240
    |||||||

QY 241 CACCATCTAAACAATCGTCGAAGCTCAGAAATGAATGTTGCTGGATGAACATTTGATT 300
    |||||||
DB 241 CACCATCTAAACAATCGTCGAAGCTCAGAAATGAATGTTGCTGGATGAACATTTGATT 300
    |||||||

QY 301 CTGGTCTTTCACAGCAAGTCTTTTAAATTCGGGTATGATGAAGTAAGACTGA 360
    |||||||
DB 301 CTGGTCTTTCACAGCAAGTCTTTTAAATTCGGGTATGATGAAGTAAGACTGA 360
    |||||||

QY 361 ATGATCTCTTCACTGATCATTCAGTCAAGTAAATTTTCGGAGTTCAAGCGGAA 420
    |||||||
DB 361 ATGATCTCTTCACTGATCATTCAGTCAAGTAAATTTTCGGAGTTCAAGCGGAA 420
    |||||||

QY 421 TTTTCGGCGAATGCTGCTTTCACAGTATAACCGAGTTGCTTGGGTTATAT 471
    |||||||
DB 421 TTTTCGGCGAATGCTGCTTTCACAGTATAACCGAGTTGCTTGGGTTATAT 471
    |||||||

RESULT 2
US-09-448-894-111
; Sequence 111, Application US/09448894
; Patent No. 6312903
; GENERAL INFORMATION:
; APPLICANT: JANNES, GEERT
; APPLICANT: ROSSAU, RUDI
; APPLICANT: VAN HEUVERSWYN, HUGO
; TITLE OF INVENTION: SIMULTANEOUS DETECTION, IDENTIFICATION
; AND DIFFERENTIATION OF EUBACTERIAL TAXA USING A
; HYBRIDIZATION ASSAY
; NUMBER OF SEQUENCES: 216
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: NIXON & VANDERHUYE P.C.
; STREET: 1100 NORTH GLEBE ROAD, 8TH FLOOR
; CITY: WASHINGTON
; STATE: D.C.
; COUNTRY: USA
; ZIP: 22201
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/448.894
; FILING DATE: 29-Apr-1993
; CLASSIFICATION: <Unknown>
; PRIORITY DATA:
; PRIOR APPLICATION DATA:
; US-09-448-894-111
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; APPLICATION NUMBER: 08/765,332
; FILING DATE: <Unknown>
; APPLICATION NUMBER: EP 95870032.0
; FILING DATE: 07-APR-1995
; APPLICATION NUMBER: EP 94870106.5
; FILING DATE: 24-JUN-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: SADOFF, B.J.
; REGISTRATION NUMBER: 36,663
; REFERENCE/DOCKET NUMBER: 1487-14
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 703-816-4091
; TELEFAX: 703-816-4100
; INFORMATION FOR SEQ ID NO: 111:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 471 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cdna
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; SEQUENCE DESCRIPTION: SEQ ID NO: 111:
US-09-448-894-111

Query Match      100.0%; Score 471; DB 4; Length 471;
Best Local Similarity 100.0%; Pred. No. 5.5e-156;
Matches 471; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATCGAAGATCCCGGCTCTTCATAAGCTCCACACGAAATGCTTACTGTTAGAC 60
    |||||||
DB 1 ATCGAAGATCCCGGCTCTTCATAAGCTCCACACGAAATGCTTACTGTTAGAC 60
    |||||||

QY 61 GATTGGGTCTGTAGCTCAGTTGGTTAGAGCGCACCCCTGATAAGGGTGAGTTCGGCAGTT 120
    |||||||
DB 61 GATTGGGTCTGTAGCTCAGTTGGTTAGAGCGCACCCCTGATAAGGGTGAGTTCGGCAGTT 120
    |||||||

QY 121 CGAATCTGCCAGACCCACCAATGTTGGTGTGCTGCTGATCCGATACGGGGCCATAGC 180
    |||||||
DB 121 CGAATCTGCCAGACCCACCAATGTTGGTGTGCTGCTGATCCGATACGGGGCCATAGC 180
    |||||||

QY 181 TCAGCTGGGAGAGCGCTGCTTGCACGAGGAGGTTCAGAGTTCGATCCTCTGGCTC 240
    |||||||
DB 181 TCAGCTGGGAGAGCGCTGCTTGCACGAGGAGGTTCAGAGTTCGATCCTCTGGCTC 240
    |||||||

QY 241 CACCATCTAAACAATCGTCGAAGCTCAGAAATGAATGTTGCTGGATGAACATTTGATT 300
    |||||||
DB 241 CACCATCTAAACAATCGTCGAAGCTCAGAAATGAATGTTGCTGGATGAACATTTGATT 300
    |||||||

QY 301 CTGGTCTTTCACAGCAAGTCTTTTAAATTCGGGTATGATGAAGTAAGACTGA 360
    |||||||
DB 301 CTGGTCTTTCACAGCAAGTCTTTTAAATTCGGGTATGATGAAGTAAGACTGA 360
    |||||||

QY 361 ATGATCTCTTCACTGATCATTCAGTCAAGTAAATTTTCGGAGTTCAAGCGGAA 420
    |||||||
DB 361 ATGATCTCTTCACTGATCATTCAGTCAAGTAAATTTTCGGAGTTCAAGCGGAA 420
    |||||||

QY 421 TTTTCGGCGAATGCTGCTTTCACAGTATAACCGAGTTGCTTGGGTTATAT 471
    |||||||
DB 421 TTTTCGGCGAATGCTGCTTTCACAGTATAACCGAGTTGCTTGGGTTATAT 471
    |||||||

RESULT 3
US-08-765-332-114
; Sequence 114, Application US/08765332
; Patent No. 6025132
; GENERAL INFORMATION:
; APPLICANT: JANNES, GEERT
; APPLICANT: ROSSAU, RUDI
; APPLICANT: VAN HEUVERSWYN, HUGO
; TITLE OF INVENTION: SIMULTANEOUS DETECTION, IDENTIFICATION
; AND DIFFERENTIATION OF EUBACTERIAL TAXA USING A
; HYBRIDIZATION ASSAY
```

Db	358	TTTGGGTATGTGATAGAAGTGA---CTAACAGCGTGTTCACCTGCACGTTGT--ATCA	412
QY	393	AGGTAATAATTTGGAGTTCACGCGGAATTTTCGGCGGAATGTCGTCTTCAC-----A	444
Db	413	AGCAAAATTTGGAGTTCACGCGGAATTTTCGGCGGAATGTCGTCTTCACGTTACGAAT	472
QY	445	GTATACACAGATTGCTTGGGGTTATAT	471
Db	473	CTATACACAGATTGCTTGGGGTTATAT	499
RESULT 4			
US-09-448-894-114			
; Sequence 114, Application US/09448894			
; Patent No. 6312903			
; GENERAL INFORMATION:			
; APPLICANT: JANNES, GEERT			
; ROSSAU, RUDI			
; VAN HEUVERSWYN, HUGO			
; TITLE OF INVENTION: SIMULTANEOUS DETECTION, IDENTIFICATION			
; AND DIFFERENTIATION OF EUBACTERIAL TAXA USING			
; HYBRIDIZATION ASSAY			
; NUMBER OF SEQUENCES: 216			
; CORRESPONDENCE ADDRESS:			
; ADDRESSEE: NIXON & VANDERHYE P.C.			
; STREET: 1100 NORTH GLEBE ROAD, 8TH FLOOR			
; CITY: WASHINGTON			
; STATE: D.C.			
; COUNTRY: USA			
; ZIP: 22201			
; COMPUTER READABLE FORM:			
; MEDIUM TYPE: Floppy disk			
; COMPUTER: IBM PC compatible			
; OPERATING SYSTEM: PC-DOS/MS-DOS			
; SOFTWARE: PatentIn Release #1.0, Version #1.30			
; CURRENT APPLICATION DATA:			
; APPLICATION NUMBER: US/09/448,894			
; FILING DATE: 29-No. 6312903-1999			
; CLASSIFICATION: <Unknown>			
; 07-APR-1995			
; 24-JUN-1994			
; PRIOR APPLICATION DATA:			
; APPLICATION NUMBER: 08/765,332			
; FILING DATE: <Unknown>			
; APPLICATION NUMBER: EP 95870032.0			
; FILING DATE: 07-APR-1995			
; APPLICATION NUMBER: EP 94870106.5			
; FILING DATE: 24-JUN-1994			
; ATTORNEY/AGENT INFORMATION:			
; NAME: SADOFF, B.J.			
; REGISTRATION NUMBER: 36,663			
; REFERENCE/DOCKET NUMBER: 1487-14			
; TELECOMMUNICATION INFORMATION:			
; TELEPHONE: 703-816-4091			
; TELEFAX: 703-816-4100			
; INFORMATION FOR SEQ ID NO: 114:			
; SEQUENCE CHARACTERISTICS:			
; LENGTH: 499 base pairs			
; TYPE: nucleic acid			
; STRANDEDNESS: single			
; TOPOLOGY: linear			
; MOLECULE TYPE: cdna			
; HYPOTHETICAL: NO			
; ANTI-SENSE: NO			
; SEQUENCE DESCRIPTION: SEQ ID NO: 114:			
US-09-448-894-114			
Query Match			
Best Local Similarity			
Matches 409; Conservative 0; Mismatches 54; Indels 44; Gaps			
QY	1	ATCGAAGATCCCGGCTTCTTCATAGCTCCACACAGAAATGCTTGATTACTACTGTTA---57	



Db 1 ATCGAAGACTTCAGTCTCTTTCATAAGTCCACACGAAATTCGTTGATTCATCTGCGGAAA 60  
QY 58 -----GACGATTGGTCTGTAGCTCAGTTCAGTTGGTTAGAGCGCA 93  
Db 61 GCGATTGGTTGAGACCGGAGAGTGAGGATGGTCTGTAGCTCAGTTGGTTAGAGCGCA 120  
QY 94 CCCTGTAAAGGTGAGTGGCGAGTTCGAATCTGCCAGACCCACCAATTTGTTGGTGTG 153  
Db 121 CCCTGTAAAGGTGAGTGGCGAGTTCGAATCTGCCAGACCCACCAATTTGTTGGGATG 180  
QY 154 CTGGGTATCCGATAGCGGCGCATAGCTCAGCTGGGAGAGCGGCTGTTGGACGAGGA 213  
Db 181 GCAGTG---TCAAAATGGGCGCATAGCTCAGCTGGGAGAGCGGCTGTTGGACGAGGA 237  
QY 214 GGTCCAGAGTTCGATCTCTTGGCTCCACCATCTA-AAACAATCGTCGAAAGCTCAGAA 272  
Db 238 GGTCCAGAGTTCGATCTCTTGGCTCCACCATCTCAGATCGCTGAAAGCTCAGAA 297  
QY 273 ATGAATGTTGGTGGATGAACATGATTCTGTGCTTTGGCACCAGAACTGTTCTTTAAAAA 332  
Db 298 ATGAACATTTGGTATGTTCAATGTTGATTCTGTGCTTTGGCCAGAACTGTTCTTTAAAAA 357  
QY 333 TTCCGGTATCTGTAGAGTAAGACTGAATGATCTCTTTCACGTGGTGAATCAATTCAGTCA 392  
Db 358 TTGGGTATGTAGAGTGA---CTAACAGCGTGTTCACGTGCAGTGTGTT--AATCA 412  
QY 393 AGTAAAAATTTGGGAGTTCGAAGCGGCAATTTTGGCGGAATGCTGCTCTCAC-----A 444  
Db 413 AGCAAAATTTGGGAGTTCGAAGCGGCAATTTTGGCGGAATGCTGCTCTCAC-----A 444  
QY 445 GTATAACAGATGCTTGGGGTTATAT 471  
Db 473 CTATAACAGATGCTTGGGGTTATAT 499

## RESULT 5

US-08-765-332-113  
; Sequence 113, Application US/08765332  
; Patent No. 6025132  
; GENERAL INFORMATION:  
; APPLICANT: JANNES, GEERT  
; APPLICANT: VAN HEUVERSWYN, HUGO  
; TITLE OF INVENTION: SIMULTANEOUS DETECTION, IDENTIFICATION  
; TITLE OF INVENTION: AND DIFFERENTIATION OF EUBACTERIAL TAXA USING A  
; NUMBER OF SEQUENCES: 216  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: NIXON & VANDERHUYE P.C.  
; STREET: 1100 NORTH GLEBE ROAD, 8TH FLOOR  
; CITY: WASHINGTON  
; STATE: D.C.  
; COUNTRY: USA  
; ZIP: 22201  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/765.332  
; FILING DATE: 23-DEC-1996  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: WO PCT/EP95/02452  
; FILING DATE: 23-JUN-1995  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: EP 95870032.0  
; FILING DATE: 07-APR-1995  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: EP 94870106.5  
; FILING DATE: 24-JUN-1994

; ATTORNEY/AGENT INFORMATION:  
; NAME: SADOFF, B.J.  
; REGISTRATION NUMBER: 36,663  
; REFERENCE/DOCKET NUMBER: 1487-14  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 703-816-4091  
; TELEFAX: 703-816-4100  
; INFORMATION FOR SEQ ID NO: 113:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 504 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: cDNA  
; HYPOHETICAL: NO  
; ANTI-SENSE: NO  
; US-08-765-332-113

Query Match 47.9%; Score 225.8; DB 3; Length 504;  
Best Local Similarity 75.1%; Pred. No. 11e-69;  
Matches 396; Conservative 0; Mismatches 52; Indels 79; Gaps 6;

QY 1 ATCGAAGATCCCGGCTTCTTCATAAGCTCCACACGAAATTCGTTGATTCATCTGTTAG-- 58  
Db 1 ATCGAAGACACCGGCTTCGTCAAGCTCCACACGAAATTCGTTGATTCATCTGCGAAAG 60  
QY 59 -----ACGATTGGTCTGTAGCTCAGTTGGTTAGAGCGCA 93  
Db 61 GCGATTGGGTTTACCCGAGAGTAAGGATGGGCTGTAGCTCAGTTGGTTAGAGCGCA 120  
QY 94 CCCTGTAAAGGTGAGTGGCGAGTTCGAATCTGCCAGACCCACCAATTTGTTGGTGTG 153  
Db 121 CCCTGTAAAGGTGAGTGGCGAGTTCGAATCTGCCAGACCCACCAATTCG----- 172  
QY 154 CTGGGTATCCGATAGCGGCGCATAGCTCAGCTGGGAGAGCGGCTGCTTTGCACGAGGA 213  
Db 173 -----AAGGGGCCATAGCTCAGCTGGGAGAGCGGCTGCTTTGCACGAGGA 218  
QY 214 GGTCCAGAGTTCGATCTCTTGGCTCCACCATCTAAACAATCGTCGAAAGCTCAGAAA 273  
Db 219 GGTCCAGGTTTCGATCCCGCTTGGCTCCACCATCTAGTCGCGGCAAGCTCAGAAA 278  
QY 274 TGAATGTT-----CGTGGATGAACATTCGTTCTGCTTTGCA 312  
Db 279 TGAGTCTTTACCAGGATGAGTTGATTGCTGGGTTGAACATTCGTTGAGACTTTGCG 338  
QY 313 CCAGAACTGTTCTTTAAAAATTCGGGTATCTGTAGAGTAAGACTGAATGATCTCTTC 372  
Db 339 CCAGAACTGTTCTTTAAAAATTTGGGTATCTGTAGTAGAAGT-AGACCGGATGTTGCTTTC 397  
QY 373 ACTGGTATCATTCAGTCAAGTAAATTTGCGAGTTC-AAGCGGCAATTTTTCGCGAA 431  
Db 398 ACTGGCAGCATGTCGCGTCAAGGTAATAATTTGCGTCTTCTATGCAAAATTTTCGCGAA 457  
QY 432 TGTGCTCTTCACAGTA-----TAACAGATTCGTTGGGGTTATAT 471  
Db 458 TGTGCTCTTCACGTTATAGACAGTAACAGATTCGTTGGGGTTATAT 504

## RESULT 6

US-09-448-894-113  
; Sequence 113, Application US/09448894  
; Patent No. 6312903  
; GENERAL INFORMATION:  
; APPLICANT: JANNES, GEERT  
; APPLICANT: ROSSAU, RUDI  
; APPLICANT: VAN HEUVERSWYN, HUGO  
; TITLE OF INVENTION: SIMULTANEOUS DETECTION, IDENTIFICATION  
; AND DIFFERENTIATION OF EUBACTERIAL TAXA USING A  
; HYBRIDIZATION ASSAY  
; NUMBER OF SEQUENCES: 216  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: NIXON & VANDERHUYE P.C.

STREET: 1100 NORTH GLEBE ROAD, 8TH FLOOR  
CITY: WASHINGTON  
STATE: D.C.  
COUNTRY: USA  
ZIP: 22201

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/448,894  
FILING DATE: 29-No. 6312903-1999  
CLASSIFICATION: <Unknown>  
07-APR-1995  
24-JUN-1994

PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/765,332  
FILING DATE: <Unknown>  
APPLICATION NUMBER: EP 95870032.0  
FILING DATE: 07-APR-1995  
APPLICATION NUMBER: EP 94870106.5  
FILING DATE: 24-JUN-1994

ATTORNEY/AGENT INFORMATION:  
NAME: SADOFF, B.J.  
REGISTRATION NUMBER: 36,663  
REFERENCE/DOCKET NUMBER: 1487-14  
TELEPHONE: 703-816-4091  
TELEFAX: 703-816-4100

INFORMATION FOR SEQ ID NO: 113:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 504 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: cdna  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
SEQUENCE DESCRIPTION: SEQ ID NO: 113:  
US-09-448-894-113

Query Match 47.9%; Score 225.8; DB 4; Length 504;  
Best Local Similarity 75.1%; Pred. No. 1.1e-69;  
Matches 396; Conservative 0; Mismatches 52; Indels 79; Gaps 6;

QY 1 ATCGAAGATCCCGGCTTCTTCATAGCTCCACAGAAATGCTTGAATCACTGGTTAG-- 58  
DB 1 ATCGAAGACACCGGCTTCGTATAAGCTCCACAGAAATGCTTGAATCACTGGCGAAG 60

QY 59 -----ACGATTGGTCTGTAGCTCAGTTCAGTTGGTTAGACGCA 93  
DB 61 GCGATTGGTTTACACCCAGAGTACAGATTGGTCTGTAGCTCAGTTGGTTAGACGCA 120

QY 94 CCCCTGATAAGGTGAGTTCGCGAGTTCGAATTCGCCAGACCCACCAATTTGTTGGTGTG 153  
DB 121 CCCCTGATAAGGTGAGTTCGCGAGTTCGAATTCGCCAGACCCACCAATTCG----- 172

QY 154 CTCGCGTATCCGATACGGGGCCATAGCTCAGCTGGGAGAGCGCTCTTTCACGACGA 213  
DB 173 -----AAGGGGCCATAGCTCAGCTGGGAGAGCGCTCTTTCACGACGA 218

QY 214 GGTGAGGATTCGATCCTCTTGGCTCCACCATCTAAAACAATCGTCGAAAGCTCAGAAA 273  
DB 219 GGTGAGGATTCGATCCTCTTGGCTCCACCATCTAAAACAATCGTCGAAAGCTCAGAAA 278

QY 274 TGAATGTT-----CGTGGATGAACATTTGATTTCTGGTCTTTGCA 312  
DB 279 TGAATGTTTACCAGGATGAGTTGATTTGCTGGTTGAACATTTGATTTCTGGACTTTCG 338

QY 313 CCAGAACTCTTTTAAATAATTCGGGTATGTGATAGAAAGTGAATGATCTCTTTC 372  
DB 339 CCAGAACTCTTTTAAATAATTTGGGTATGTGATAGAAAGT-AGACCGGATGTGTTGCTTTC 397

QY 373 ACTGTGATCATTCAGTCAAGTAAATTTCCGAGTTC-AAGCCGAATTTTCGGCGAA 431  
DB 398 ACTGGCAGCATGTCGCTCAAGGTAATTTCCGTTCTCTATGCAAAATTTTCGGCGAA 457

QY 432 TGTCGTCTTCACAGTA-----TAACACAGATTGCTTGGGTTATAT 471  
DB 458 TGTCGTCTTCACAGTATATAGACAGTACAGATTGCTTGGGTTATAT 504

RESULT 7  
US-08-765-332-115  
; Sequence 115, Application US/08765332  
; Patent No. 6025132  
; GENERAL INFORMATION:  
; APPLICANT: JANNES, GEERT  
; APPLICANT: ROSSAU, RUDI  
; APPLICANT: VAN HEUVERSWYN, HUGO  
; TITLE OF INVENTION: SIMULTANEOUS DETECTION, IDENTIFICATION  
; TITLE OF INVENTION: AND DIFFERENTIATION OF EUBACTERIAL TAXA USING A  
; TITLE OF INVENTION: HYBRIDIZATION ASSAY  
; NUMBER OF SEQUENCES: 216  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: NIXON & VANDERHUYE P.C.  
; STREET: 1100 NORTH GLEBE ROAD, 8TH FLOOR  
; CITY: WASHINGTON  
; STATE: D.C.  
; COUNTRY: USA  
; ZIP: 22201  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/765,332  
; FILING DATE: 23-DEC-1996  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: WO PCT/EP95/02452  
; FILING DATE: 23-JUN-1995  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: EP 95870032.0  
; FILING DATE: 07-APR-1995  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: EP 94870106.5  
; FILING DATE: 24-JUN-1994  
; ATTORNEY/AGENT INFORMATION:  
; NAME: SADOFF, B.J.  
; REGISTRATION NUMBER: 36,663  
; REFERENCE/DOCKET NUMBER: 1487-14  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 703-816-4091  
; TELEFAX: 703-816-4100  
; INFORMATION FOR SEQ ID NO: 115:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 468 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: cdna  
; HYPOTHETICAL: NO  
; ANTI-SENSE: NO  
; US-08-765-332-115

Query Match 45.9%; Score 216; DB 3; Length 468;  
Best Local Similarity 74.9%; Pred. No. 3.1e-66;  
Matches 370; Conservative 0; Mismatches 75; Indels 49; Gaps 6;

QY 1 ATCGAAGATCCCGGCTTCTTCATAGCTCCACAGAAATGCTTGAATCACTGGTTAG- 59  
DB 1 ATCGAAGACATCAGCTGCTCATAAGCTCCACAGAAATGCTTGAATCACTGGTTAG- 60





Db 61 AATGCTGTAACGCGACCGCTGTTATAGTCTCTAGCTCAGTTGGTTAGAGCCACCCCTG 120  
Qy 100 ATAAGGCTGAGTCGCGAGTTCGAATCTGCCAGACCCACCAATTTGTTGGTGTGCTGCT 159  
Db 121 ATAAAGGCTGAGTCGCGAGTTCGAATCTGCCAGACCCACCAATTTGTTGGTGTGCTGCT 179  
Qy 160 GATCCGATACGCGGCGATAGCTCAGCTGGGAGAGCGCTGCTTTCACGCGAGGAGTCCAG 219  
Db 180 -----AATACGGGCGCATAGCTCAGCTGGGAGAGCGCTGCTTTCACGCGAGGAGTCCAG 234  
Qy 220 GAGTTCGATCTCTTGGCTCCACCA-----TCTAAACAATCTCGAAGAGTCA 269  
Db 235 CGGTTCGATCCGCTTGGCTCCACCACTCTCTCGTGTGCGGTGATCTTAAAGAGTTCA 294  
Qy 270 GAAATGA-----ATGTCGTGATGACATGATTTCTGCTTT-----CCA 312  
Db 295 GAAATGATGCGCTCAGTTTGTCTCTGTTGAGTCTGATTTCTGCTTTTGTACCGGTA 354  
Qy 313 CCAGAATCTTTTAAATTCGGTATGTCATAGAGTAAAGACTGAATGATCTCTTTTC 372  
Db 355 CGAAATCTTTTAAATTTGGATATGATAGAGT--GACTGATTAATTCCTTC 412  
Qy 373 ACTGCTGATCATCAAGTCAAGTAAATTTG--CGAGTTCAAGCGGCAATTTTCGGCGA 430  
Db 413 ACTGCAATGATCTGTCAGGTAAGTAAATTTGTTAGTCTCAAGACGCAATTTTCGGCGA 472  
Qy 431 ATGCTGCTTCCAC-----AGTATAACGAGATGCTTGGGTTATAT 471  
Db 473 ATGCTGCTTCCAGATTGAGACAGTAACGAGATGCTTGGGTTATAT 520

## RESULT 11

US-08-765-332-195  
; Sequence 195, Application US/08765332  
; Patent No. 6025132  
; GENERAL INFORMATION:  
; APPLICANT: JANNES, GEERT  
; APPLICANT: ROSSAU, RUDI  
; APPLICANT: VAN HEUVERSWYN, HUGO  
; TITLE OF INVENTION: SIMULTANEOUS DETECTION, IDENTIFICATION  
; AND DIFFERENTIATION OF EUBACTERIAL TAXA USING A  
; TITLE OF INVENTION: HYBRIDIZATION ASSAY  
; NUMBER OF SEQUENCES: 216  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: NIXON & VANDERHYE P.C.  
; STREET: 1100 NORTH GLEBE ROAD, 8TH FLOOR  
; CITY: WASHINGTON  
; STATE: D.C.  
; COUNTRY: USA  
; ZIP: 22201  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/765,332  
; FILING DATE: 23-DEC-1996  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: WO PCT/EP95/02452  
; FILING DATE: 23-JUN-1995  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: EP 95870032.0  
; FILING DATE: 07-APR-1995  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: EP 94870106.5  
; FILING DATE: 24-JUN-1994  
; ATTORNEY/AGENT INFORMATION:  
; NAME: SADOFF, B.J.  
; REGISTRATION NUMBER: 36,663  
; REFERENCE/DOCKET NUMBER: 1487-14  
; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 703-816-4091  
; TELEFAX: 703-816-4100  
; INFORMATION FOR SEQ ID NO: 195:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 470 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: cDNA  
; HYPOTHETICAL: NO  
; ANTI-SENSE: NO  
US-08-765-332-195

Query Match 24.1%; Score 113.4; DB 3; Length 470;  
Best Local Similarity 73.1%; Pred. No. 3.9e-30;  
Matches 163; Conservative 0; Mismatches 51; Indels 9; Gaps 1;

Qy 64 TGGGTCCTAGCTCAGTTGGTTAGAGCGCACCCCTGATAAGGTCAGGTCGCGAGTTCA 123  
Db 75 TAGGCTTCTAGCTCAGTGGTTAGAGCGCACCCCTGATAAGGTCAGGTCGCGAGTTCA 134  
Qy 124 ATCTGCCAGACCCCAATTTGTTGGTGTG-----CTGCGTGTATCCGATACGGGCG 174  
Db 135 GTCCACTCAGCGCTACCACTTCTCGAAGTGGAAAAAGTACTGCACGTGACTGTATGGGCG 194  
Qy 175 CATAGCTCAGCTGGGAGAGCGCTGCTTTCACGCGAGGTCAGAGGTCGATCCTCT 234  
Db 195 TATAGCTCAGCTGGGAGAGCGCTGCTTTCACGCGAGGTCAGGTCGATCCTCT 254  
Qy 235 TGGTCCACCATCTAAACAATCTGTCGAAAGCTCAGAAATGAA 277  
Db 255 TAGTCCACCATATAGTCTCTATTCTTCAATCTTCCAGAGTGA 297

## RESULT 12

US-09-448-894-195  
; Sequence 195, Application US/09448894  
; Patent No. 6312903  
; GENERAL INFORMATION:  
; APPLICANT: JANNES, GEERT  
; APPLICANT: ROSSAU, RUDI  
; APPLICANT: VAN HEUVERSWYN, HUGO  
; TITLE OF INVENTION: SIMULTANEOUS DETECTION, IDENTIFICATION  
; AND DIFFERENTIATION OF EUBACTERIAL TAXA USING A  
; TITLE OF INVENTION: HYBRIDIZATION ASSAY  
; NUMBER OF SEQUENCES: 216  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: NIXON & VANDERHYE P.C.  
; STREET: 1100 NORTH GLEBE ROAD, 8TH FLOOR  
; CITY: WASHINGTON  
; STATE: D.C.  
; COUNTRY: USA  
; ZIP: 22201  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/448,894  
; FILING DATE: 29-NOV-1999  
; CLASSIFICATION: <Unknown>  
; 07-APR-1995  
; 24-JUN-1994  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/765,332  
; FILING DATE: <Unknown>  
; APPLICATION NUMBER: EP 95870032.0  
; FILING DATE: 07-APR-1995  
; APPLICATION NUMBER: EP 94870106.5  
; FILING DATE: 24-JUN-1994  
; ATTORNEY/AGENT INFORMATION:  
; NAME: SADOFF, B.J.

us-09-931-486-111.rni

Mon Feb 3 16:48:53 2003

```

; APPLICATION NUMBER: EP 94870106.5
; FILING DATE: 24-JUN-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: SADOFF, B.J.
; REGISTRATION NUMBER: 36,663
; REFERENCE/DOCKET NUMBER: 1487-14
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 703-816-4091
; TELEFAX: 703-816-4091
; INFORMATION FOR SEQ ID NO: 128:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 249 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cdna
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; SEQUENCE DESCRIPTION: SEQ ID NO: 195:
US-09-448-894-195

```

```

Query Match 24.1%; Score 113.4; DB 4; Length 470;
Best Local Similarity 73.1%; Pred. No. 3.9e-30;
Matches 163; Conservative 0; Mismatches 51; Indels 9; Gaps 1;

QY 64 TGGGCTCTAGCTCAGTTGGTTAGAGCGCACCCCTGTGATAGGGTGAGGTGCGGAGTTCGA 123
Db 75 TAGGCTTGTAGCTCAGTTGGTTAGAGCGCACCCCTGTGATAGGGTGAGGTGCGGAGTTCGA 134
QY 124 ATCTGCCAGACCCACCAATTGTTGGTGTG-----CTGCGTGATCCGATAGCGGGC 174
Db 135 GTCCACTAGGCTACCACTTCTCGAAGTGGAAAGGACTGACGCTGACTGTATGGGGC 194
QY 175 CATAGCTCAGCTGGGAGAGCGCTGTTTGCACGAGGAGTTCAGAGTTCGATCCTCT 234
Db 195 TATAGCTCAGCTGGGAGAGCGCTGCTTGCACGAGGAGTTCAGAGTTCGATCCTCT 254
QY 235 TGGCTCCACCTATAAACAATCGTCGAAGCTCAGAAATGAA 277
Db 255 TAGCTCCACCATATATCTCTGTATTTCATATCTTACAGAGTGTA 297

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RESULT 13
US-08-765-332-128
; Sequence 128, Application US/08765332
; Patent No. 6025132
; GENERAL INFORMATION:
; APPLICANT: JANNES, GEERT
; APPLICANT: ROSSAU, RUDI
; APPLICANT: VAN HEUVERSWYN, HUGO
; TITLE OF INVENTION: SIMULTANEOUS DETECTION, IDENTIFICATION
; TITLE OF INVENTION: AND DIFFERENTIATION OF EUBACTERIAL TAXA USING A
; TITLE OF INVENTION: HYBRIDIZATION ASSAY
; NUMBER OF SEQUENCES: 216
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: NIXON & VANDERHYE P.C.
; STREET: 1100 NORTH GLEBE ROAD, 8TH FLOOR
; CITY: WASHINGTON
; STATE: D.C.
; COUNTRY: USA
; ZIP: 22201
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08765,332
; FILING DATE: 23-DEC-1996
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: WO PCT/EP95/02452
; FILING DATE: 23-JUN-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: EP 95870032.0
; FILING DATE: 07-APR-1995
; PRIOR APPLICATION DATA:

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Query Match 22.0%; Score 103.8; DB 3; Length 249;
Best Local Similarity 76.2%; Pred. No. 6.5e-27;
Matches 144; Conservative 0; Mismatches 37; Indels 8; Gaps 1;

QY 65 GGGTCTCTAGCTCAGTTGGTTAGAGCGCACCCCTGTGATAGGGTGAGGTGCGGAGTTCGAA 124
Db 61 GGGTCTCTAGCTCAGTTGGTTAGAGCGCACCCCTGTGATAGGGTGAGGTGCGGAGTTCGAA 120
QY 125 TCTGCCAGACCCACCAATTGT-----TGGTGTGCTGCGTGATCCGATAGCGGGCCA 176
Db 121 TCTTGTGACAGCCCAAAATCTGAAAGATATGTCGTTCAATATGATTAAAGCTGGGGACT 180
QY 177 TAGCTCAGCTGGGAGAGCGCTGTTTGCACGAGGAGTTCAGAGTTCGATCCTCTCTTG 236
Db 181 TAGCTTGTGTTAGAGCGCTGCTTTGCACGAGGAGTTCAGAGTTCGACTCTCTCTAG 240
QY 237 GCTCCACCA 245
Db 241 TCTCCACCA 249

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RESULT 14
US-09-448-894-128
; Sequence 128, Application US/09448894
; Patent No. 6312903
; GENERAL INFORMATION:
; APPLICANT: JANNES, GEERT
; APPLICANT: ROSSAU, RUDI
; APPLICANT: VAN HEUVERSWYN, HUGO
; TITLE OF INVENTION: SIMULTANEOUS DETECTION, IDENTIFICATION
; TITLE OF INVENTION: AND DIFFERENTIATION OF EUBACTERIAL TAXA USING A
; TITLE OF INVENTION: HYBRIDIZATION ASSAY
; NUMBER OF SEQUENCES: 216
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: NIXON & VANDERHYE P.C.
; STREET: 1100 NORTH GLEBE ROAD, 8TH FLOOR
; CITY: WASHINGTON
; STATE: D.C.
; COUNTRY: USA
; ZIP: 22201
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/448,894
; FILING DATE: 29-NOV-1999
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/765,332

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; FILING DATE: <Unknown>  
; APPLICATION NUMBER: EP 95870032.0  
; FILING DATE: 07-APR-1995  
; APPLICATION NUMBER: EP 94870106.5  
; FILING DATE: 24-JUN-1994  
; ATTORNEY/AGENT INFORMATION:  
; NAME: SADOFF, B.J.  
; REGISTRATION NUMBER: 36,663  
; REFERENCE/DOCKET NUMBER: 1487-14  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 703-816-4091  
; TELEFAX: 703-816-4100  
; INFORMATION FOR SEQ ID NO: 128:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 249 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: CDNA  
; HYPOTHETICAL: NO  
; ANTI-SENSE: NO  
; SEQUENCE DESCRIPTION: SEQ ID NO: 128:  
US-09-448-894-128

Query Match 22.0%; Score 103.8; DB 4; Length 249;  
Best Local Similarity 76.2%; Pred. No. 6.5e-27;  
Matches 144; Conservative 0; Mismatches 37; Indels 8; Gaps 1;  
QY 65 GGGTCGTAGCTAGCTAGGCGCACCCCTGATAAGGCTGAGGTCGGCAGTTCGAA 124  
Db 61 GGGTCGTAGCTAGCTAGGCGCACCCCTGATAAGGCTGAGGTCGGCAGTTCGAA 120  
QY 125 TCTGCCACAGCCACCAATTGT-----TGGTGTGCTGCTGATCCGATACGGGGCCA 176  
Db 121 TCTGCCACAGCCACCAATTGT-----TGGTGTGCTGCTGATCCGATACGGGGCCA 180  
QY 177 TAGCTCAGCTGGGAGAGCGCTGCTTTGACGACGAGGTGAGGTCGATCCCTCTTG 236  
Db 181 TAGCTCAGCTGGGAGAGCGCTGCTTTGACGACGAGGTGAGGTCGATCCCTCTTG 236  
QY 237 GCTCCACCA 245  
Db 241 TCTCCACCA 249

RESULT 15  
US-08-765-332-215  
; Sequence 215, Application US/08765332  
; Patent No. 6025132  
; GENERAL INFORMATION:  
; APPLICANT: JANNES, GEERT  
; APPLICANT: ROSSAU, RUDI  
; APPLICANT: VAN HEUVERSWYN, HUGO  
; TITLE OF INVENTION: SIMULTANEOUS DETECTION, IDENTIFICATION  
; TITLE OF INVENTION: AND DIFFERENTIATION OF EUBACTERIAL TAXA USING A  
; TITLE OF INVENTION: HYBRIDIZATION ASSAY  
; NUMBER OF SEQUENCES: 216  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: NIXON & VANDERHVE P.C.  
; STREET: 1100 NORTH GLEBE ROAD, 8TH FLOOR  
; CITY: WASHINGTON  
; STATE: D.C.  
; COUNTRY: USA  
; ZIP: 22201  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/765,332  
; FILING DATE: 23-DEC-1996  
; CLASSIFICATION: 435

; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: WO PCT/EP95/02452  
; FILING DATE: 23-JUN-1995  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: EP 95870032.0  
; FILING DATE: 07-APR-1995  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: EP 94870106.5  
; FILING DATE: 24-JUN-1994  
; ATTORNEY/AGENT INFORMATION:  
; NAME: SADOFF, B.J.  
; REGISTRATION NUMBER: 36,663  
; REFERENCE/DOCKET NUMBER: 1487-14  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 703-816-4091  
; TELEFAX: 703-816-4100  
; INFORMATION FOR SEQ ID NO: 215:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 463 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: CDNA  
; HYPOTHETICAL: NO  
; ANTI-SENSE: NO  
; US-08-765-332-215

Query Match 21.2%; Score 100; DB 3; Length 463;  
Best Local Similarity 75.0%; Pred. No. 2e-25;  
Matches 141; Conservative 0; Mismatches 40; Indels 7; Gaps 1;  
QY 65 GGGTCGTAGCTAGCTAGGCGCACCCCTGATAAGGCTGAGGTCGGCAGTTCGAA 124  
Db 115 GGGTCGTAGCTAGCTAGGCGCACCCCTGATAAGGCTGAGGTCGGCAGTTCGAG 174  
QY 125 TCTGCCACAGCCACCAATTGTGCTGCTGATCCG-----ATACGGGGCCAT 177  
Db 175 TCTGCCACAGCCACCAATTGTGCTGCTGATCCG-----ATACGGGGCCAT 177  
QY 178 AGCTCAGCTGGGAGAGCGCTGCTTTGACGACGAGGTGAGGTCGATCCCTCTTG 237  
Db 235 AGCTCAGCTGGGAGAGCGCTGCTTTGACGACGAGGTGAGGTCGATCCCTCTTG 234  
QY 238 CTCCACCA 245  
Db 295 CTCCACCA 302

Search completed: February 1, 2003, 04:24:12  
Job time : 26.4874 secs



GenCore version 5.1.3  
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: February 1, 2003, 03:05:22 ; Search time 26.2092 Seconds  
(without alignments)  
8073.649 Million cell updates/sec

Title: US-09-931-486-111

Perfect score: 471

Sequence: 1 ATCGAAGATCCCGCTCT.....CAGATTGCTGGGGTTATAT 471

Scoring table: IDENTITY\_NUC

Gapop 10.0 , Gapext 1.0

Searched: 396772 seqs, 224632407 residues

Total number of hits satisfying chosen parameters: 793544

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications NA:\*

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- 2: /cgn2\_6/ptodata/1/pubpna/PCP\_NEW\_PUB.seq:\*
- 3: /cgn2\_6/ptodata/1/pubpna/PCP\_NEW\_PUB.seq:\*
- 4: /cgn2\_6/ptodata/1/pubpna/US06\_PUBCOMB.seq:\*
- 5: /cgn2\_6/ptodata/1/pubpna/US07\_NEW\_PUB.seq:\*
- 6: /cgn2\_6/ptodata/1/pubpna/US07\_PUBCOMB.seq:\*
- 7: /cgn2\_6/ptodata/1/pubpna/US08\_PUBCOMB.seq:\*
- 8: /cgn2\_6/ptodata/1/pubpna/US08\_NEW\_PUB.seq:\*
- 9: /cgn2\_6/ptodata/1/pubpna/US09\_PUBCOMB.seq:\*
- 10: /cgn2\_6/ptodata/1/pubpna/US09\_NEW\_PUB.seq:\*
- 11: /cgn2\_6/ptodata/1/pubpna/US10\_PUBCOMB.seq:\*
- 12: /cgn2\_6/ptodata/1/pubpna/US10\_NEW\_PUB.seq:\*
- 13: /cgn2\_6/ptodata/1/pubpna/US60\_PUBCOMB.seq:\*
- 14: /cgn2\_6/ptodata/1/pubpna/US60\_PUBCOMB.seq:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

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1	95.2	20.2	640681	10	US-09-790-988-1
2	94.4	20.0	243	10	US-09-815-242-1358
3	93.8	19.9	255	10	US-09-815-242-1377
4	93.8	19.9	255	10	US-09-815-242-1402
5	93.8	19.9	255	10	US-09-815-242-1415
6	93.8	19.9	255	10	US-09-815-242-1423
7	93.8	19.9	255	10	US-09-815-242-1431
8	93.8	19.9	255	10	US-09-815-242-1454
9	93.8	19.9	255	10	US-09-815-242-1459
10	93.8	19.9	255	10	US-09-815-242-1473
11	93.8	19.9	255	10	US-09-815-242-1475
12	93.8	19.9	255	10	US-09-815-242-1544
13	93.8	19.9	255	10	US-09-815-242-1638
14	92.6	19.7	582	10	US-09-863-086-87
15	92.6	19.7	590	10	US-09-863-086-88
16	87.2	18.5	3309400	9	US-09-738-626-1
17	85.2	18.1	549	10	US-09-863-086-92
18	82.6	17.5	498	10	US-09-863-086-90
19	81.8	17.4	603	10	US-09-863-086-85

20	81.8	17.4	603	10	US-09-863-086-86
21	68.6	14.6	836	9	US-09-894-467-5
22	66.4	14.1	76	10	US-09-974-300-4361
23	66.4	14.1	76	10	US-09-974-300-4403
24	66.4	14.1	76	10	US-09-974-300-4409
25	66.4	14.1	76	10	US-09-974-300-4418
26	66.4	14.1	76	10	US-09-974-300-8396
27	66.4	14.1	76	10	US-09-974-300-8438
28	66.4	14.1	76	10	US-09-974-300-8444
29	66.4	14.1	76	10	US-09-974-300-8453
30	66.4	14.1	290	10	US-09-815-242-4692
31	66.4	14.1	495	10	US-09-815-242-2687
32	66.4	14.1	495	10	US-09-815-242-2691
33	65.8	14.0	1069	10	US-09-070-927A-869
34	65.4	13.9	279	10	US-09-863-086-96
35	64.8	13.8	9797	10	US-09-070-927A-550
36	64.6	13.7	2336	10	US-09-842-552-102
37	64.4	13.7	74	10	US-09-974-300-4363
38	64.4	13.7	76	10	US-09-974-300-8398
39	63.8	13.5	246	10	US-09-863-086-95
40	62.8	13.3	654	10	US-09-863-086-89
41	61.6	13.1	1883	10	US-09-927-483-3
42	61.6	13.1	1883	10	US-09-927-483-4
43	61.6	13.1	1919	10	US-09-927-483-1
44	61.6	13.1	1919	10	US-09-927-483-2
45	59.4	12.6	77	10	US-09-974-300-4362

## ALIGNMENTS

## RESULT 1

US-09-790-988-1  
; Sequence 1, Application US/09790988  
; Patent No. US20020127687A1  
; GENERAL INFORMATION:  
; APPLICANT: SHIGENOBU, SHUJI  
; APPLICANT: WATANABE, HIDEKI  
; APPLICANT: HATTORI, MASAHIRA  
; APPLICANT: SAKAKI, YOSHIYUKI  
; TITLE OF INVENTION: GENOME DNA OF BACTERIAL SYMBIONT OF APHIDS  
; FILE REFERENCE: 081356/0159  
; CURRENT APPLICATION NUMBER: US/09/790.988  
; PRIOR FILING DATE: 2001-02-23  
; PRIOR APPLICATION NUMBER: JP2000-107160  
; FILING DATE: 2000-04-07  
; NUMBER OF SEQ ID NOS: 7  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 1  
; LENGTH: 640681  
; TYPE: DNA  
; ORGANISM: Buchnera sp.  
US-09-790-988-1

Query Match 20.2%; Score 95.2; DB 10; Length 640681;  
Best Local Similarity 69.7%; Pred. No. 2e-20;  
Matches 166; Conservative 0; Mismatches 53; Indels 19; Gaps 2;  
QY 5 AAGATCCCGCTTCTTCATTAAGCTCCACACAGAAATTCCTTGAATCTACCTGGTTAGACGATT 64  
Db 275585 AAAATATATATCTTTTGAAGTCCACACAAATATCTAATAAAAAATTTAGA----- 275639  
QY 65 GGCTCTAGCTCAGTTGGTTAGAGCGCACCCCTGTATAGGTTAGGTCGGCAGTTTCGAA 124  
Db 275640 AGGCTTGTAGCTCAGATGGTTAGAGCGCACCCCTGTATAGGTTAGGTCGGTTCGTTCAAT 275699  
QY 125 TCTGCCACGACCCACCAATTTGGTGTCTGCTGCTATCCGATACGGGCCCATAGCTCAG 184  
Db 275700 TCACCTCAGGCTACCAAT-----AAAAATCATCTGGGCTTATAGTCAG 275745  
QY 185 CTGGAGAGCGCTGCTTTTTCACGAGGAGGTCAGAGGTTTCATCTCTTGGCTCCA 242  
Db 275746 CTGGAGAGCGCTGCTTTTTCACGAGGAGGTCAGGCTTCAATCCCGCTTAGCTCCA 275803







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; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Kari L.
; APPLICANT: Zyskind, Judith W.
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John D.
; APPLICANT: Carr, Grant J.
; APPLICANT: Yamamoto, Robert T.
; APPLICANT: Xu, H. Howard
; TITLE OF INVENTION: Identification of Essential Genes in
; FILE REFERENCE: ELITRA.011a
; CURRENT APPLICATION NUMBER: US/09/815,242
; CURRENT FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; NUMBER OF SEQ ID NOS: 14110
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1459
; LENGTH: 255
; TYPE: DNA
; ORGANISM: Staphylococcus aureus
US-09-815-242-1473

Query Match          19.9%; Score 93.8; DB 10; Length 255;
Best Local Similarity 72.8%; Pred. No. 8.1e-22;
Matches 139; Conservative 0; Mismatches 42; Indels 10; Gaps 1;

QY 39 TTGCTTGATTCACGTGGTGTAGACGATGGGCTCTAGCTCAGTTGGTTAGAGCCGCCCT 98
Db 181 TTGAATGTTGTTTCATTCAAATTAATGGCCTATAGCTCAGCTGGTTAGAGCCGCCCT 122

QY 99 GATAAGGGTGGAGTGGCGGCGGCTTCCAAATCTGCCAGACCCACCAATTTGTTGCTGCG 158
Db 121 GATAAGCGTGAGTGGTGGTGGTTCGAGTCCACTTAGGCCCCACCAATTAATT-----T 72

QY 159 TGATCCGATACGGGCGGCGGCTAGCTCAGCTGGGAGAGCGCGCTTTGCACCGAGGAGTCA 218
Db 71 AATACCTATTGGGGGCTTAGCTCAGCTGGGAGAGCGCGCTTTGCACCGAGGAGTCA 12

QY 219 GGAGTTCGATC 229
Db 11 GCGGTTTCGATC 1

RESULT 10
US-09-815-242-1473/c
; Sequence 1473, Application US/09815242
; Patent No. US20020061569A1
; GENERAL INFORMATION:
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Kari L.
; APPLICANT: Zyskind, Judith W.
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John D.
; APPLICANT: Carr, Grant J.
; APPLICANT: Yamamoto, Robert T.
; APPLICANT: Xu, H. Howard
; TITLE OF INVENTION: Identification of Essential Genes in
; FILE REFERENCE: ELITRA.011a
; CURRENT APPLICATION NUMBER: US/09/815,242
; CURRENT FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; CURRENT APPLICATION NUMBER: US/09/815,242
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; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Kari L.
; APPLICANT: Zyskind, Judith W.
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John D.
; APPLICANT: Carr, Grant J.
; APPLICANT: Yamamoto, Robert T.
; APPLICANT: Xu, H. Howard
; TITLE OF INVENTION: Identification of Essential Genes in
; FILE REFERENCE: ELITRA.011a
; CURRENT APPLICATION NUMBER: US/09/815,242
; CURRENT FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; CURRENT APPLICATION NUMBER: 60/257,931
; RESULT 11
US-09-815-242-1475/c
; Sequence 1475, Application US/09815242
; Patent No. US20020061569A1
; GENERAL INFORMATION:
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Kari L.
; APPLICANT: Zyskind, Judith W.
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John D.
; APPLICANT: Carr, Grant J.
; APPLICANT: Yamamoto, Robert T.
; APPLICANT: Xu, H. Howard
; TITLE OF INVENTION: Identification of Essential Genes in
; FILE REFERENCE: ELITRA.011a
; CURRENT APPLICATION NUMBER: US/09/815,242
; CURRENT FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; CURRENT APPLICATION NUMBER: 60/257,931
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Db 210 CTGGGAGAGCGCTGCTTTTGCACGAGGATGTCATCGGTCGATCCGTTACCTCCACC 269

QY 245 A 245

Db 270 A 270

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RESULT 15
US-09-863-086-88
: Sequence 88, Application US/09863086
: Patent No. US20020048762A1
: GENERAL INFORMATION:
: APPLICANT: Rossau, Rudi
: TITLE OF INVENTION: HYBRIDIZATION PROBES DERIVED FROM THE SPACER
: REGION BETWEEN THE 16S A
: NUMBER OF SEQUENCES: 104
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Merchant, Gould, Smith, Edell, Welter & Schmidt
: STREET: 3100 No. US20020048762Alwest Center, 90 S. 7th Street
: CITY: Minneapolis
: STATE: MN
: COUNTRY: U.S.A.
: ZIP: 55402
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Diskette
: COMPUTER: IBM Compatible
: OPERATING SYSTEM: DOS
: SOFTWARE: FastSeq Version 1.5
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/09/863,086
: FILING DATE: 22-May-2001
: CLASSIFICATION: <Unknown>
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: 09/312,520
: FILING DATE: <Unknown>
: APPLICATION NUMBER: 08/412,614
: FILING DATE: 29-MAR-1995
: ATTORNEY/AGENT INFORMATION:
: NAME: Hillson, Randall A
: REGISTRATION NUMBER: 31,838
: REFERENCE/DOCKET NUMBER: 8076.75USC1
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: 612/332-5300
: TELEFAX: 612/332/9081
: TELEX: <Unknown>
: INFORMATION FOR SEQ ID NO: 88:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 590 base pairs
: TYPE: nucleic acid
: STRANDEDNESS: single
: TOPOLOGY: linear
: MOLECULE TYPE: Genomic DNA
: HYPOTHETICAL: NO
: ANTI-SENSE: NO
: FRAGMENT TYPE: <Unknown>
: ORIGINAL SOURCE:
: SEQUENCE DESCRIPTION: SEQ ID NO: 88:
US-09-863-086-88

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db	98	GGGTCCTAGCTCAGTCGGTTAGAGCACCCCTCTTGATAAGGGGGGGTCTGGTGGTTCGAA	157		
2Y	125	TCTGCCAGACCCACCAATTTGGTGTGCTGCGTGATCCGATACGGGGCCATAGCTCAG	184		
db	158	TCCAAACAGACCCACCAAGGTTTCTCAGAGG-----GAAATGGGGGTCTAGCTCAG	209		
2Y	185	CTGGGAGAGCGCTGCTTTTCACGACGAGGAGGTTCAGAGTTCTGATCTCTCGTGGCTCCACC	244		

Db 210 CTGGAGAGCGCCTGCTTTGCAAGCAGGATGTCATCGGTTGATCCCGTTTCACCTCCACC 269  
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Db 270 A 270

Search completed: February 1, 2003, 06:47:34  
Job time : 247.209 secs



GenCore version 5.1.3  
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: February 1, 2003, 01:09:56 ; Search time 878.868 Seconds  
(without alignments)  
8679.427 Million cell updates/sec

Title: US-09-931-486-111

Perfect score: 471

Sequence: 1 ATCGAAGATCCGCTTCTT.....CAGATTGCTGGGTATAT 471

Scoring table: IDENTITY\_NUC

Gapop 10.0 , Gapext 1.0

Searched: 16154066 seqs, 8097743376 residues

Total number of hits satisfying chosen parameters: 32308132

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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3: em\_estin:\*

4: em\_estmu:\*

5: em\_estov:\*

6: em\_estpl:\*

7: em\_estro:\*

8: em\_hic:\*

9: gb\_est1:\*

10: gb\_est2:\*

11: gb\_hic:\*

12: gb\_est3:\*

13: gb\_est4:\*

14: gb\_est5:\*

15: em\_estfun:\*

16: em\_estom:\*

17: gb\_gss:\*

18: em\_gss\_hum:\*

19: em\_gss\_inv:\*

20: em\_gss\_pln:\*

21: em\_gss\_vrt:\*

22: em\_gss\_fun:\*

23: em\_gss\_mam:\*

24: em\_gss\_mus:\*

25: em\_gss\_other:\*

26: em\_gss\_pro:\*

27: em\_gss\_rod:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Match	Length	DB	ID	Description
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C 3	184.6	39.2	639	17	AO509640	AO509640 nbxb0096P
C 4	121.6	25.8	319	10	BE092111	BE092111 IL2-BY073
C 5	73.6	15.6	754	17	BH405252	BH405252 AG-ND-127
C 6	71.6	15.2	712	17	BH397037	BH397037 AG-ND-137

RESULT 1  
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LOCUS  
DEFINITION  
ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM  
REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
COMMENT

BH200120  
Sm1-57J2.TF Sm1 Schistosoma mansoni genomic clone Sm1-57J2, DNA sequence.  
BH200120  
BH200120.1 GI:16370164  
GSS.  
Schistosoma mansoni.  
Schistosoma mansoni.  
Eukaryota; Metazoa; Platyhelminthes; Trematoda; Digenea;  
Strigoida; Schistosomatidae; Schistosomatidae; Schistosoma.  
1 (bases 1 to 507)  
Shetty,J., Simpson,A., Malek,J., Koo,H., LoVerde,P.T. and El-Sayed,N.M.  
Use of end sequences from Schistosoma mansoni (Puerto Rico strain) Sm1 BAC library for gene discovery and map construction  
Unpublished (2001)  
Other\_GSSs: Sm1-57J2.TF  
Contact: Najib M. El-Sayed  
Department of Eukaryotic Genomics  
The Institute for Genomic Research  
9712 Medical Center Dr., Rockville, MD 20850, USA  
Tel: 301 838 0200  
Fax: 301 838 0208  
Email: nelsayed@tigr.org  
lo.edu).  
Seq primer: M13 For  
Class: BAC ends.

ALIGNMENTS

507 bp DNA linear GSS 24-OCT-2001  
Sm1-57J2.TF Sm1 Schistosoma mansoni genomic clone Sm1-57J2, DNA sequence.

BH200120  
BH200120  
BH200120.1  
GI:16370164  
GSS.  
Schistosoma mansoni.  
Schistosoma mansoni.  
Eukaryota; Metazoa; Platyhelminthes; Trematoda; Digenea;  
Strigoida; Schistosomatidae; Schistosomatidae; Schistosoma.  
1 (bases 1 to 507)  
Shetty,J., Simpson,A., Malek,J., Koo,H., LoVerde,P.T. and El-Sayed,N.M.  
Use of end sequences from Schistosoma mansoni (Puerto Rico strain) Sm1 BAC library for gene discovery and map construction  
Unpublished (2001)  
Other\_GSSs: Sm1-57J2.TF  
Contact: Najib M. El-Sayed  
Department of Eukaryotic Genomics  
The Institute for Genomic Research  
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Tel: 301 838 0200  
Fax: 301 838 0208  
Email: nelsayed@tigr.org  
lo.edu).  
Seq primer: M13 For  
Class: BAC ends.

AA680996 SW3D9CA51  
BH771024 LMGtag74  
BH819575 BACPPI3-E  
BH400944 AG-ND-158  
BH393190 AG-ND-168  
BH393241 AG-ND-137  
BH544108 S071 Grac  
BH614410 IC22AG2 S  
BH544086 S042 Grac  
BH375641 AG-ND-133  
AZ578476 23h03 Sho  
A1526132 PC3-2.B11  
BH159957 ENTS113TF  
AQ012191 430PIA043  
BH1941477 GQ07G11.Y  
BH387664 AG-ND-157  
AQ989869 RfC00532  
BH586090 BOHOK43TF  
BH375975 AG-ND-133  
AZ683938 ENT1J28TR  
BI263958 NF107H06P  
AQ959605 LBREL81TF  
AQ967686 LERI16TR  
AW238039 xpl13H02.X  
AW238064 xpl16A02.X  
BG272878 naJ02e02.  
BH584916 BOGFM79TR  
BH427885 BOHOK30TF  
BH427896 BOHOK30TR  
BH463934 BOGR220TR  
BH646171 BOME267TF  
AZ672622 ENTMR14TR  
BH855109 SALK\_0866  
BH169234 SALK\_0008

FEATURES  
Source

## Location/Qualifiers

1..507  
/organism="Schistosoma mansoni"  
/strain="Puerto Rico"  
/db\_xref="taxon:6183"  
/clone="Sml-57J2"  
/clone\_lib="Sml"  
/note="Vector: pBelOBAC11; Site.1: Hin dIII; Constructed in the laboratory of Dr. Denis Le Paslier at the Fondation Jean Dausset, CEPH, Paris, France. Briefly, Schistosoma mansoni agarose embedded DNA was partially digested with Hin dIII. High molecular weight fragments were ligated in pBelOBAC11 digested with Hin dIII. The average insert size is 100 kb. Total clone coverage: approx. 7.95 x the haploid genome. Further information can be found in Le Paslier et al. (2000) Construction and characterization of a Schistosoma mansoni bacterial artificial chromosome library. Genomics 65: 87-94."

BASE COUNT 136 a 129 c 117 g 125 t

Query Match 56.6%; Score 266.6; DB 17; Length 507;

Best Local Similarity 81.1%; Pred. No. 5.3e-73;

Matches 385; Conservative 0; Mismatches 54; Indels 36; Gaps 5;

QY 1 ATCGAAGATCCGGCTTCTTCATAAGCTCCACACGAAATGCTTGATTCAGTGTGA-- 57

Db 485 ATCAAGACCTCAGCTCTTCTATAAGTCCACACGAATGCTTGATTCAGTGTGGA 426

QY 58 -----GACGATTGGTCTGTAGCTCAGTGTGGTTAGAGCGCA 93

Db 425 GCGATTGGTGTAGACCCGAGAGTGAGGATTGGGTCTGTAGCTCAGTGTGGTTAGAGCGCA 366

QY 94 CCCTGTATAGGTTGAGTGGCGAGTTCGAATCTGCCAGACCCAGCCACCAATTTGGTGTG 153

Db 365 CCCTGTATAGGTTGAGTGGCGAGTTCGAATCTGCCAGACCCAGCCACCAATTTGGGATG 306

QY 154 CTGCGTATCCGATACGAGGCGCATAGCTCAGCTGGGAGAGCGCCTGCTTTGCACGACGGA 213

Db 305 GCCAGTG---TCAATGGGCGCATAGCTCAGCTGGGAGAGCGCCTGCTTTGCACGACGGA 249

QY 214 GGTGAGAGTTCGATCTCTCTTGGCTCCACCATCTA-AAACAATCGTGAAGCTCAGAA 272

Db 248 GGTGAGAGTTCGATCTCTCTTGGCTCCACCATCTA-AAACAATCGTGAAGCTCAGAA 189

QY 273 ATGAATCTTCGTGATGAACATTTGATTTCTGCTTTTGCACGAGAACTGTTCTTTAAAAA 332

Db 188 ATGAACATTTGCTAGTTCATGTTGATTTCTGCTTTTGCACGAGAACTGTTCTTTAAAAA 129

QY 333 TTGCGGTATGTGATAGTAAGTAAGTGAATGATCTCTTTTCACTGCTGATCAATTCAGTCA 392

Db 128 TTTGGGTATGTGATAGTAAGTGA---CTAACAGCGTGTCTTCACTGACCGTTGTT--AATCA 74

QY 393 AGGTAAATTTGCGAGTTCAGCGCGGAATTTTCGCGGAATCTCGTCTTTCACAGTA 447

Db 73 AGCAAAATTTGCGAGTTCAGCGCGGAATTTTCGCGGAATCTCGTCTTTCACAGTTA 19

## RESULT 2

BH201541/c

LOCUS

DEFINITION

SM1-57P13.TF Sml Schistosoma mansoni genomic clone Sml-57P13, DNA

sequence.

VERSION

BH201541

KEYWORDS

GSS.

SOURCE

Schistosoma mansoni.

ORGANISM

Eukaryota; Metazoa; Platyhelminthes; Trematoda; Digenea;

Strigeidida; Schistosomatidae; Schistosomatidae; Schistosoma.

REFERENCE

Shetty, J., Simpson, A., Malek, J., Koo, H., LoVerde, P.T. and El-Sayed

, N.M.

## TITLE

## JOURNAL

## COMMENT

Use of end sequences from Schistosoma mansoni (Puerto Rico strain) Sml BAC library for gene discovery and map construction

Unpublished (2001)

Other\_GSSs: Sml-57P13.TF

Contact: Najib M. El-Sayed

Department of Eukaryotic Genomics

The Institute for Genomic Research

9712 Medical Center Dr., Rockville, MD 20850, USA

Tel: 301 838 0200

Fax: 301 838 0208

Email: neilsayed@tigr.org

lo.edu).

Seq primer: M13 For

Class: BAC ends.

Location/Qualifiers

1..629

/organism="Schistosoma mansoni"

/strain="Puerto Rico"

/db\_xref="taxon:6183"

/clone="Sml-57P13"

/clone\_lib="Sml"

/note="Vector: pBelOBAC11; Site.1: Hin dIII; Constructed in the laboratory of Dr. Denis Le Paslier at the Fondation Jean Dausset, CEPH, Paris, France. Briefly, Schistosoma mansoni agarose embedded DNA was partially digested with Hin dIII. High molecular weight fragments were ligated in pBelOBAC11 digested with Hin dIII. The average insert size is 100 kb. Total clone coverage: approx. 7.95 x the haploid genome. Further information can be found in Le Paslier et al. (2000) Construction and characterization of a Schistosoma mansoni bacterial artificial chromosome library. Genomics 65: 87-94."

BASE COUNT 157 a 172 c 146 g 154 t

## ORIGIN

Query Match 56.2%; Score 264.8; DB 17; Length 629;

Best Local Similarity 84.1%; Pred. No. 2.3e-72;

Matches 348; Conservative 0; Mismatches 57; Indels 9; Gaps 4;

QY 35 CGAATTCGTTGATTCAGTGGTGTAGAGGATTTGGTCTGTAGCTCAGTTGGTTAGAGCGCAC 94

Db 424 CGATTGGTGTAGACCCGAGAGTGAGGATTTGGTCTGTAGCTCAGTTGGTTAGAGCGCAC 365

QY 95 CCCTGTATAGGTTGAGTGGCGAGTTCGAATCTGCCAGACCCACCAATTTGTTGGTGTGC 154

Db 364 CCCTGTATAGGTTGAGTGGCGAGTTCGAATCTGCCAGACCCACCAATTTGTTGGTGTGC 305

QY 155 TCGGTGATCCGATACGAGGCGCATAGCTCAGCTGGGAGAGCGCCTGCTTTGCACGACGAG 214

Db 304 CCAAGTG---TCAATGGGCGCATAGCTCAGCTGGGAGAGCGCCTGCTTTGCACGACGAG 248

QY 215 GTCAGGAGTTCGATCTCTTGGCTCCACCATCTA-AAACAATCGTGGAAAGCTCAGAAA 273

Db 247 GTCAGGAGTTCGATCTCTTGGCTCCACCATCTA-AAACAATCGTGGAAAGCTCAGAAA 188

QY 274 TGAATCTTCGTGATGAACATTTGATTTCTGCTTCCACAGAACTGTTCTTTAAAAAT 333

Db 187 TGAACATTTGCGAGTTCGATTTGATTTCTGCTTCCACAGAACTGTTCTTTAAAAAT 128

QY 334 TCGGGTATGTAGTAAGTAAGTGAATGATCTCTTCACTGGTGTGATTCATTCAGTCAAA 393

Db 127 TTTGGGTATGTAGTAAGTGA---CTAACAGCGTGTCTTCACTGACCGTTGTT--AATCAA 73

QY 394 GGTAAATTTGCGAGTTCAGCGCGGAATTTTCGCGGAATGTCGCTCTTCACAGTA 447

Db 72 GGCAGAAATTTGCGAGTTCAGCGCGGAATTTTCGCGGAATGTCGCTCTTCACAGTTA 19

## RESULT 3

AQ509640/c

LOCUS

DEFINITION

639 bp DNA linear GSS 04-MAY-1999

nbxb0096P15f CUGI Rice BAC Library Oryza sativa genomic clone

nbxb0096P15f, DNA sequence.

Db	428	CTTTGGCTCCACCATTCCACCCCTGTGTCGATACACGATTGCTTGAAGAGCTCAGAAGT	369
QY	276	AATGTTCCG-TGGATGAACATTGATTTCTGTCTTTTCCACGACAACTGTTCTTTAAAAAT	334
Db	368	AGTGTTCCGTTGCGGAATCCTGACTTCTGGTCTTTG-ATCAGAACATGTTCTTTAAAAAT	310
QY	335	CGGGTATGTGATAGAAGTAGACTGAATGATCTCTTTTCACTGGTGATCAATCAAGTCAAG	394
Db	309	TGGGAAGTGTAGAAGT-AGACACATTTGACTGTTTTCACCTGGCAGCTGATGTCGTCAG	251
QY	395	GTAATAAT-TTGGCAGATTCAAGCGCGAATTTTCGGCG- AATGTGCTCTTCC	443
Db	250	GTAATAATCTTGGCACTCAAGCGCAAGTTTTCGGCGAAATGTCGCTCTTCC	200
RESULT 4			
LOCUS	BE092111	319 bp mRNA linear	EST 12-JUN-2000
DEFINITION	IL2-BF0733-240400-073-G03 BF0733 Homo sapiens cDNA, mRNA sequence.		
ACCESSION	BE092111		
VERSION	BE092111.1	GI:8482563	
KEYWORDS	EST.		
SOURCE	human.		
ORGANISM	Homo sapiens		
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.		
AUTHORS	1 (bases 1 to 319)		
	Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R., Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F., Simpson,D.H., Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H., Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and Simpson,A.J.		
TITLE	Shotgun sequencing of the human transcriptome with ORF expressed sequence tags		
JOURNAL	Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)		
MEDLINE	20202663		
COMMENT	Contact: Simpson A.J.G. Laboratory of Cancer Genetics Ludwig Institute for Cancer Research Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP, Brazil Tel: +55-11-2704922 Fax: +55-11-2707001 Email: asimpson@ludwig.org.br This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL (http://www.ludwig.org.br/scripts/gethtml2.pl?tl=et3-IL2-BF0733-240400-073-G03&t3=2000-04-24&t4=1) Seq primer: puc 18 forward High quality sequence stop: 298. Location/Qualifiers 1. 319 /organism="Homo sapiens" /db_xref="taxon:9606" /clone_lib="BF0733" /dev_stage="Adult" /note="Organ: breast; Vector: puc18; Site1: Sma1; Site2: Sma1; A mini-library was made by cloning products derived from ORESPEs PCR (U.S. Letters Patent application No. 196716 - Ludwig Institute for Cancer Research) profiles into the puc 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."		
FEATURES			
source	73 a 62 c 91 g 93 t		
BASE COUNT			
ORIGIN			
Query Match	25.8%	Score 121.6; DB 10; Length 319;	
Best Local Similarity	85.1%	Pred. No. 2.5e-27;	
Matches 148; Conservative	0; Mismatches 24; Indels 2; Gaps 1;		
QY	78	AGTTGTTAGCGGACCCCTGATAAGGTTGAGTGGCGAGTTCGAATCTGCCAGACC	137

QY	228	TCCTCCTGGCTCCACCA	245	
Db	469	TCCCGTCATCCTCCACCA	452	
RESULT	6			
BH397037/c				
LOCUS				
DEFINITION		712 bp DNA linear GSS 11-DEC-2001		
		AG-ND-137F22.TF.1 ND-TAM Anopheles gambiae genomic clone		
ACCESSION		BH397037		
VERSION		BH397037		
KEYWORDS		BH397037.1 GI:17343253		
SOURCE		GSS.		
ORGANISM		African malaria mosquito.		
		Anopheles gambiae		
		Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;		
		Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea;		
		Anopheles.		
REFERENCE		1 (bases 1 to 712)		
AUTHORS		Shetty,J., Malek,J., Koo,H., Collins,F., Gardner,M. and Loftus,B.J.		
TITLE		Direct Submission of BAC-end sequences from Anopheles gambiae		
JOURNAL		Unpublished (2001)		
COMMENT		Other_GSSs: AG-ND-137F22.TR.1		
		Contact: Brendan J Loftus		
		Department of Eukaryotic Genomics		
		The Institute for Genomic Research		
		9712 Medical Center Dr., Rockville, MD 20850, USA		
		Tel: 301 838 0208		
		Fax: 301 838 3543		
		Email: bilofus@ig.rockefeller.edu		

This clone is from an *A. gambiae* BAC library (ND-TAM) provided by F.H. Collins and sequenced by The Institute for Genomic Research (TIGR). The BAC library was generated from *A. gambiae* PEST strain DNA. All DNA was extracted from newly hatched first instar larvae to minimize the inclusion of DNA from microorganisms that inhabit the gut. The DNA is derived from mixed sexes of larvae. The BAC library was constructed at Texas A&M University BAC Center University, College Station, Texas 77843-2123, USA using a HindIII partial digest.

Seq primer: M13 For  
Class: BAC ends.

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Class: BAC ends.
Location/Qualifiers
1..712
/organism="Anopheles gambiae"
/strain="PEST"
/db_xref="taxon:7165"
/clone="AG-ND-137F22"
/clone_lib="ND-TAM"
/notice="vector: pECBAC1; Site_1: HindIII"
BASE COUNT      168 a 187 c 148 g 209 t

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BASE COUNT
ORIGIN
168 a 187 c 148 g 209 t
/note=vector: pECBAC1; Site_1: HindIII#

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Query Match	15.2%	Score 71.6;	DB 17;
Best Local Similarity	65.1%	Pred. No. 2.8e-11;	
Matches 121; Conservative	0;	Mismatches 64;	Indels 1

QY	61	GATTGGGTCTGTAGCTCAGTGTGGTTAGAGCGCACCCCTGATAGGAGGTGAGGTCGCGCAGTT	120
Db	672	GAAGGGGCTGTAGCTCAGCTCAGCTGTGTTAGAGCACCTGTGTTGATACGACAGGGGCTGTTGGTT	613
QY	121	CGAATCTGCCAGACACCCACCAATTGTTGGTGTGCTCGGTGATCCGATACGGGGCCATAGC	180
Db	612	CGAGGCCCAACTAGACCCACCCAGATTCCTGTTTCGAGGATCCAGGGGGATTAGC	553
QY	181	TCAGCTGGGAGAGCGCGCTGCTT-TGCACACGAGGAGTTCAGGAGTTCGATCCCTCTTGGCT	239
Db	552	TCAGCTGGGAGAGACATGCTTCGCGACACAGGGGGTCTCGGTTTCGATCCCGTCATCCT	493
QY	240	CCACCA	245
Db	492	CCACCA	487

```

RESULT 7
AA680996/c
LOCUS
DEFINITION
  AA680996 619 bp mRNA linear EST 30-DEC-1997
  SW3D9CA514SK Brugia malayi L3 molting-day 9 larva cDNA
  (SAW97MLW-Bml3d9) Brugia malayi cDNA clone SW3D9CA514 5', mRNA
  sequence.
ACCESSION
  AA680996.1 GI:2663001
VERSION
  EST.
KEYWORDS
  Brugia malayi.
ORGANISM
  Brugia malayi
  Eukaryota; Metazoa; Nematoda; Chromadorea; Spirurida; Filarioidea;
  Onchocercidae; Brugia.
REFERENCE
  1 (bases 1 to 619)
  Williams, S.A. and Lizotte-Waniewski, M.
  Genes expressed in day 9 post-infection, third stage larvae of
  Brugia malayi
  Unpublished (1997)
JOURNAL
  Contact: Steven A. Williams
  Molecular Parasitology
  Smith College Department of Biological Sciences
  Department of Biological Sciences Clark Science Center, Smith
  College, Northampton, MA, 01063, USA
  Tel: 4135853826
  Fax: 4135853786
  Email: genome@smith.edu
  Seq primer: pBluescript SK.
  Location/Qualifiers
    1..619
    /organism="Brugia malayi"
    /db_xref="taxon:6279"
    /clone_lib="SW3D9CA514"
    /clone="SW3D9CA514"
    (SAW97MLW-Bml3d9)
    /db_xref="E. coli XLI-Blue MRF."
    /lab_host="third stage larvae, nine days after infection"
    /note="Vector: LambdaZap II (Unizap XR); Site_1: Eco RI
    (5' end); Site_2: Xho I (3' end); Brugia malayi is a
    lymphatic filarial nematode parasite of humans. mRNA was
    prepared from third stage larvae of Brugia malayi
    isolated from the peritoneal cavity of birds nine days
    after infection. The mRNA was converted to double
    stranded cDNA using reverse transcriptase and oligo (dT)
    followed by Knaase H and DNAPol I. The library was
    constructed by Michelle Lizotte-Waniewski. The library is
    available from the Filarial Genome Project Resource
    Center: contact Dr. S.A. Williams, Clark Science Center,
    Smith College, Northampton, MA 01063 USA phone +1 413
    585-3826 fax +1 413 585-3786 email genome@smith.edu"
BASE COUNT 148 a 148 c 121 g 168 t 34 others
ORIGIN
  Query Match 14.9%; Score 70; DB 9; Length 619;
  Best Local Similarity 68.8%; Pred. No. 8.1e-11;
  Matches 130; Conservative 0; Mismatches 43; Indels 16; Gaps 2;

QY 76 TCAGTTGGTTAGAGCGCACCCTGATAGGTTGAGTGGCGAGTTTCAAGTCTGCCAGAC 135
  ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 518 TCAGTTGGTTAGAGCGCACCCTGATAGGTTGAGTGGCGAGTTTCAAGTCTGCCAGC 459
  ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

QY 136 CCACCAATTTGTTGTTGCTGCTGATCCGA-----TACGGGGCCCATAGCT 181
  ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 458 CTACCAAAATTTGCACGGCAAAATTTGAGAGGTTTAACTACATGCTATGGGTTATAGCT 399
  ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

QY 182 CAGCTGGGAGAGCGCTGCTTTGCA--CCGAGAGGTAGGAGTTCGATCCTCCTTGCT 239
  ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 398 CAGCTGGGAGAGCGCTGCTTTGCA--CCGAGAGGTAGGAGTTCGATCCTCCTTGCT 339
  ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

QY 240 CCACCATCT 248
  ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 338 CCACCATCT 330
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RESULT 8
BH771024
LOCUS
DEFINITION
  BH771024 6499 bp DNA linear GSS 01-MAY-2002
  LLMGTAG746 MG1363 Random Sequence Tag Library Lactococcus lactis
  subsp. cremoris genomic, DNA sequence.
ACCESSION
  BH771024.1 GI:20373981
VERSION
  GSS.
KEYWORDS
  Lactococcus lactis subsp. cremoris.
  Lactococcus lactis subsp. cremoris
  Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
  Lactococcus.
REFERENCE
  1 (bases 1 to 6499)
  Bolotin, A., Ehrlich, S.D. and Sorokin, A.
  Studies of genomes of dairy bacteria Lactococcus lactis
  Sci. Aliments, (2002) In press
  Contact: Sorokin A
  Genetique Microbienne
  INRA
  CRJ INRA, Domaine de Vilvert, 78352 Jouy en Josas cedex, France
  Tel: 33 1 34 65 25 16
  Fax: 33 1 34 65 25 21
  Email: sorokine@jouy.inra.fr
  best homologue in strain Il1403 is ywgA (78%)
  Class: shotgun
  High quality sequence start: 30
  High quality sequence stop: 6471.
  Location/Qualifiers
    1..6499
    /organism="Lactococcus lactis subsp. cremoris"
    /strain="MG1363"
    /db_xref="taxon:1359"
    /clone_lib="MG1363 Random Sequence Tag Library"
    /note="Vector: pSGM2; Site_1: SmaI; Library of
    chromosomal fragments of L.lactis strain MG1363 was
    prepared by partial AluI digestion or by sonication."
BASE COUNT 1946 a 1228 c 1683 g 1642 t
ORIGIN
  Query Match 13.5%; Score 63.8; DB 17; Length 6499;
  Best Local Similarity 85.5%; Pred. No. 3.8e-08;
  Matches 71; Conservative 0; Mismatches 12; Indels 0; Gaps 0;

QY 170 GGGGCCATAGCTCAGCTGGGAGAGCGCTGCTTTGCACGAGGAGTTCGAGTTCGATC 229
  ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 2165 GGGGCCATAGCTCAGCTGGGAGAGCGCTGCTTTGCACGAGGAGTTCGAGTTCGATC 2224
  ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

QY 230 CTCCTTGGCTCCACCATCTAAA 252
  ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 2225 CCGCTAGGCTCCATTTGCAGACA 247
  ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

RESULT 9
BH819575
LOCUS
DEFINITION
  BH819575 577 bp DNA linear GSS 20-MAY-2002
  BACP13-E14.y Pristionchus pacificus BAC ends Pristionchus
  pacificus genomic, DNA sequence.
ACCESSION
  BH819575
VERSION
  BH819575.1 GI:20993843
KEYWORDS
  GSS.
  Pristionchus pacificus.
  Pristionchus pacificus
  Pristionchus pacificus
  Eukaryota; Metazoa; Nematoda; Chromadorea; Diplogasterida;
  Neodiplogasteridae; Pristionchus.
REFERENCE
  1 (bases 1 to 577)
  Srinivasan, J., Sinz, W., Lanz, C., Brand, A., Nandakumar, R., Raddatz
  G., Witte, H., Keller, H., Pires da Silva, A., Jesse, T.,
  Millare, J., de Both, M., Schuster, S.C. and Sommer, R.J.
  A BAC-based genetic linkage map of the nematode Pristionchus
  pacificus
  Unpublished (2002)
  Contact: Sommer RJ
  Evolutionary Biology

```

Max-Planck-Institute for Developmental Biology  
 Spemannstr. 37-39, Tuebingen D-72076, Germany  
 Tel: 00497071601371  
 Fax: 00497071601498  
 Email: ralf.sommer@tuebingen.mpg.de  
 Class: BAC ends.

## FEATURES

source

Location/Qualifiers  
 1. .577

/organism="Pristionchus pacificus"  
 /strain="var. California"  
 /db\_xref="taxon:54126"

/clone\_lib="Pristionchus pacificus BAC ends"  
 129 a 142 c 139 g 167 t

BASE COUNT

ORIGIN

Query Match 13.4%; Score 63.2; DB 17; Length 577;  
 Best Local Similarity 66.1%; Pred. No. 1.1e-08;  
 Matches 127; Conservative 0; Mismatches 53; Indels 12; Gaps 2;

QY 65 GGTCTGTAGCTCAGTTGGTTAGAGCGCACCCCTGTAAGGTTGAGGTGAGGTGCGGAGTTTCGAA 124  
 Db 4 GGGCTATAGCTCAGCTGG-GAGAGCGCTTGCATGCATGCAAGAGGTGCGGTTTCGAT 62

QY 125 TCTGCCAGACGACCAATTTGTG-----GTGTCCTCGTGATCGGTAACGCATCGTGGG 173  
 Db 63 CCGCTTAGCTCCACCAATTTTGACCCAGCAACTTGGTAGCTAAACGCATCGTGGG 122

QY 174 CCATAGCTCAGCTGGAGAGCGCTGTTTGCACGAGGAGTTCGATCGATCCCTCC 233  
 Db 123 CTATAGCTCAGCTGGAGAGCGCTTGCATGCATGCAAGAGGTGCGGTTTCGATCCCGC 182

QY 234 TTGGCTCCACCA 245  
 Db 183 TTAGCTCCACCA 194

## RESULT 10

BH400944/c

LOCUS

DEFINITION AG-ND-158022.TF ND-TAM Anopheles gambiae genomic clone AG-ND-158022

ACCESSION

BH400944

VERSION

BH400944.1 GI:17347147

KEYWORDS

GSS.

SOURCE

African malaria mosquito.

ORGANISM

Anopheles gambiae

REFERENCE

1 (bases 1 to 593)

AUTHORS

Shetty,J., Malek,J., Koo,H., Collins,F., Gardner,M. and Loftus,B.J.

TITLE

Direct Submission of BAC-end sequences from Anopheles gambiae

JOURNAL

Unpublished (2001)

COMMENT

Other\_GSSs: AG-ND-158022.TF

Contact: Brendan J Loftus

Department of Eukaryotic Genomics

The Institute for Genomic Research

9712 Medical Center Dr., Rockville, MD 20850, USA

Tel: 301 838 0208

Fax: 301 838 3543

Email: bjlloftus@tigr.org

This clone is from an A. gambiae BAC library (ND-TAM) provided by

F.H. Collins and sequenced by The Institute for Genomic Research

(TIGR). The BAC library was generated from A. gambiae PEST strain

DNA. All DNA was extracted from newly hatched first instar larvae

to minimize the inclusion of DNA from microorganisms that inhabit

the gut. The DNA is derived from mixed sexes of larvae. The BAC

library was constructed at Texas A&amp;M University BAC Center

partial digest.

Seq primer: M13 For

Class: BAC ends.

## FEATURES

Location/Qualifiers

1. .577

/organism="Pristionchus pacificus"

/strain="var. California"

/db\_xref="taxon:54126"

/clone\_lib="Pristionchus pacificus BAC ends"

129 a 142 c 139 g 167 t

source

1. .593  
 /organism="Anopheles gambiae"  
 /strain="PEST"  
 /db\_xref="taxon:7165"  
 /clone="AG-ND-158022"  
 /clone\_lib="ND-TAM"  
 /note="Vector: pECBAC1; Site\_1: HindIII"  
 119 a 157 c 118 g 199 t

BASE COUNT

ORIGIN

Query Match 13.4%; Score 63; DB 17; Length 593;  
 Best Local Similarity 69.3%; Pred. No. 1.3e-08;  
 Matches 124; Conservative 0; Mismatches 35; Indels 20; Gaps 2;

QY 71 GTAGCTCAGTTGGTTAGAGCGCACCCCTGTAAGGTTGAGGTGCGGAGTTTCGATCTGCC 130  
 Db 574 GTAGCTCAGCTGGTTAGAGCGCTACACTGATATGATAGAGTTCGAGCTGCC 515

QY 131 CAGACCCACCAATTTGTTGTCGTCGATCCGATACGGGCCATAGCTAGCTGGG- 189  
 Db 514 CGAGCTACTAATTA-----AAAAGGGGAATAGCTCAGCTGGCT 474

QY 190 AGAGCGCCTGCTTTCACGCGAGGAGTTCAGAGTTCGATCTCTTGGTCCACCATCT 248  
 Db 473 AGAGCGCCTGCTTTCACGCGAGGAGTTCAGAGTTCGATCTCTTGGTCCACCATCT 415

## RESULT 11

BH393190/c

LOCUS

DEFINITION AG-ND-168H12.TR ND-TAM Anopheles gambiae genomic clone AG-ND-168H12

ACCESSION

BH393190

VERSION

BH393190.1 GI:17339331

KEYWORDS

GSS.

SOURCE

African malaria mosquito.

ORGANISM

Anopheles gambiae

REFERENCE

1 (bases 1 to 760)

AUTHORS

Shetty,J., Malek,J., Koo,H., Collins,F., Gardner,M. and Loftus,B.J.

TITLE

Direct Submission of BAC-end sequences from Anopheles gambiae

JOURNAL

Unpublished (2001)

COMMENT

Other\_GSSs: AG-ND-168H12.TF

Contact: Brendan J Loftus

Department of Eukaryotic Genomics

The Institute for Genomic Research

9712 Medical Center Dr., Rockville, MD 20850, USA

Tel: 301 838 0208

Fax: 301 838 3543

Email: bjlloftus@tigr.org

This clone is from an A. gambiae BAC library (ND-TAM) provided by

F.H. Collins and sequenced by The Institute for Genomic Research

(TIGR). The BAC library was generated from A. gambiae PEST strain

DNA. All DNA was extracted from newly hatched first instar larvae

to minimize the inclusion of DNA from microorganisms that inhabit

the gut. The DNA is derived from mixed sexes of larvae. The BAC

library was constructed at Texas A&amp;M University BAC Center

partial digest.

Seq primer: M13 Rev

Class: BAC ends.

## FEATURES

source

Location/Qualifiers

1. .760

/organism="Anopheles gambiae"

/strain="PEST"

/db\_xref="taxon:7165"

/clone="AG-ND-168H12"

/clone\_lib="ND-TAM"

/note="Vector: pECBAC1; Site\_1: HindIII"

BASE COUNT

ORIGIN

171 a 187 c 139 g 263 t





Db 285 TCCAGGATAGCCACCATGAATA-----AAGGGGTATAGCTCAG 324  
 Qy 185 CTGGAGAGCGCTCTTTGACGAGGAGGTTCAGAGTTCAGTCTCTCTGGCTCCACC 244  
 Db 325 CTGGTAGAGCGCTGCTTTGCAAGGAGGATGTCAGCGGTTCAAATCCGCTTATCTCCAAG 384  
 Qy 245 ATCTAAAA 252  
 Db 385 TTAAAAA 392

RESULT 14  
 BI544155  
 LOCUS  
 DEFINITION S129 Gracilaria lemaneiformis gametophyte cDNA library Gracilaria lemaneiformis cDNA 5', mRNA sequence.  
 ACCESSION BI544155  
 VERSION BI544155.1 GI:19033837  
 KEYWORDS EST.  
 SOURCE Gracilaria lemaneiformis.  
 ORGANISM Gracilaria lemaneiformis.  
 Eukaryota; Rhodophyta; Florideophyceae; Gracilariiales; Gracilariaceae; Gracilaria.  
 REFERENCE 1 (bases 1 to 548)  
 AUTHORS Sun, X., Yang, G.P., Mao, Y.X. and Zhang, X.C.  
 TITLE Analysis of expressed sequence tags of a marine red alga, Gracilaria lemaneiformis  
 JOURNAL Unpublished (2001)  
 COMMENT Contact: Sun, X.; Zhang, X. C.  
 College of Marine Life Sciences  
 Ocean University of Qingdao  
 Yushan Road 5, Qingdao, 266003, Shandong, China  
 Tel: +86-0532-2032789  
 Fax: +86-0532-2032276  
 Email: xc Zhang@ouqd.edu.cn  
 PCR PRIMERS  
 FORWARD: 5' -CGTGATACCATGGTCTAGAGT-3'  
 BACKWARD: 5' -CTGATCTAGACCTGCAGGCTC-3'  
 Seq primer: 5' -CGTGATACCATGGTCTAGAGT-3'  
 POLYA=Yes.

FEATURES  
 source  
 1..548  
 Location/Qualifiers  
 /organism="Gracilaria lemaneiformis"  
 /db\_xref="taxon:2778"  
 /clone\_lib="Gracilaria lemaneiformis gametophyte cDNA library"  
 /tissue\_type="gametophyte thalli"  
 /note="Vector: pMD 18-T; site:1; EcoR V with a T hang; Wild type Gracilaria lemaneiformis were harvested from Zhanshan Bay, Qingdao (China). After rinsed with boiled seawater, younger thalli was cut and washed every 3-4 days until 1 month. Then thalli was cultivated in Provasoli medium. Total RNA was isolated from thalli of gametophyte algae, using UNIQ-10 Trizol Total RNA Preparation Kit (Sangon Inc., Shanghai, China). The cDNA was synthesized, amplified and cloned using cDNA Synthesis Kit, cDNA PCR Library Kit and pMD 18-T vector (Takara Biotechnology Co., Ltd., Dalian, China), respectively."  
 BASE COUNT 183 a 92 c 107 g 166 t  
 ORIGIN

Query Match 12.7%; Score 59.6; DB 13; Length 548;  
 Best Local Similarity 63.3%; Pred. No. 1.4e-07;  
 Matches 119; Conservative 0; Mismatches 49; Indels 20; Gaps 1;  
 Qy 65 GGGCTGTAGCTCAGTTGGTTAGCGCACCCCTGATAGGCTGAGGTGGGAGTTCGAA 124  
 Db 81 GGGCTATTAGCTCAGTTGGTTAGCGCACCCCTGATAGGCTGAGGTGGGAGTTCGAA 140  
 Qy 125 TCTGCCAGAGCCACCAATTTGTTGTTGCTGCTGATCCGATACGGGGCCATAGCTCAG 184

Db 141 TCCAGGATAGCCACCATGAATA-----AAGGGGTATAGCTCAG 180  
 Qy 185 CTGGAGAGCGCTCTTTGACGAGGAGGTTCAGAGTTCAGTCTCTCTGGCTCCACC 244  
 Db 181 CTGGTAGAGCGCTGCTTTGCAAGGAGGATGTCAGCGGTTCAAATCCGCTTATCTCCAAG 240  
 Qy 245 ATCTAAAA 252  
 Db 241 TTAAAAA 248

RESULT 15  
 BH614410  
 LOCUS  
 DEFINITION IC22A62 Subclones from overlapping BAC clones spanning the hrp cluster of Erwinia carotovora subsp. atroseptica Pectobacterium carotovorum subsp. atrosepticum genomic, DNA sequence.  
 ACCESSION BH614410  
 VERSION BH614410.1 GI:18078210  
 KEYWORDS GSS.  
 SOURCE Pectobacterium carotovorum subsp. atrosepticum.  
 ORGANISM Pectobacterium carotovorum subsp. atrosepticum.  
 Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae; Pectobacterium.  
 REFERENCE 1 (bases 1 to 287)  
 AUTHORS Bell, K.S., Avrova, A.O., Holeva, M.C., Cardle, L., Morris, W., De Jong, W., Toth, I.K., Waugh, R., Bryan, G.J. and Birch, P.R.J.  
 TITLE Sample sequencing of a selected region of the genome of Erwinia carotovora subsp. atroseptica reveal candidate phytopathogenicity genes and allows comparison with Escherichia coli  
 JOURNAL Unpublished (2002)  
 COMMENT Contact: Bell KS  
 Scottish Crop Research Institute  
 Invergowrie, Dundee, United Kingdom, DD2 5DA  
 Email: kbell@scri.sari.ac.uk  
 Class: BAC subclone.

FEATURES  
 source  
 1..287  
 Location/Qualifiers  
 /organism="Pectobacterium carotovorum subsp. atrosepticum"  
 /strain="SCRI039"  
 /db\_xref="taxon:29471"  
 /clone\_lib="Subclones from overlapping BAC clones spanning the hrp cluster of Erwinia carotovora subsp. atroseptica"  
 /note="Vector: pGEM 3zf; DNA from BAC clones Eca2B8 and Eca1C22 was nebulised and cloned into pGEM 3zf and sequenced with SP6 or T7 primers."  
 BASE COUNT 74 a 62 c 78 g 73 t  
 ORIGIN

Query Match 12.4%; Score 58.6; DB 17; Length 287;  
 Best Local Similarity 82.7%; Pred. No. 1.9e-07;  
 Matches 67; Conservative 0; Mismatches 14; Indels 0; Gaps 0;  
 Qy 66 GGCTCTAGCTCAGTTGGTTAGAGCGCACCCCTGATAGGCTGAGGTGGGAGTTCGAAT 125  
 Db 174 GGCTTGTAGCTCAGTTGGTTAGAGCGCACCCCTGATAGGCTGAGGTGGGAGTTCGAAT 233  
 Qy 126 CTGCCAGAGCCACCAATTTGT 146  
 Db 234 CCACTCAGGCTTACCAATTT 254

Search completed: February 1, 2003, 04:21:48  
 Job time : 886.868 secs



GenCore version 5.1.3  
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OM nucleic - nucleic search, using sw model

Run on: February 1, 2003, 01:06:21 ; Search time 1070.63 Seconds  
(without alignments)  
14135.156 Million cell updates/sec

Title: US-09-931-486-112

Perfect score: 520

Sequence: 1 ATCGAAGACATCAGCTCTT.....CAGATTCCTGGGGTTATAT 520

Scoring table: IDENTITY\_NUC

Gapop 10.0 , Gapext 1.0

Searched: 2054640 seqs, 14551402878 residues

Total number of hits satisfying chosen parameters: 4109280

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

GenEmbl.\*

1: gb\_ba.\*

2: gb\_hgt.\*

3: gb\_in.\*

4: gb\_om.\*

5: gb\_ov.\*

6: gb\_pat.\*

7: gb\_ph.\*

8: gb\_pl.\*

9: gb\_pr.\*

10: gb\_ro.\*

11: gb\_sts.\*

12: gb\_sy.\*

13: gb\_un.\*

14: gb\_vi.\*

15: em\_ba.\*

16: em\_fun.\*

17: em\_hum.\*

18: em\_in.\*

19: em\_mu.\*

20: em\_om.\*

21: em\_or.\*

22: em\_ov.\*

23: em\_pat.\*

24: em\_ph.\*

25: em\_pi.\*

26: em\_ro.\*

27: em\_sts.\*

28: em\_un.\*

29: em\_vi.\*

30: em\_hgt\_hum.\*

31: em\_hgt\_inv.\*

32: em\_hgt\_other.\*

33: em\_hgt\_mus.\*

34: em\_hgt\_pln.\*

35: em\_hgt\_rod.\*

36: em\_hgt\_mam.\*

37: em\_hgt\_vrt.\*

38: em\_sy.\*

39: em\_hgt\_hum.\*

40: em\_hgt\_mus.\*

41: em\_hgt\_other.\*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Match %	Length	DB	ID	Description
1	520	100.0	520	6	A48045	A48045 Sequence 11
2	520	100.0	520	6	AR177090	AR177090 Sequence
3	520	100.0	520	6	AX191053	AX191053 Sequence
4	438.2	84.3	707	1	PSEDFO	L28162 Pseudomonas
5	397	76.3	587	1	PSED29245	AJ279245 Pseudomonas
6	396.4	76.2	705	1	PSEDEF	L28160 Pseudomonas
7	393.2	75.6	705	1	PSEDEF	L28161 Pseudomonas
8	351.2	67.5	702	1	PSEDEF	L28159 Pseudomonas
9	278.2	53.5	616	1	AF422492	AF422492 Unculture
10	258.4	49.7	528	1	PST390589	AJ390589 Pseudomon
11	258	49.6	528	1	PST251905	AJ251905 Pseudomon
12	252.4	48.5	529	1	PST251904	AJ251904 Pseudomon
13	252.4	48.5	529	1	PST390587	AJ390587 Pseudomon
14	249	47.9	504	6	A48046	A48046 Sequence 11
15	249	47.9	504	6	AR177091	AR177091 Sequence
16	249	47.9	504	6	AX191054	AX191054 Sequence
17	249	47.9	505	1	PST251910	AJ251910 Pseudomon
18	248.8	47.8	528	1	PST251903	AJ251903 Pseudomon
19	248.6	47.8	505	1	PST390585	AJ390585 Pseudomon
20	247.4	47.6	505	1	PST390584	AJ390584 Pseudomon
21	246.6	47.4	505	1	PST390582	AJ390582 Pseudomon
22	245.8	47.3	505	1	PST390583	AJ390583 Pseudomon
23	242.6	46.7	505	1	PST251900	AJ251900 Pseudomon
24	241.2	46.4	506	1	PST390588	AJ390588 Pseudomon
25	238.2	45.8	530	1	PST251906	AJ251906 Pseudomon
26	238.2	45.8	530	1	PST251907	AJ251907 Pseudomon
27	238	45.8	530	1	PST251908	AJ251908 Pseudomon
28	235.2	45.2	560	1	AF356514	AF356514 Pseudomon
29	224.4	43.2	529	1	PST251901	AJ251901 Pseudomon
30	224.4	43.2	529	1	PST251902	AJ251902 Pseudomon
31	222	42.7	529	1	PST390590	AJ390590 Pseudomon
32	219.8	42.3	477	1	PST390586	AJ390586 Pseudomon
33	219.8	42.3	523	1	PST390581	AJ390581 Pseudomon
34	218.2	42.0	477	1	PST251909	AJ251909 Pseudomon
35	209.4	40.3	5785	1	PSU65012	U65012 Pseudomonas
36	207.6	39.9	527	1	AF127584	AF127584 Pseudomon
37	207	39.8	521	1	AF364306	AF364306 Pseudomon
38	207	39.8	521	1	AF364307	AF364307 Pseudomon
39	205.8	39.6	526	1	AF127583	AF127583 Pseudomon
40	200.8	38.6	584	1	AF197570	AF197570 Alcanivor
41	200.8	38.6	584	1	AF197571	AF197571 Alcanivor
42	200.2	38.5	567	1	PSEGRDAA	L06304 Pseudomonas
43	200.2	38.5	567	1	PSEGRDAA	L06306 Pseudomonas
44	198	38.1	523	1	AF364308	AF364308 Pseudomon
45	197.6	38.0	5679	1	AF134704	AF134704 Pseudomon

#### ALIGNMENTS

RESULT 1  
A48045  
LOCUS A48045 Sequence 112 from Patent WO9600298.  
DEFINITION A48045  
ACCESSION A48045  
VERSION A48045.1 GI:2301907  
KEYWORDS  
SOURCE  
ORGANISM  
unidentified.  
unclassified.  
REFERENCE 1 (bases 1 to 520)  
AUTHORS  
TITLE  
Jannes G., Rossau R. and Van H.H.  
EUBACTERIAL TAXA USING A HYBRIDIZATION ASSAY  
PATENT: WO 9600298-A 112 04-JAN-1996;  
JOURNAL

linear PAT 07-MAR-1997

INNOGENETICS NV (BE)  
Other publication AU 2924695 960119.  
Location/Qualifiers  
1. .520

BASE COUNT	126 a	109 c	134 g	151 t
ORIGIN				

```
Query Match      100.0%; Score 520; DB 6; Length 520;
Best Local Similarity 100.0%; Pred. No. 6.4e-120;
Matches 520: Conservative 0; Mismatches 0; Indels
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Qy	1	ATGGAAGACATCAGCTCTTCATCAAGTATCCACACAAATGCTTGATTCATAGTCGAAGC	60
Db	1	ATCGAAGACATCAGCTCTTCATCAAGTATCCACACAAATGCTTGATTCATAGTCGAAGC	60
Qy	61	AANTGCTTAACGGCAGCCGGTGTATAGTCTGTAGCTCAGTTGGTTPAGAGCGCACCCCTG	120
Db	61	AANTGCTTAACGGCAGCCGGTGTATAGTCTGTAGCTCAGTTGGTTPAGAGCGCACCCCTG	120
Qy	121	ATRAGGGTGAGGTGGCGAGTTCAAAATCTGCCAGACCTACCAATTCCTTTGGTTCGAGAAGA	180
Db	121	ATRAGGGTGAGGTGGCGAGTTCAAAATCTGCCAGACCTACCAATTCCTTTGGTTCGAGAAGA	180
Qy	181	ATACGGGGCCATAGCTCAGCTGGGAGAGCGCCTTGCCACGACGAGGTGACGCGGTC	240
Db	181	ATACGGGGCCATAGCTCAGCTGGGAGAGCGCCTTGCCACGACGAGGTGACGCGGTC	240
Qy	241	GATCCCGCTTGGCTCCACCACTCTCTCGTGTTCGGGTGAGTGTTAAAGAGTTCAGAAAATG	300
Db	241	GATCCCGCTTGGCTCCACCACTCTCTCGTGTTCGGGTGAGTGTTAAAGAGTTCAGAAAATG	300
Qy	301	ATGCCGCTTCAGGTTTGCTCGTGTGAGTGCTGATTTCTGGTCTTTTACCGGTACGAAA	360
Db	301	ATGCCGCTTCAGGTTTGCTCGTGTGAGTGCTGATTTCTGGTCTTTTACCGGTACGAAA	360
Qy	361	TCGTTCTTTAAAAATTTGGATGTGATAGAAGTGACTGATTAATTCCTTCACTCGCAA	420
Db	361	TCGTTCTTTAAAAATTTGGATGTGATAGAAGTGACTGATTAATTCCTTCACTCGCAA	420
Qy	421	TTGATCTGGTCAAGGTAAAAATTTGTAGTCTCAGACGCCAAATTTTCGGCGATATGTCGTC	480
Db	421	TTGATCTGGTCAAGGTAAAAATTTGTAGTCTCAGACGCCAAATTTTCGGCGATATGTCGTC	480
Qy	481	TTCAAGATTGAGACAGTAAACCAAGATTGCTTTGGGGTTATAT	520
Db	481	TTCAAGATTGAGACAGTAAACCAAGATTGCTTTGGGGTTATAT	520

RESULT 2				
AR177090	LOCUS	AR177090	520 bp	DNA
	DEFINITION	Sequence 112 from patent US 6312903.		linear
				PAT 17-DEC-2001

REFERENCE  
1 (bases 1 to 520)  
AUTHORS  
Jannes, G., Rossau, R. and Van Hooverswyn, H.  
TITLE  
Simultaneous detection, identification and differentiation of  
eubacterial taxa using a hybridization assay  
JOURNAL  
Patent: US 6312903-A 112 06-NOV-2001:

BASE COUNT	126 a	109 c	134 g	151 t
ORIGIN				

Query Match	100.0%;	Score 520;	DB 6;	Length 520;
Best Local Similarity	100.0%;	Pred. No. 6.4e-120;		

	Matches	Conservative	Mismatches	Indels	Gaps	
Qy	1	ATCGAAGACATCAGCTCTTCATAAGTATCCACACGAATTGCTTGATTCATATCGAACG	60			
Db	1	ATCGAAGACATCAGCTCTTCATAAGTATCCACACGAATTGCTTGATTCATATCGAACG	60			
Qy	61	AATGCTCTAAAGCGACCCGGTGTATAGTCTGTAGCTCAGTTGGTTAGAGCGCACCCCTG	120			
Db	61	AATGCTCTAAAGCGACCCGGTGTATAGTCTGTAGCTCAGTTGGTTAGAGCGCACCCCTG	120			
Qy	121	ATAAGGGTGAGGTCGGCAGTTCAAATCTGCCAGACCTACCAATTGCTTGGTCAGAGA	180			
Db	121	ATAAGGGTGAGGTCGGCAGTTCAAATCTGCCAGACCTACCAATTGCTTGGTCAGAGA	180			
Qy	181	ATACGGGGCCATAGCTCAGCTGGAGAGCGCTGCCCTTGACGACGAGGTCACGGGTTTC	240			
Db	181	ATACGGGGCCATAGCTCAGCTGGAGAGCGCTGCCCTTGACGACGAGGTCACGGGTTTC	240			
Qy	241	GATCCCGCTTGGCTCCACCACTCTCTCGTGTGGGTGAGTGTAAAGAGTTCAGAATG	300			
Db	241	GATCCCGCTTGGCTCCACCACTCTCTCGTGTGGGTGAGTGTAAAGAGTTCAGAATG	300			
Qy	301	ATGCGCGTTCAGGTTGTGCCCTGTGAGTGTGATTTCTGGCTTTTGGACCGGTACGAAA	360			
Db	301	ATGCGCGTTCAGGTTGTGCCCTGTGAGTGTGATTTCTGGCTTTTGGACCGGTACGAAA	360			
Qy	361	TCGTTCTTTAAAAATTTGGATATCGATAGAAGTGACTGATTAATTCGTTTCACTGGCAA	420			
Db	361	TCGTTCTTTAAAAATTTGGATATCGATAGAAGTGACTGATTAATTCGTTTCACTGGCAA	420			
Qy	421	TTGATCTGGTCAAGGTAAATTTCTAGTTCACAGACGCAATTTCTGGCGCAATGTCGTC	480			
Db	421	TTGATCTGGTCAAGGTAAATTTCTAGTTCACAGACGCAATTTCTGGCGCAATGTCGTC	480			
Qy	481	TTACAGATTGAGACAGTAACACAGATTGCTTGGGGTTATAT	520			
Db	481	TTACAGATTGAGACAGTAACACAGATTGCTTGGGGTTATAT	520			

AX191053	AX191053	520 bp	DNA	linear	PAT 10-AUG-2001
LOCUS					
DEFINITION	Sequence	112 from Patent	EP1091004.		
ACCESSION	AX191053				
VERSION	AX191053.1	GI:15149698			

REFERENCE	1 (bases 1 to 520)
AUTHORS	JAMES, G., ROSSAU, R. and van Heuverswyn, H.
TITLE	Simultaneous detection, identification and differentiation of eubacterial taxa using a hybridization assay
JOURNAL	Patent: EP 1091004-A 112 11-APR-2001;

BASE COUNT	126 a	109 c	134 g	151 t
ORIGIN				

Query Match	100.0%	Score 520;	DB 6;	Length 520;
Best Local Similarity	100.0%	Pred. No. 6.4e-120;		
Matches 520;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;

Accession	Sequence	Length
QY	1 ATCGAAGACATCAGCTTCTTCATATAGTATCCACACGAATTCGTTGATTCATAGTCGAACG	60
DB	1 ATCGAAGACATCAGCTTCTTCATATAGTATCCACACGAATTCGTTGATTCATAGTCGAACG	60
QY	61 AATGCTGTAAGCGACCGCGTGTATTAGTCTGTAGCTCAGTTGGTTAGAGCGCACCCCTTG	120
DB	61 AATGCTGTAAGCGACCGCGTGTATTAGTCTGTAGCTCAGTTGGTTAGAGCGCACCCCTTG	120



## FEATURES

source 1. .587  
 misc\_feature 1. .587  
 gene 95. .171  
 tRNA 95. .171  
 gene 195. .269  
 tRNA 195. .269  
 BASE COUNT 146 a 120 c 149 g 172 t  
 ORIGIN  
 Query Match 76.3%; Score 397; DB 1; Length 587;  
 Best Local Similarity 87.3%; Pred. No. 4.7e-89;  
 Matches 507; Conservative 0; Mismatches 10; Indels 64; Gaps 4;  
 QY 1 ATCGAGACATCAGCTTCTTCATAGTATCCACAGCAATGCTGTGATTCATAGTCGAA-C 59  
 Db 10 ATCGAGACATCAGCTTCTTCATAGTATCCACAGCAATGCTGTGATTCATAGTCGAA 69  
 QY 60 GAATGCTGAACGCGACCGCTGTATAGTCTGTAGTCTAGTGTAGAGCGCACCCCT 119  
 Db 70 CGATGCTGAACGCGACCGCTGTATAGTCTGTAGTCTAGTGTAGAGCGCACCCCT 128  
 QY 120 GATAAGGTGAGGTGGCGAGTTCAAATCTGCCAGACCTACCAATGCTTGTGTCGAGAG 179  
 Db 129 GATAAGGTGAGGTGGCGAGTTCAAATCTGCCAGACCTACCAATGCTTGTGTCGAGAG 188  
 QY 180 AATACGGGGCCATAGCTCAGCTGGGAGAGCGCTCCCTTGCACGAGAGTTCAGCGGT 239  
 Db 189 AATACGGGGCCATAGCTCAGCTGGGAGAGCGCTCCCTTGCACGAGAGTTCAGCGGT 248  
 QY 240 CGATCCCGCTTGGCTCCACCACTCTCTCGTGTGGGTGAGTGTAAAGAGTTCAGAA 299  
 Db 249 CGATCCCGCTTGGCTCCACCACTCTCTCGTGTGGGTGAGTGTAAAGAGTTCAGAA 308  
 QY 300 GATGCGGCTTCAGGTTTCTCTGTGAGTGC----- 330  
 Db 309 GA--GCATTCAGGTTTCTCTGTGAGTGTAAAGAGTTCAGAA 366  
 QY 331 -----TGATTTCTGCTCTTTGACCGGTACGAA 359  
 Db 367 ATAGACGGGACCTCTTCTACTGGTGTGATTTCTGCTCTTTGACCGGTACGAA 426  
 QY 360 ATCGTTCTTAAAGTTGGATATGTGATAGAGTACTGATTAATGCTTTCACTGSCA 419  
 Db 427 ATCGTTCTTAAAGTTGGATATGTGATAGAGTACTGATTAATGCTTTCACTGSCA 486  
 QY 420 ATTGATCTGTCAAGTAAATTTGATGTTCTCAAGACGCAAAATTTTCGGCGAATGCGT 479  
 Db 487 ATTGATCTGTCAAGTAAATTTGATGTTCTCAAGACGCAAAATTTTCGGCGAATGCGT 546  
 QY 480 CTTACGATTGAGACGATACCAAGATTGCTTGGGTTTATAT 520  
 Db 547 CTTACGATTGAGACGATACCAAGATTGCTTGGGTTTATAT 587

## RESULT 6

PSDFM Pseudomonas mendocina 705 bp DNA linear BCT 04-DEC-1995  
 LOCUS  
 DEFINITION

## ACCESSION

VERSION L28160.1 GI:453550

## KEYWORDS

16S ribosomal RNA; 23S ribosomal RNA; tRNA; transfer RNA.

## SOURCE

Pseudomonas mendocina (tissue library: ATCC 25411) DNA.

## ORGANISM

Bacteria; Proteobacteria; gamma subdivision; Pseudomonadaceae;

## REFERENCE

1. (bases 1 to 705)

## AUTHORS

Tyler, S.D., Strathdee, C.A., Rozee, K.R. and Johnson, W.M.

## TITLE

Oligonucleotide primers designed to differentiate pathogenic

## JOURNAL

Pseudomonas on the basis of the sequencing of genes coding for

## MEDLINE

16S-23S rRNA internal transcribed spacers

## PUBMED

Clin. Diagn. Lab. Immunol. 2 (4), 448-453 (1995)

## FEATURES

7583922

## Source

Location/Qualifiers

## gene

1. .705

## rRNA

/organism="Pseudomonas mendocina"

## tRNA

/db\_xref="taxon:300"

## tRNA

/tissue\_lib="ATCC 25411"

## gene

1. .142

## rRNA

/gene="16S rRNA"

## tRNA

<1. .142

## tRNA

/gene="16S rRNA"

## gene

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## rRNA

/note="putative"

## tRNA

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## tRNA

/product="tRNA-Ile"

## gene

/note="codon recognized: AUC; putative"

## rRNA

/anticodon=(pos:262. .264,aa:Ile)

## tRNA

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## tRNA

/product="tRNA-Ala"

## gene

/note="codon recognized: GCA; putative"

## rRNA

/anticodon=(pos:358. .360,aa:Ala)

## tRNA

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## tRNA

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## tRNA

/note="putative"

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Matches 496; Conservative 0; Mismatches 16; Indels 10; Gaps 8;

QY 1 ATCGAGACATCAGCTTCTTCATAGTATCCACAGCAATGCTGTGATTCATAGTCGAA-C 59

Db 143 ATCGAGACATCAGCTTCTTCATAGTATCCACAGCAATGCTGTGATTCATAGTCGAA 202

QY 60 GAATGCTGAACGCGACCGCTGTATAGTCTGTAGTCTAGTGTAGAGCGCACCCCT 119

Db 203 CCATGCTGTACGCGACCGCTGTATAGTCTGTAGTCTAGTGTAGAGCGCACCCCT 261

QY 120 GATAAGGTGAGGTGGCGAGTTCAAATCTGCCAGACCTACCAATGCTTGTGTCGAGAG 179

Db 262 GATAA-GGTGAGGTGGCGAGTTCAAATCTGCCAGACCTACCAATGCTTGTGTCGAGAG 320

QY 180 AATACGGGGCCATAGCTCAGCTGGGAGAGCGCTTGCCTTGCACGAGAGTTCAGCGGT 239

Db 321 ATTAC-GGGCCATAGCTCAGCTGGGAGAGCGCTTGCCTTGCACGAGAGTTCAGCGGT 379

QY 240 CGATCCCGCTTGGCTCCACCACTCTCT-CGTGTTGCGGTGAGTGTAAAGAGTTCAGAA 298

Db 380 CGATCCCGCTTGGCTCCACCACTCTCTACGTTGTCGGGTGA--GTTAAGAGTTCAGAA 437

QY 299 TGATGCGGCTTCAAGTTGTCCTGTTGAGTGTGCTGCTGTTGACCGGTACGAA 358

Db 438 TGA--GGCTTTCAGGGTAAGCGCTGGCGAGTGTGCTGCTGTTGACCGGTGA-GAA 494

Db	262	GATAA--GGTGGAGTCGGCAGTTCAAATCTGCCAGACCTTACCAATTCGTTGGTGCGAGAAG	320
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Db	321	ATTAC--GGGCGCATAGCTCCGCTGGGAGAGCGCCTGCTTGCACGCAGGAGGTTCAGCGGTT	379
Qy	240	CGATCCCGCTTGGGCTCCACCACCTCTCT--CGTGTTCGGGTGAGTGTAAAGAGTTCAGAA	298
Db	380	CGATCCCGATTGGGCTCCACCACCTCTCTACGTGTTCGGGTGA--GTTAAAGAGTTCAGAA	437
Qy	299	TGATGCCGCTTCAGGTTTTCCTGTTGAGTGCTGATTTCTGCTCTTTGACCGGTACGAA	358
Db	438	TGA--GCCTTCAGGGTAAGCTGGCGAGTGCTGATTCTCTGGGTCTTTTGACCGGTA--GAA	494
Qy	359	RATCGTCTTTAAAAATTTGGATATGTGATAGAAGTGACTGATTAATTCGTTTCACATGGC	418
Db	495	AATCGTCTTTAAAAATTTGGATATGTGATAGAAGTGACTGATTAATTCGTTTCACATGGC	554
Qy	419	AATTGATCTGGTCAAGGTAAATTTGTAGTTCTCAAGACGCAATTTTCGGCGAATGTCG	478
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Qy	479	TCTTCACGATTGAGACAGTAACGAGATTGCTTGGGGTTATAT	520
Db	615	TCTTCACGATTGAGACAGTAACGAGATTGCTTGGGGTTATAT	556
RESULT 8			
PSDFL	702 bp DNA linear BCT 04-DEC-1995		
LOCUS	Pseudomonas mendocina 16S ribosomal RNA (16S rRNA) gene, transfer		
DEFINITION	RNA-1le (tRNA-1le) gene, transfer RNA-Ala (tRNA-Ala) gene, 23S ribosomal RNA (23S rRNA) gene.		
ACCESSION	L28159		
VERSION	L28159.1 GI:453549		
KEYWORDS	16S ribosomal RNA; 23S ribosomal RNA; tRNA; transfer RNA.		
SOURCE	Pseudomonas mendocina (tissue library: ATCC 25411) DNA.		
ORGANISM	Pseudomonas mendocina		
REFERENCE	Bacteria; Proteobacteria; gamma subdivision; Pseudomonadaceae; Pseudomonas.		
AUTHORS	1 (bases 1 to 702)		
TITLE	Tyler, S.D., Strathdee, C.A., Rozee, K.R. and Johnson, W.M.		
JOURNAL	Oligonucleotide primers designed to differentiate pathogenic pseudomonads on the basis of the sequencing of genes coding for 16S-23S rRNA internal transcribed spacers		
MEDLINE	Clin. Diagn. Lab. Immunol. 2 (4), 448-453 (1995)		
PUBMED	96082422		
FEATURES	7583922		
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Db	143	ATCGAAGACATCAGCTTCTTCATAGTATCCACACCAATTCGTTGATTTCATAGTCGAA	202
Qy	60	GAATGCTCTACGCGACCGGTTATAGGTCGTAGCTAGTTGGTTAGAGCGCACCCCT	119
Db	203	CGATGCTGTACGCGACCC--TGTTATAGGTCGTAGCTAGTTGGTTAGAGCGCACCCCT	261
Qy	120	GATAGGCTGAGGTCGGCAGTTCAAATCTGCCAGACCTTACCAATTCGTTGGTCGAGAAG	179







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DEFINITION Pseudomonas stutzeri internal transcribed spacer 1 (ITS1), trna-ile
and trna-Ala, strain AN10.
ACCESSION AJ251904
VERSION AJ251904.1 GI:9844592
KEYWORDS RNA-ile; trna-Ala; trna-Ile.
SOURCE Pseudomonas stutzeri.
ORGANISM Pseudomonas stutzeri.
REFERENCE 1 (bases 1 to 529)
AUTHORS Guasp, C., Moore, E.R., Lalucat, J. and Bannasar, A.
TITLE Utility of internally transcribed 16S-23S rDNA spacer regions for
the definition of Pseudomonas stutzeri genomovars and other
Pseudomonas species
JOURNAL Int. J. Syst. Evol. Microbiol. 50 Pt 4, 1629-1639 (2000)
MEDLINE 20393664
PUBMED 10939670
REFERENCE 2 (bases 1 to 529)
AUTHORS Bannasar, A.
TITLE Direct Submission
JOURNAL Submitted (14-DEC-1999) Bannasar A., Division of Microbiology,
National Research Centre for Biotechnology, Mascheroder Weg 1,
D-38124 Braunschweig, GERMANY
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Matches 396; Conservative 0; Mismatches 116; Indels 24; Gaps 5;
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415 TCACCTTTCACCTGGTGATTATTCAAGTCAAGGTAATAATTTG-CGTGTTCTCTATGCAAAAT 473
QY 465 TTGCGGCAATGTCGCTTCACAGTTCAGACAGTACACAGATTCGTTGGGTTATAT 520
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RESULT 13
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DEFINITION Pseudomonas stutzeri intergenic spacer, trna-ile and trna-Ala
genes, strain AER5.1.
ACCESSION AJ390587
VERSION AJ390587.1 GI:9844760
KEYWORDS IGS: intergenic spacer; transfer RNA Ile; transfer RNA-Ala;
trna-Ala gene; trna-Ile gene.
SOURCE Pseudomonas stutzeri.
ORGANISM Pseudomonas stutzeri.
REFERENCE 1 (bases 1 to 529)
AUTHORS Guasp, C., Moore, E.R., Lalucat, J. and Bannasar, A.
TITLE Utility of internally transcribed 16S-23S rDNA spacer regions for
the definition of Pseudomonas stutzeri genomovars and other
Pseudomonas species
JOURNAL Int. J. Syst. Evol. Microbiol. 50 Pt 4, 1629-1639 (2000)
MEDLINE 20393664
PUBMED 10939670
REFERENCE 2 (bases 1 to 529)
AUTHORS Bannasar, A.
TITLE Direct Submission
JOURNAL Submitted (15-DEC-1999) Bannasar A., Division of Microbiology,
National Research Centre for Biotechnology, Mascheroder Weg 1,
D-38124 Braunschweig, GERMANY
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BASE COUNT 123 a 111 c 141 g 154 t
ORIGIN
Query Match 48.5%; Score 252.4; DB 1; Length 529;
Best Local Similarity 73.9%; Pred. No. 9.4e-53;
Matches 396; Conservative 0; Mismatches 116; Indels 24; Gaps 5;
QY 1 ATCGAAGACATCAGCTTCTCATAAGTATCCACACGAATTGCTTGATTTCATAGTCGAACG 60
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QY 61 AATGCTGTAAACCGCCCGCTGTATA-----GGTCTGTAGCTCAGTTCGTTAGACGCGA 114
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115 CCCTGATAGGGTGGAGTGGCGAGTCAAAATCTGCCAGACCTACCAATTG----- 166  
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ACCESSION A48046  
VERSION A48046.1 GI:2301908  
KEYWORDS  
SOURCE unidentified.  
ORGANISM unidentified.  
REFERENCE 1 (bases 1 to 504)  
AUTHORS James G. Rossau, R. and Van H. H.  
TITLE SIMULTANEOUS DETECTION, IDENTIFICATION AND DIFFERENTIATION OF  
EUBACTERIAL TAXA USING A HYBRIDIZATION ASSAY  
JOURNAL Patent: WO 9600298-A 113 04-JAN-1996;  
COMMENT INNOGENETICS NV (BE)  
FEATURES Other publication AU 2924695 960119.  
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Qy 61 AATGCTGTAACGCGACCGTGTATATA-----GGTCTGTAGCTCAGTTGGTTAGAGCGCA 114  
Db 61 GCGATTGGGTTTAGACCCGAGAGTAACGATTGGGTCGTAGCTCAGTTGGTTAGAGCGCA 120  
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ACCESSION ARI77091  
VERSION ARI77091.1 GI:17919446  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unclassified.  
REFERENCE 1 (bases 1 to 504)  
AUTHORS James G. Rossau, R. and Van Heuvel, H.  
TITLE Simultaneous detection, identification and differentiation of  
eubacterial taxa using a hybridization assay  
JOURNAL Patent: US 6312903-A 113 06-NOV-2001;  
FEATURES Location/Qualifiers  
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BASE COUNT 119 a 111 c 137 g 137 t  
ORIGIN

Query Match 47.9%; Score 249; DB 6; Length 504;  
Best Local Similarity 74.4%; Pred. No. 6.7e-52;  
Matches 392; Conservative 0; Mismatches 105; Indels 30; Gaps 5;

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Job time : 1073.63 secs

GenCore version 5.1.1.3  
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OM nucleic - nucleic search, using sw model

Run on: January 31, 2003, 19:23:36 ; Search time 123.136 Seconds  
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Title: US-09-931-486-112  
Perfect score: 520  
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Scoring table: IDENTITY\_NUC

Gap 10.0 , Gapext 1.0

Searched: 2185239 seqs, 1125999159 residues

Total number of hits satisfying chosen parameters: 4370478

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	520	100.0	520	17 AAT11843	P. pseudoalcaligenes
2	249	47.9	504	17 AAT11844	P. stutzeri LMG 23
3	193.2	37.2	499	17 AAT11845	P. alcaligenes LMG
4	178	34.2	468	17 AAT11846	P. putida LMG 2322
5	174	33.5	471	17 AAT11842	P. aeruginosa U2G
6	168.6	32.4	588	22 AAI69774	16S/23S rRNA spacer
7	129.2	24.8	640681	24 ABA92787	Buchnera sp. genom
8	113.8	21.9	470	17 AAT11898	Yersinia enterocol
9	111.2	21.4	582	12 AAQ14104	B. pertussis ATCC 1

C	10	110.8	21.3	1396	22 AAH55089	S. epidermidis gen
	11	110.8	21.3	2839	22 AAH54998	S. epidermidis gen
	12	110.8	21.3	3444	22 AAH54992	S. epidermidis gen
	13	110.8	21.3	4429	22 AAH54300	S. epidermidis gen
C	14	109.4	21.0	400	18 AAV78022	Staphylococcus aur
	15	109.4	21.0	400	18 AAV77902	Staphylococcus aur
	16	109.4	21.0	1311	18 AAV77852	Staphylococcus aur
C	17	106.8	20.5	400	18 AAV77984	Staphylococcus aur
	18	106.8	20.5	400	18 AAV78405	Staphylococcus aur
C	19	104.2	20.0	351	18 AAV78405	Staphylococcus aur
	20	104	20.0	463	17 AAT11870	Listeria-like isol
	21	101.4	19.5	475	17 AAT11869	Listeria-like isol
	22	100	19.2	590	12 AAQ14105	B. bronchiseptica N
C	23	100	19.2	5097	20 AAQ24983	E. coli MGI655 rrr
	24	97.8	18.8	5341	20 AAQ24986	E. coli MGI655 rrr
	25	97.4	18.7	808	17 AAT11865	L. ivanovii CIP 78
	26	97.4	18.7	808	17 AAT11889	Brucella melitensi
	27	97.4	18.7	809	17 AAT11890	Brucella suis NIDO
	28	96.8	18.6	5105	20 AAQ24989	Brucella abortus
C	29	96	18.5	243	23 AAS48781	E. coli MGI655 rrr
	30	95.4	18.3	255	23 AAS48800	Staphylococcus aur
C	31	95.4	18.3	255	23 AAS48825	Staphylococcus aur
	32	95.4	18.3	255	23 AAS48838	Staphylococcus aur
C	33	95.4	18.3	255	23 AAS48846	Staphylococcus aur
	34	95.4	18.3	255	23 AAS48854	Staphylococcus aur
C	35	95.4	18.3	255	23 AAS48877	Staphylococcus aur
	36	95.4	18.3	255	23 AAS48882	Staphylococcus aur
C	37	95.4	18.3	255	23 AAS48896	Staphylococcus aur
	38	95.4	18.3	255	23 AAS48898	Staphylococcus aur
C	39	95.4	18.3	255	23 AAS48967	Staphylococcus aur
	40	95.4	18.3	255	23 AAS49061	Staphylococcus aur
C	41	95.4	18.3	343	18 AAV78492	Staphylococcus aur
	42	95	18.3	496	17 AAT11866	L. monocytogenes I
	43	95	18.3	1265	24 ABQ69060	Listeria monocytog
	44	95	18.3	1409	24 ABQ70714	Listeria monocytog
	45	95	18.3	5015	24 ABQ71078	Listeria monocytog

#### ALIGNMENTS

RESULT 1  
AAT11843  
ID AAT11843 standard; DNA; 520 BP.  
AC AAT11843;  
XX  
XX 03-SEP-1996 (first entry)  
XX  
DE P. pseudoalcaligenes LMG 1225 16S-23S rRNA spacer region.  
XX  
XX Probe; detection; identification; microorganism; amplify;  
KW 16S-23S rRNA spacer region; respiratory tract; universal;  
KW species-specific; ss.  
XX  
OS Pseudomonas pseudoalcaligenes.  
XX  
XX WO9600298-A1.  
PN  
XX  
XX 04-JAN-1996.  
XX  
XX 23-JUN-1995; 95WO-EP02452.  
PF  
XX  
XX 07-APR-1995; 95EP-0870032.  
PR  
XX 24-JUN-1994; 94EP-0870106.  
XX  
(INNO-) INNOGENETICS NV.  
XX  
XX Jannes G, Rossau R, Van Heuverswyn H;  
XX WPI; 1996-068882/07.  
XX  
XX Novel hybridisation assay for the detection of eubacteria - esp

```
PT Mycobacterium, comprises amplifying the 16S-23S rRNA spacer region
XX Claim 2; Fig 37; 248pp; English.
XX
CC The sequences given in AAT11791-857 represent the 16S-23S rRNA spacer
CC regions derived from various microorganisms. These sequences were
CC used in the method of the invention for the detection and identification
CC of at least one or more microorganisms. The method comprises amplifying
CC the 16S-23S rRNA spacer region and hybridising one or more of the probes
CC given in AAT34011-77 to the amplified sequence. These probes were
CC specifically used to detect microorganisms in samples originating from
CC the respiratory tract. This spacer region is derived from Pseudomonas
CC pseudoalcaligenes LMG 1225.
XX
SQ Sequence 520 BP; 126 A; 109 C; 134 G; 151 T; 0 other;

Query Match 100.0%; Score 520; DB 17; Length 520;
Best Local Similarity 100.0%; Pred. No. 4e-157;
Matches 520; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATCGAAGACATCAGCTTCTTCATAGTATCCACACGAATGCTGATTCATAGTGAACG 60
DB |||||
1 ATCGAAGACATCAGCTTCTTCATAGTATCCACACGAATGCTGATTCATAGTGAACG 60
QY 61 ATGCTGTAAACGCGCCGCTGTATAGGCTCTGTAGCTAGTGTGGTTAGAGCGCACCCCTG 120
DB |||||
61 AATGCTGTAAACGCGCCGCTGTATAGGCTCTGTAGCTAGTGTGGTTAGAGCGCACCCCTG 120
QY 121 ATAAGGCTGAGGTGCGGAGTCAAAATCTGCCAGACCTACCAATTCGTTGGTCGAGAAGA 180
DB |||||
121 ATAAGGCTGAGGTGCGGAGTCAAAATCTGCCAGACCTACCAATTCGTTGGTCGAGAAGA 180
QY 181 ATACGGGCCATAGCTCAGCTGGGAGAGCGCCTGCTTCAGCAGGAGGTACGCGGTTC 240
DB |||||
181 ATACGGGCCATAGCTCAGCTGGGAGAGCGCCTGCTTCAGCAGGAGGTACGCGGTTC 240
QY 241 GATCCCGCTTGGCTCCACACTCTCTCGTGTGGGTGAGTGTAAAGAGTTTCAGAAATG 300
DB |||||
241 GATCCCGCTTGGCTCCACACTCTCTCGTGTGGGTGAGTGTAAAGAGTTTCAGAAATG 300
QY 301 ATGCGCTTCAGGTTTGTCTGCTGAGTGTCTGATTCGCTGCTTGTGCTTGTGACCGGTACCAAAA 360
DB |||||
301 ATGCGCTTCAGGTTTGTCTGAGTGTCTGATTCGCTGCTTGTGCTTGTGACCGGTACCAAAA 360
QY 361 TCGTCTTTAAAAATTTGGATATGTAGTAAAGTCACTGATTAATGCTTTCACGTGGCAA 420
DB |||||
361 TCGTCTTTAAAAATTTGGATATGTAGTAAAGTCACTGATTAATGCTTTCACGTGGCAA 420
QY 421 TTGATCTGGTCAAGTAAATTTGTAGTCTCAAGACGCAATTTTCGCGCAATGTCGTC 480
DB |||||
421 TTGATCTGGTCAAGTAAATTTGTAGTCTCAAGACGCAATTTTCGCGCAATGTCGTC 480
QY 481 TTCAGATTGAGACAGTAACCAAGATTGCTTGGGGTTATAT 520
DB |||||
481 TTCAGATTGAGACAGTAACCAAGATTGCTTGGGGTTATAT 520

RESULT 2
AAT11844
ID AAT11844 standard; DNA; 504 BP.
XX
AC AAT11844;
XX
DT 03-SEP-1996 (first entry)
XX
DE P. stutzeri LMG 2333 16S-23S rRNA spacer region.
XX
KW Probe: detection; identification; microorganism; amplify;
KW 16S-23S rRNA spacer region; respiratory tract; universal;
KW species-specific; ss.
XX
OS Pseudomonas stutzeri.
XX
```

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PN WO9600298-Al.
XX
PD 04-JAN-1996.
XX
PF 23-JUN-1995; 95WO-EP02452.
XX
PR 07-APR-1995; 95EP-0870032.
PR 24-JUN-1994; 94EP-0870106.
XX
PA (INNO-) INNOGENETICS NV.
XX
PI Jannes G, Rossau R, Van Heuverswyn H;
XX
XX WPI; 1996-068882/07.
XX
PT Novel hybridisation assay for the detection of eubacteria - esp
PT Mycobacterium, comprises amplifying the 16S-23S rRNA spacer region
PS Claim 2; Fig 38; 248pp; English.
XX
CC The sequences given in AAT11791-857 represent the 16S-23S rRNA spacer
CC regions derived from various microorganisms. These sequences were
CC used in the method of the invention for the detection and identification
CC of at least one or more microorganisms. The method comprises amplifying
CC the 16S-23S rRNA spacer region and hybridising one or more of the probes
CC given in AAT34011-77 to the amplified sequence. These probes were
CC specifically used to detect microorganisms in samples originating from
CC the respiratory tract. This spacer region is derived from Pseudomonas
CC stutzeri LMG 2333.
XX
SQ Sequence 504 BP; 119 A; 111 C; 137 G; 137 T; 0 other;

Query Match 47.9%; Score 249; DB 17; Length 504;
Best Local Similarity 74.4%; Pred. No. 8.1e-70;
Matches 392; Conservative 0; Mismatches 105; Indels 30; Gaps 5;

QY 1 ATCGAAGACATCAGCTTCTTCATAGTATCCACACGAATGCTGATTCATAGTGAACG 60
DB |||||
1 ATCGAAGACATCAGCTTCTTCATAGTATCCACACGAATGCTGATTCATAGTGAACG 60
QY 61 AATGCTGTAAACGCGCCGCTGTATAGGCTCTGTAGCTAGTGTGGTTAGAGCGCAC 114
DB |||||
61 GCGATTGGGTTAGACCCGAGAGTAACGATTGGGTCCTAGCTCACTGTTAGAGCGCA 120
QY 115 CCCTGTATAGGTTGAGTGGCGAGTTCAAATCTGCCAGACCTACCAATGCTTGGTGG 174
DB |||||
121 CCCTGTATAGGTTGAGTGGCGAGTTCGAATCTGCCAGACCCACCAATCG----- 172
QY 175 AGAAGAATACGGGCCATAGCTCAGCTGGGAGAGCGCTGCTTCCACGAGGAGGTGAG 234
DB |||||
173 -----AAGGGCCATAGCTCAGCTGGGAGAGCGCTGCTTCCACGAGGAGGTGAG 224
QY 235 CGGTTCCGATCCCGCTTGGCTCCACACTCTCTCGTGTGCGGTGAGTGTAAAGAGTTCA 294
DB |||||
225 CGGTTCCGATCCCGCTTGGCTCCACACTTAACTCTAGTCTGCCGGAAGCTCAGAAATGAGTG 284
QY 295 GAATGATGCCGCTTTCAGGTTTGTCTGCTGCTGAGTGTGATTTGGTGTGATTTGACCGGTA 354
DB |||||
285 TTACACGAGTATGAGGTTGATTGGCTTGAACATTGATTTCTGGACTTT-----GCG 338
QY 355 CGAAATCGTCTTTAAAAATTTGGATATGTAGTAGAGT-GACTGATTAATTTGCTTTCA 413
DB |||||
339 CCAGAACTGTTCTTTAAAAATTTGGGTTATGTATAGAGTAGACCGGATGTTGCTTTCA 398
QY 414 CTGGCAATGATCTGGTCAAGTAAATTTGTAGTCTCAAGACCGCAAAATTTTCGGCGAA 473
DB |||||
399 CTGGCAGCATGTGCGCTCAAGGTAATTTG-CGTGTTCTCTATGCAAAATTTTCGGCGAA 457
QY 474 TCTCGTCTTTCAGGATTGACAGTAAACGAGTTCGTTGGGGTTATAT 520
DB |||||
458 TCTCGTCTTTCAGGATTGACAGTAAACGAGTTCGTTGGGGTTATAT 504
```

RESULT 3  
 AAT11845  
 ID AAT11845 standard; DNA; 499 BP.  
 XX AAT11845;  
 XX AAT11845;  
 DT 03-SEP-1996 (first entry)  
 XX  
 DE P. alcaligenes LMG 1224 16S-23S rRNA spacer region.  
 XX  
 KW Probe; detection; identification; microorganism; amplify;  
 KW 16S-23S rRNA spacer region; respiratory tract; universal;  
 KW species-specific; ss.  
 XX  
 OS Pseudomonas alcaligenes.  
 XX  
 PN WO9600298-A1.  
 XX  
 PD 04-JAN-1996.  
 XX  
 PF 23-JUN-1995; 95WO-EP02452.  
 XX  
 PR 07-APR-1995; 95EP-0870032.  
 PR 24-JUN-1994; 94EP-0870106.  
 XX  
 XX (INNO-) INNOGENETICS NV.  
 XX  
 PI Jannes G, Rossau R, Van Heuverswyn H;  
 XX  
 DR WPI; 1996-068882/07.  
 XX  
 PT Novel hybridisation assay for the detection of eubacteria - esp  
 PT Mycobacterium, comprises amplifying the 16S-23S rRNA spacer region  
 XX  
 PS Claim 2; Fig 39; 248pp; English.  
 XX  
 CC The sequences given in AAT11791-857 represent the 16S-23S rRNA spacer  
 CC regions derived from various microorganisms. These sequences were  
 CC used in the method of the invention for the detection and identification  
 CC of at least one or more microorganisms. The method comprises amplifying  
 CC the 16S-23S rRNA spacer region and hybridising one or more of the probes  
 CC given in AAT34011-77 to the amplified sequence. These probes were  
 CC specifically used to detect microorganisms in samples originating from  
 CC the respiratory tract. This spacer region is derived from Pseudomonas  
 CC alcaligenes LMG 1224.  
 XX  
 SQ Sequence 499 BP; 123 A; 109 C; 130 G; 137 T; 0 other;  
 Query Match 37.2%; Score 193.2; DB 17; Length 499;  
 Best Local Similarity 72.8%; Pred. No. 7.6e-52;  
 Matches 386; Conservative 0; Mismatches 103; Indels 41; Gaps 9;  
 QY 1 ATCGAGACATCAGCTTCTTCATAGTATCCACACGAATTGCTTGAATTCATAGTCGAACG 60  
 DB 1 ATCGAGACATCAGCTTCTTCATAGTATCCACACGAATTGCTTGAATTCATAGTCGAACG 60  
 QY 61 AATGCTGTAAACGCGACCCGCTTTATA-----GCTGTAGCTCAGTGTGTTAGAGCGCA 114  
 DB 61 GCATTTGGTGTAGACCCGAGAGTGAGTGGTCTGTAGCTCAGTGTGTTAGAGCGCA 120  
 QY 115 CCCTGATAGGCTGAGGTGCGGAGTCAATCTGCCAGACCTACCAATTGCTTG---G 171  
 DB 121 CCCTGATAGGCTGAGGTGCGGAGTCAATCTGCCAGACCTACCAATTGCTTGCGGAGT 180  
 QY 172 TCAGAGAAGATACGGGGCCATAGCTCAGCTGGGAGAGCGCTGCCCTTGCACGAGGAGT 231  
 DB 181 GCCAGTGTCAATGGGGCCATAGCTCAGCTGGGAGAGCGCTGCCCTTGCACGAGGAGT 240  
 QY 232 CAGCGCTTCGATCCCGCTTGGCTCCACCACTCTCTGCTGTGCGGTGACGTGTTAAAGAGT 291  
 DB 241 CAGAGTTCGATCTCTTGGCTCCACCACTCAACTCAGC-----ATCGCTGAAGC 291  
 QY 292 TCAGAAATGATCGCGCTTCAGGTTTGTCTGTGTAGTGTGCTGATTTCTGCTTTTGACCG 351

DB 292 TCAGAAATGA-----ACATGGTAGTTCAATGTTGATTTCTGGTCTTT----- 334  
 QY 352 GTACGAAATCGTCTTTAAATAATTTGGATATGTGATAGAGTCACTGATTAATTCGCTTT 411  
 DB 335 GCGCCAGAACTGTCTTTAAATAATTTGGTATGTGATAGAGTCACTGATTAATTCGCTTT 393  
 QY 412 CACTGGCAATTGATCTGGTCAAGTAAATTTGTAGTCTCAAGACGCAAAATTTTCGCG 471  
 DB 394 CACTGCAGTTG--TTAATCAAGCAAAATTTG--CGAGTCAAGCGCGAATTTTCGCG 449  
 QY 472 AATGCTGCTTCTCAGAT-TGAGACAGTAAACCAGATTCCTTGGGTTATAT 520  
 DB 450 AATGCTGCTTCTCAGAT-TGAGACAGTAAACCAGATTCCTTGGGTTATAT 499  
 RESULT 4  
 AAT11846  
 ID AAT11846 standard; DNA; 468 BP.  
 XX AAT11846;  
 AC AAT11846;  
 XX  
 DT 03-SEP-1996 (first entry)  
 XX  
 DE P. putida LMG 2232 16S-23S rRNA spacer region.  
 XX  
 KW Probe; detection; identification; microorganism; amplify;  
 KW 16S-23S rRNA spacer region; respiratory tract; universal;  
 KW species-specific; ss.  
 XX  
 OS Pseudomonas putida.  
 XX  
 PN WO9600298-A1.  
 XX  
 PD 04-JAN-1996.  
 XX  
 PF 23-JUN-1995; 95WO-EP02452.  
 XX  
 PR 07-APR-1995; 95EP-0870032.  
 PR 24-JUN-1994; 94EP-0870106.  
 XX  
 XX (INNO-) INNOGENETICS NV.  
 XX  
 PI Jannes G, Rossau R, Van Heuverswyn H;  
 XX  
 DR WPI; 1996-068882/07.  
 XX  
 PT Novel hybridisation assay for the detection of eubacteria - esp  
 PT Mycobacterium, comprises amplifying the 16S-23S rRNA spacer region  
 XX  
 PS Claim 2; Fig 40; 248pp; English.  
 XX  
 CC The sequences given in AAT11791-857 represent the 16S-23S rRNA spacer  
 CC regions derived from various microorganisms. These sequences were  
 CC used in the method of the invention for the detection and identification  
 CC of at least one or more microorganisms. The method comprises amplifying  
 CC the 16S-23S rRNA spacer region and hybridising one or more of the probes  
 CC given in AAT34011-77 to the amplified sequence. These probes were  
 CC specifically used to detect microorganisms in samples originating from  
 CC the respiratory tract. This spacer region is derived from Pseudomonas  
 CC putida LMG 2232.  
 XX  
 SQ Sequence 468 BP; 117 A; 101 C; 117 G; 133 T; 0 other;  
 Query Match 34.2%; Score 178; DB 17; Length 468;  
 Best Local Similarity 71.1%; Pred. No. 5.8e-47;  
 Matches 371; Conservative 0; Mismatches 95; Indels 56; Gaps 8;  
 QY 1 ATCGAGACATCAGCTTCTTCATAGTATCCACACGAATTGCTTGAATTCATAGTCGAACG 60  
 DB 1 ATCGAGACATCAGCTTCTTCATAGTATCCACACGAATTGCTTGAATTCATAGTCGAACG 60  
 QY 61 AATGCTGTAAACGCGACCCGCTTTATAGTCTGTAGTGTGTTAGAGCGCACCCCTG 120

Db 61 CGATTAGGTAGCAACCTTCGAT - TGGGTCTGTAGCTCAGTTGGTTAGAGCGCACCCCTG 119  
 QY 121 ATAGAGGTGAGTGGCGAGTTCGAATCTGCCAGACCTACCAATTCGTTGGTCGAGAGA 180  
 Db 120 ATAGAGGTGAGTGGCGAGTTCGAATCTGCCAGACCTACCAATTCGTTGGTCGAGAGA 180  
 QY 181 ATAGAGGTGAGTGGCGAGTTCGAATCTGCCAGACCTACCAATTCGTTGGTCGAGAGA 180  
 Db 169 - - - - - GGGGCGCATAGCTCAGCTGGGAGAGCGGCTGCTTTCGACGAGGAGTTCGAGGTTTC 224  
 QY 241 GATCCCGCTTGGCTCCACCACTCTCTGCTGTTGGGAGTGTAAAGAGTTCAGAAATG 300  
 Db 225 GATCCCGCTTGGCTCCACCACTCTCTGCTGTTGGGAGTGTAAAGAGTTCAGAAATG 300  
 QY 301 ATGCCCGCTTGGCTCCACCACTCTCTGCTGTTGGGAGTGTAAAGAGTTCAGAAATG 360  
 Db 278 A - - - - - ATATTCGCGTGAATATTCGTTGCTGAACTT - - - - - TATCAGAA 317  
 QY 361 TCGTCTCTTAAATTTGGATATGTAGAGTGAAGTGAATTTG - - - - - CTTTCACTGTC 418  
 Db 318 TCGTCTCTTAAATTTGGATATGTAGAGTGAAGTGAATTTG - - - - - CTTTCACTGTC 418  
 QY 419 AATTGATCTGGTCAAGTAAATTTGATTTCTCAAGACGCAAAATTTTCGGCGAATGTCG 478  
 Db 378 GTGTGTTTCAGGCTAAGCTAAATTTGAGT - - - - - AATTCAAGTTTTCGGCGAATGTCG 478  
 QY 479 TCTTCAGGATGACAGTACACAGATTCACAGATTCGTTGGGTTATAT 520  
 Db 434 TCTTCAC - - - - - AGTATAACACAGATTCGTTGGGTTATAT 468

## RESULT 5

AAT11842

ID AAT11842 standard; DNA; 471 BP.

XX AAT11842;

XX 03-SEP-1996 (first entry)

DE P. aeruginosa UZG 5669 16S-23S rRNA spacer region.

KW Probe; detection; identification; microorganism; amplify;

KW 16S-23S rRNA spacer region; respiratory tract; universal;

KW species-specific; ss.

XX Pseudomonas aeruginosa.

OS WO9600298-A1.

PN 04-JAN-1996.

XX 23-JUN-1995; 95WO-EP02452.

XX 07-APR-1995; 95EP-0870032.

XX 24-JUN-1994; 94EP-0870106.

XX (INNO-) INNOGENETICS NV.

XX Jannes G, Rossau R, Van Heuverswyn H;

XX WPI; 1996-068882/07.

XX Novel hybridisation assay for the detection of eubacteria - esp

PT Mycobacterium, comprises amplifying the 16S-23S rRNA spacer region

XX Claim 2; Fig 36; 248pp; English.

CC The sequences given in AAT11791-857 represent the 16S-23S rRNA spacer  
 CC regions derived from various microorganisms. These sequences were  
 CC used in the method of the invention for the detection and identification  
 CC of at least one or more microorganisms. The method comprises amplifying  
 CC the 16S-23S rRNA spacer region and hybridising one or more of the probes

CC given in AAT34011-77 to the amplified sequence. These probes were  
 CC specifically used to detect microorganisms in samples originating from  
 CC the respiratory tract. This spacer region is derived from *Pseudomonas*  
 CC *aeruginosa* UZG 5669.

SQ Sequence 471 BP; 116 A; 103 C; 120 G; 132 T; 0 other;

Query Match 33.5%; Score 174; DB 17; Length 471;  
 Best Local Similarity 70.6%; Pred. No. 1.1e-45;

Matches 373; Conservative 0; Mismatches 90; Indels 65; Gaps 8;

QY 1 ATCGAAGACATCATGCTTCTTATAGTATCCACACGAATTCGTTGATTCATAGTCGAACG 60  
 Db 1 ATCGAAGATCCCGCTTCTTATAGTATCCACACGAATTCGTTGATTCATAGTCGAACG 60

QY 61 AATGCTGTAAACGCGACCCCTGTTATAGTCTGTAGCTCAGTTGGTTAGAGCGCACCCCTG 120  
 Db 61 GAT - - - - - TGGGTCTGTAGCTCAGTTGGTTAGAGCGCACCCCTG 99

QY 121 ATAAGGTCAGGTCGCGCAGTTCAAATCTGCCAGACCTACCAATTCGTTGTCGAGAAG- 179  
 Db 100 ATAAGGTCAGGTCGCGCAGTTCGAATCTGCCAGACCTACCAATTCGTTGTCGCGT 159

QY 180 - - - - - AATACGGGGCCATAGCTCAGCTGGGAGAGCGCTGCCTTGCACGAGGAGTCA 234  
 Db 160 GATCCGATAGCGGGCCATAGCTCAGCTGGGAGAGCGCTGCCTTGCACGAGGAGTCA 219

QY 235 CGGTCGATCCCGCTTGGCTCCACCACTCTCTGCTGTGGGTGAGTGTAAAGAGTTC 294  
 Db 220 GAGTTCGATCCCTCTTGGCTCCACCA - - - - - TCTAAACAATCGTCGAAAGTCA 269

QY 295 GAAATGATCCCGCTTGGCTCCACCACTCTCTGCTGTGGGTGAGTGTAAAGAGTTC 354  
 Db 270 GAAATGA - - - - - ATGTTCTGGATGAACATTCGTTGCTGCTTTT 312

QY 355 CGAAATATCTCTTAAATAATTTGGATATGTATAGTGAAGT - - - - - GACTGATTAATTCGTTTC 412  
 Db 313 CCAGAACTGTTCTTAAATAATTCGGGTATGTATAGTAAGTGAAGTGAAGTATCTCTTC 372

QY 413 ACTGCCAATTCGTTCTCAAGTAAATAATTTAGTTCCTCAAGACGCAAAATTTTCGCGCA 472  
 Db 373 ACTGGTGATCATTCGAAGTCAAGTAAATAATTTG - - - - - CGAGTTCAAGCGCGAATTTTCGCGCA 430

QY 473 ATGTCGTCCTTCAGGATGAGACAGTAACCAAGATTCGTTGGGGTTATAT 520  
 Db 431 ATGTCGTCCTTCAC - - - - - AGTATAACCAAGATTCGTTGGGGTTATAT 471

## RESULT 6

AAI69774

ID AAI69774 standard; DNA; 588 BP.

XX AAI69774;

XX 13-DEC-2001 (first entry)

XX 16S/23SrRNA spacer region.

KW Bacterium detection; 16S/23SrRNA spacer region; ds.  
 OS *Pseudomonas putida*.

XX JP2001190279-A.  
 XX 17-JUL-2001.

XX 13-JAN-2000; 2000JP-0004160.  
 XX 13-JAN-2000; 2000JP-0004160.

XX (MITO ) MITSUBISHI JUKOGYO KK.  
 XX WPI; 2001-605311/69.

```
XX Detection method of Pseudomonas bacteria -
XX Claim 6; Page 7; 11pp; Japanese.
XX The present invention relates to a method for the detection of the
XX present DNA sequence; the 16S/23S rRNA spacer region of Pseudomonas
XX putida. The method can be used to detect Pseudomonas bacteria.
XX Sequence 588 BP; 147 A; 134 C; 153 G; 149 T; 5 other;
XX
XX Query Match 32.4%; Score 168.6; DB 22; Length 588;
XX Best Local Similarity 67.5%; Pred. No. 7e-44;
XX Matches 359; Conservative 0; Mismatches 99; Indels 74; Gaps 6;
XX
QY 1 ATCGAGACATCAGCTTCTTATAGATATCCACAGAAATGCTTATCATAGTGAAGC 60
Db 63 ATCGAGACATCAGCTTCTTATAGATATCCACAGAAATGCTTATCATAGTGAAGC 120
QY 61 AATGCTGTAACCGCCGCTGTATAGTCTCTAGTCTAGTGGTTAGAGCGCACCCCTG 120
Db 121 -----GAGCATCAGACCTATATAGTCTAGTCTAGTGGTTAGAGCGCACCCCTG 174
QY 121 ATAGGGTGAAGTGGCGAGTCAAAATCTGCCAGACCTACCAATGCTTGGTCGAGA 180
Db 175 ATAANGGTGAGTGGCGAGTCAAAATCTGCCAGACCTACCAAT----- 218
QY 181 ATACGGGGCCATAGCTCAGCTGGGAGAGCGCTGCTGCACGAGGAGGTGAGCGGTT 240
Db 219 ATGCGGGGCCATAGCTCAGCTGGGAGAGCGCTGCTGCACGAGGAGGTGAGCGGAT 278
QY 241 GATCCCGCTTGCTCCACACCTCTCTCGTGTGCGGTGAGTGTAAAGAGTTCAGAAATG 300
Db 279 GATCCCGCTTGCTCCACACCTGCTGTACCTTGATCAACTCANAATGAGCA----- 332
QY 301 ATGCGCGCTTCAGGTTGCTGCTGAGTGTCTGATTCGTGCTGTTGACCGGTACGAAA 360
Db 333 -----TTCCCGTCTAAATGTTGATTTCTGGCTTT-----GTCAGA 367
QY 361 TCGTCTCTTAAATTTGATATGATAGAGTGAAGTGAATTAATGCTTCACTGGCAA 420
Db 368 TCGTCTCTTAAATTTGATATGATAGATATGATAGTGAAGTGAATTAATGCTTCACTGG 427
QY 421 TTGATCTGTGCAAGTAAATTTGT-----AGTCTCAAGACGCCAAATTTTCG 468
Db 428 TGSATCAGCTAANGTAAATTTGAGTCTGCTCGAAGAGCAACTTNCGAATTTTCG 487
QY 469 GCGAATGCTGCTTCAAGATTCAGACAGTAAACAGATTCCTTGGGGTTATAT 520
Db 488 GCGAATGCTGCTTCAAC-----AGTATAACAGATTCCTTGGGGTTATAT 532
XX
RESULT 7
ABA92787
ID ABA92787 standard; DNA; 640681 BP.
XX
AC ABA92787;
XX
DT 27-MAR-2002 (first entry)
XX
DE Buchnera sp. genomic DNA SEQ ID NO:1.
XX
KW Buchnera; cockroach-symbiotic bacterium; cockroach extermination;
KW circular; ds.
XX
OS Buchnera sp.
XX
PN JP2001292771-A.
XX
PD 23-OCT-2001.
XX
PF 07-APR-2000; 2000JP-0107160.
XX
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PR 07-APR-2000; 2000JP-0107160.
XX (RIKA ) RIKAGAKU KENKYUSHO.
XX WPI; 2002-126043/17.
XX A genomic DNA of cockroach-symbiotic bacterium -
XX Claim 1; Page 16-230; 237pp; Japanese.
XX
XX The present invention describes a gene (T) derived from Buchnera sp.
XX containing the DNA (a) or (b), (a) has a fully defined base pair
XX sequence selected from a table of sequences found in the Buchnera sp.
XX genomic DNA of ABA92787 given in the specification or is a DNA selected
XX from complementary DNA sequences, and (b) is a DNA which hybridises with
XX the DNA (a) and encodes a protein. Also described are: (1) a recombinant
XX vector (II) containing (1); (2) a transformant (III) containing (II);
XX (3) a genomic DNA of Buchnera sp. containing the sequence given in
XX ABA92787; (4) a plasmid derived from Buchnera sp. containing DNA (c) or
XX (d), (c) is a DNA containing a fully defined sequence given in ABA92788
XX or ABA92789 and (d) is a plasmid which hybridises with a DNA; and (5) a
XX method for the preparation of a protein in which (III) is cultured and
XX the expression protein of the objective protein is collected from the
XX resultant culture. The DNA is useful for developing agricultural
XX chemicals for exterminating cockroaches. The present sequence represents
XX the specifically claimed Buchnera sp. genomic DNA sequence, from the
XX present invention.
XX
XX Query Match 24.8%; Score 129.2; DB 24; Length 640681;
XX Best Local Similarity 73.4%; Pred. No. 1.1e-29;
XX Matches 182; Conservative 0; Mismatches 58; Indels 8; Gaps 1;
XX
QY 86 AGGCTGTAGTCTGAGTGGTTAGAGCGACCCCTGATAGAGGTGAGTCCGAGTCAAA 145
Db 275640 AGGCTGTAGTCTGAGTGGTTAGAGCGACCCCTGATAGAGGTGAGTCCGAGTCAAA 275699
QY 146 TCTGCCAGACCTACCAATGCTTGTGCGAAGATACGCGCCATAGCTCAGCTGGGA 205
Db 275700 TCCACTCAGCGCTTACCAC-----TAAAAATCATCTGGGCTATAGCTCAGCTGGGA 275751
QY 205 GAGCGCTGCTTGCACGAGGAGTACGCGGTTCGATCCCGCTTGGCTCCACACTCTC 265
Db 275752 GAGCGCTGCTTGCACGAGGAGTACGCGGTTCGATCCCGCTTGGCTCCACACTCTC 275811
QY 266 TCGTGTGGGTGAGTGTAAAGAGTTCAGAAATGATGCGCCTTCAGGTTTGTCTGTTG 325
Db 275812 TTTTAACTCTTAATCTTTTAAAAACTTCAAAATCAGTGCACGTAATTTTAAATCAAT 275871
QY 326 AGTGTCTGA 333
Db 275872 ATTTCTTA 275879
XX
RESULT 8
AAT11898
ID AAT11898 standard; DNA; 470 BP.
XX
AC AAT11898;
XX
DT 03-SEP-1996 (first entry)
XX
DE Versinia enterocolitica strain P95 16S-23S rRNA spacer region (#1).
XX
KW Probe; detection; identification; microorganism; amplify;
KW 16S-23S rRNA spacer region; food; universal;
KW species-specific; ss.
XX
OS Versinia enterocolitica.
XX
PN WO9600298-A1.
XX
```

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PD 04-JAN-1996.
XX
XX PF 23-JUN-1995; 95WO-EP02452.
XX
XX PR 07-APR-1995; 95EP-0870032.
XX
XX PR 24-JUN-1994; 94EP-0870106.
XX
XX PA (INNO-) INNOGENETICS NV.
XX
XX PI Jannes G, Rossau R, Van Heuverswyn H;
XX
XX WIPI; 1996-068882/07.
XX
XX Novel hybridisation assay for the detection of eubacteria - esp
XX Mycobacterium, comprises amplifying the 16S-23S rRNA spacer region
XX
XX PS Claim 5; Fig 98; 248pp; English.
XX
XX CC The sequences given in AAT11889-905 represent the 16S-23S rRNA spacer
XX regions derived from various microorganisms. These sequences were
XX used in the method of the invention for the detection and identification
XX of at least one or more microorganisms. The method comprises amplifying
XX the 16S-23S rRNA spacer region and hybridising one or more probes to
XX the amplified sequence. These probes were specifically used to detect
XX microorganisms in samples originating from food. This spacer region is
XX derived from Yersinia enterocolitica strain P95.
XX
XX SQ Sequence 470 BP; 129 A; 101 C; 120 G; 120 T; 0 other;

Query Match 21.9%; Score 113.8; DB 17; Length 470;
Best Local Similarity 77.1%; Pred. No. 2.8e-26;
Matches 158; Conservative 0; Mismatches 32; Indels 15; Gaps 1;

QY 82 TTATAGGCTGTAGCTCAGTTGGTTAGAGCGCACCCCTGATAGGGTGAGGTGGCGAGTT 141
Db 72 TTATAGGCTGTAGCTCAGTTGGTTAGAGCGCACCCCTGATAGGGTGAGGTGGTGTT 131
QY 142 CAAATCTGCCAGACCTACCAATTTGCTTGGTCGAGAGAAATAC-----GG 186
Db 132 CAAGTCCACTCAGGCGCTACCACTTCTCGAAGTGGAAGGACTACTGCACGTGACTGTATGG 191
QY 187 GGCCATAGTCAGCTGGGAGAGCGCTGCTTCACGCAGGAGGTGACGGTTCGATCCC 246
Db 192 GGCATAGTCAGCTGGGAGAGCGCTGCTTCACGCAGGAGGTGACGGTTCGATCCC 251
QY 247 GCTTGGCTCCACACCTCTCTCGGT 271
Db 252 GCTTACTCCACCATATAGTCTCTGT 276

RESULT 9
AAQ14104
ID AAQ14104 standard; DNA; 582 BP.
XX
XX AC AAQ14104;
XX
XX DT 10-JAN-1992 (first entry)
XX
XX DE B.pertussis ATCC 10380 16S to 23S rRNA gene spacer region.
XX
XX KW rRNA gene; ribosomal RNA; probe; ss.
XX
XX OS Bordetella pertussis ATCC 10380.
XX
XX PN EP452596-A.
XX
XX PD 23-OCT-1991.
XX
XX PF 18-APR-1990; 90EP-0401054.
XX
XX PR 18-APR-1990; 90EP-0401054.
XX
XX PA (INNO-) INNOGENETICS NV SA.

XX Rossau R, Van Heuverswyn H;
XX
XX WIPI; 1991-311940/43.
XX
XX Hybridisation probes for detecting non-viral microorganisms -
XX derived from spacer region between 16S and 23S rRNA genes, for
XX detecting e.g. BORDETELLA PERTUSSIS, NEISSERIA GONORRHOEA
XX
XX PS Disclosure; Fig 2; 41pp; English.
XX
XX CC This sequence is the non-coding strand of the 16S-23S rRNA gene
XX spacer region; the 5'-end is proximal to the 16S rRNA gene and the 3'-
XX end proximal to the 23S rRNA gene. A set of probes were designed
XX based on this sequence which were specific for B.pertussis. A kit
XX is provided for detection of this species using the probes.
XX
XX SQ Sequence 582 BP; 136 A; 114 C; 181 G; 148 T; 3 other;

Query Match 21.4%; Score 111.2; DB 12; Length 582;
Best Local Similarity 63.4%; Pred. No. 2.2e-25;
Matches 201; Conservative 0; Mismatches 111; Indels 5; Gaps 2;

QY 67 GTAACGCGACCGCTGTATAGTCTGTAGCTCAGTTGGTTAGAGCGCACCCCTGATAAGG 126
Db 79 GGAGAGAGAAAGGTTTCGCGGGTCTGTAGCTCAGTCTGAGTGTAGAGCACCCGCTTGTGATAAGG 138
QY 127 GTGAGTGGCGAGTTCAATCTGCCAGACCTACCAATTCCTTGGTCGAGAAAGATACGG 186
Db 139 CGGGGGTGGTGGTTGGAATCAACACGACCCACCAA--GGTTTCTCTGAGAGGGAATGG 196
QY 187 GGCCATAGTCAGCTGGGAGAGCGCTGCTTCACGCAGGAGGTGACGGTTCGATCCC 246
Db 197 GGGTGTAGCTCAGCTGGGAGAGCGCTGCTTTCGACAGCAGGATGTCATCGTTCGATCCC 256
QY 247 GCTTGGCTCCACCACTCTCTCGTGTGGTTCGAGTGTAAAGAGTTCAGAAATGATGCCG 306
Db 257 GTTCACCTCCACCAAGGCTGTCAGAGGATGGGTGTGNNNGAGACCAAGAGCGGAGAG 316
QY 307 CTTCAGGTTTGCTCTG---TTGAGTGTCTGATTTCTGTCTTTTGACCGGTACGAAATCG 363
Db 317 AGCAACGTTAGTGTGCGAGTCAGTGTAAAGCGTTTAAAGCGTTTGGCCGACGCTATATG 376
QY 364 TTCTTTAAATTTTGA 380
Db 377 TTCTTTAAATTTTGA 393

RESULT 10
AAH5089
ID AAH5089 standard; DNA; 1396 BP.
XX
XX AC AAH5089;
XX
XX DT 03-SEP-2001 (first entry)
XX
XX DE S. epidermidis genomic polynucleotide sequence SEQ ID NO:4453.
XX
XX KW Staphylococcus epidermidis SR1 strain; infection; diagnosis;
XX vaccination; endocarditis; ds.
XX
XX OS Staphylococcus epidermidis.
XX
XX PN WO200134809-A2.
XX
XX PD 17-MAY-2001.
XX
XX PF 09-NOV-2000; 2000WO-US30782.
XX
XX PR 09-NOV-1999; 99US-0164258.
XX
XX PA (GLAXO) GLAXO GROUP LTD.
XX
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PN WO200134809-A2.
XX 17-MAY-2001.
XX 09-NOV-2000; 2000WO-US30782.
XX 09-NOV-1999; 99US-0164258.
XX (GLAX ) GLAXO GROUP LTD.
XX Kimmerly WJ;
XX WPI; 2001-316495/33.
XX Nucleic acids encoding polypeptides from Staphylococcus epidermidis,
XX useful for vaccinating against infections, e.g. endocarditis -
XX Claim 8; Page 2096-2097; 2188pp; English.
XX
XX AAH52304 to AAH53970 represent nucleic acids (I) encoding polypeptides
XX (II), given in AAG81454 to AAG83120, from Staphylococcus epidermidis.
XX (I) and (II) can have antibacterial activity and therefore can be used
XX in vaccination. The nucleic acids (I) may be used to produce the
XX S. epidermidis polypeptides (II) via the production of vectors
XX containing them which are used to produce hosts cells which express the
XX polypeptides. The polypeptides (II) (and/or nucleic acids) may then be
XX used to vaccinate subjects and to raise antibodies against the bacteria.
XX The polypeptides may also be used to assay for other inhibitors of their
XX activity and therefore identify compounds that may be used for the
XX treatment of S. epidermidis infections, e.g. endocarditis. AAH53971 to
XX AAH55090 represent specifically claimed S. epidermidis genomic DNA
XX polynucleotide sequences from the present invention. AAH55091 to
XX AAH55098 represent oligonucleotide sequences and primers which are used
XX in the exemplification of the present invention.
XX N.B. The present invention specifically claims all the polynucleotide
XX sequences given in the sequence listing of the present specification,
XX however the sequence listing only goes up to SEQ ID NO:4454 so even
XX though sequences are given in the disclosure for SEQ ID NO:4465 to 4472,
XX no sequences are present for SEQ ID NO:4455 to 4464.
XX
XX Sequence 3444 BP; 1203 A; 597 C; 723 G; 921 T; 0 other;
XX
XX Query Match 21.3%; Score 110.8; DB 22; Length 3444;
XX Best Local Similarity 77.1%; Pred. No. 7.1e-25;
XX Matches 148; Conservative 0; Mismatches 42; Indels 2; Gaps 1;
XX
QY 80 TGTATAGTCTGTAGCTCAGTTGGTTAGAGCGCACCCCTGTATAGGTCAGGTCGGCAG 139
DB 2705 TTTAATGGCCCTATAGCTCAGCTGGTTAGAGCGCACGCCCTGTATAGGTCAGGTCGGTGG 2764
QY 140 TTCAAATCGCCAGACCTACCAATTCGTTGGTCGAGAGAAATACGGGGCCATAGCTCAG 199
DB 2765 TTCGAGTCACCTTAGGCCACCATTCATTAATT--TAAACACCTTAGGGGCTTAGCTCAG 2822
QY 200 CTGGAGAGCGCCTGCTTGCAGCGAGGAGGTCAGGTCGATCCGCTTGGCTCCACC 259
DB 2823 CTGGAGAGCGCCTGCTTGCAGCGAGGAGGTCAGGTCGATCCGCTTGGCTCCACC 2882
QY 260 ACTCTCTCGTGT 271
DB 2883 ATTATATTTTGT 2894
XX
RESULT 13
AAH54300
ID AAH54300 standard; DNA; 4429 BP.
XX
XX AC AAH54300;
XX
XX 03-SEP-2001 (first entry)
XX
XX S. epidermidis genomic polynucleotide sequence SEQ ID NO:3664.
XX
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KW Staphylococcus epidermidis SRI strain; infection; diagnosis;
XX vaccination; endocarditis; ds.
OS Staphylococcus epidermidis.
XX
XX WO200134809-A2.
XX 17-MAY-2001.
XX 09-NOV-2000; 2000WO-US30782.
XX 09-NOV-1999; 99US-0164258.
XX (GLAX ) GLAXO GROUP LTD.
XX Kimmerly WJ;
XX WPI; 2001-316495/33.
XX
XX Nucleic acids encoding polypeptides from Staphylococcus epidermidis,
XX useful for vaccinating against infections, e.g. endocarditis -
XX Claim 8; Page 1270-1272; 2188pp; English.
XX
XX AAH52304 to AAH53970 represent nucleic acids (I) encoding polypeptides
XX (II), given in AAG81454 to AAG83120, from Staphylococcus epidermidis.
XX (I) and (II) can have antibacterial activity and therefore can be used
XX in vaccination. The nucleic acids (I) may be used to produce the
XX S. epidermidis polypeptides (II) via the production of vectors
XX containing them which are used to produce hosts cells which express the
XX polypeptides. The polypeptides (II) (and/or nucleic acids) may then be
XX used to vaccinate subjects and to raise antibodies against the bacteria.
XX The polypeptides may also be used to assay for other inhibitors of their
XX activity and therefore identify compounds that may be used for the
XX treatment of S. epidermidis infections, e.g. endocarditis. AAH53971 to
XX AAH55090 represent specifically claimed S. epidermidis genomic DNA
XX polynucleotide sequences from the present invention. AAH55091 to
XX AAH55098 represent oligonucleotide sequences and primers which are used
XX in the exemplification of the present invention.
XX N.B. The present invention specifically claims all the polynucleotide
XX sequences given in the sequence listing of the present specification,
XX however the sequence listing only goes up to SEQ ID NO:4454 so even
XX though sequences are given in the disclosure for SEQ ID NO:4465 to 4472,
XX no sequences are present for SEQ ID NO:4455 to 4464.
XX
XX Sequence 4429 BP; 1327 A; 928 C; 1004 G; 1170 T; 0 other;
XX
XX Query Match 21.3%; Score 110.8; DB 22; Length 4429;
XX Best Local Similarity 77.1%; Pred. No. 8e-25;
XX Matches 148; Conservative 0; Mismatches 42; Indels 2; Gaps 1;
XX
QY 80 TGTATAGTCTGTAGCTCAGTTGGTTAGAGCGCACCCCTGTATAGGTCAGGTCGGCAG 139
DB 2765 TTTAATGGCCCTATAGCTCAGCTGGTTAGAGCGCACGCCCTGTATAGGTCAGGTCGGTGG 2824
QY 140 TTCAAATCGCCAGACCTACCAATTCGTTGGTCGAGAGAAATACGGGGCCATAGCTCAG 199
DB 2825 TTCGAGTCACCTTAGGCCACCATTCATTAATT--TAAACACCTTAGGGGCTTAGCTCAG 2882
QY 200 CTGGAGAGCGCCTGCTTGCAGCGAGGAGGTCAGGTCGATCCGCTTGGCTCCACC 259
DB 2883 CTGGAGAGCGCCTGCTTGCAGCGAGGAGGTCAGGTCGATCCGCTTGGCTCCACC 2942
QY 260 ACTCTCTCGTGT 271
DB 2943 ATTATATTTTGT 2954
XX
RESULT 14
AAV78022
ID AAV78022 standard; DNA; 400 BP.
XX
XX AC AAV78022;
```

XX 16-MAR-1999 (first entry)  
XX Staphylococcus aureus contig SEQ ID #3711.  
XX  
XX Computer readable medium; vaccine; S.aureus infection; immunodetection;  
KW cellulitis; eyelid infection; food poisoning; osteomyelitis; therapy;  
KW skin infection; surgical wound infection; scalded skin syndrome;  
KW toxic shock syndrome; ds.  
XX Staphylococcus aureus.  
XX  
XX EP786519-A2.  
XX 30-JUL-1997.  
XX 07-JAN-1997; 97EP-0100117.  
XX 05-JAN-1996; 96US-0009861.  
XX (HUMA-) HUMAN GENOME SCI INC.  
XX Barash SC, Choi GH, Dillon PJ, Fannon MR, Kunsch CA;  
XX Rosen CA;  
XX WPI; 1997-374922/35.  
XX Polynucleotide(s) and proteins derived from Staphylococcus aureus -  
PT stored on computer readable medium and used in the production of  
PT anti-S.aureus vaccines  
XX  
PS Claim 1; Page 2654; 3271pp; English.  
XX  
XX This sequence represents one of 5191 Staphylococcus aureus DNA sequences  
CC of the invention. The DNA sequences are recorded on a computer readable  
CC medium, preferably selected from a floppy or hard disk, random access  
CC memory (RAM), read-only memory (ROM) or CD-ROM. Homology searches using  
CC the S.aureus DNA sequences allows putative functions to be assigned so  
CC that protein-encoding or regulatory regions of commercial, therapeutic or  
CC industrial importance can be obtained. Specifically, sequences which are  
CC likely to encode antigens have been identified and these polypeptides can  
CC be used in a vaccine composition against S.aureus infection. The  
CC polypeptides can also be used in a kit for the immunodetection of  
CC S.aureus in a sample. S.aureus is implicated in numerous human diseases,  
CC including cellulitis, eyelid infections, food poisoning, osteomyelitis,  
CC skin and surgical wound infections, scalded skin syndrome, toxic shock  
CC syndrome, etc. Organisms transformed with the DNA sequences can be used  
CC for recombinant production of the polypeptides. The new DNA sequences  
CC (and their fragments) are useful as primers or probes for isolating  
CC homologues of any of the S.aureus DNA sequences contained on the  
XX computer readable medium.  
XX  
SQ Sequence 400 BP; 104 A; 79 C; 104 G; 113 T; 0 other;  
Query Match 21.0%; Score 109.4; DB 18; Length 400;  
Best Local Similarity 78.4%; Pred. No. 6.8e-25;  
Matches 145; Conservative 0; Mismatches 36; Indels 4; Gaps 1;  
QY 82 TTATAGGCTGTAGCTGAGTGGTTAGAGCGCACCCCTGTAGAGGTGAGGTGCGCAGTT 141  
DB 186 TAATGGCCCTATAGCTAGCTGAGTGGTTAGAGCGCACCCCTGTAGAGGTGAGGTGCGTGGT 245  
QY 142 CAAATCTGCCAGACCTACCAATCTGTTGGTCGAGAGAAATACGGGGCCATCAGTCAGCT 201  
DB 246 CGAGTCCACTTAGGCCCCACCAATTAATTT-----AATACCTATTGTTGGGCTTAGCTCAGCT 301  
QY 202 GGGAGAGCGCCCTGCTTGCACGAGGAGGTGAGTGGTTCGATCCCGCTTGGCTCCACCAC 261  
DB 302 GGGAGAGCGCCCTGCTTGCACGAGGAGGTGAGTGGTTCGATCCCGCTTGGCTCCACCAC 361  
QY 262 TCTCT 266  
DB 362 TATTT 366

RESULT 15  
AAV77902/c  
ID AAV77902 standard; DNA; 400 BP.  
XX  
XX AAV77902;  
AC  
XX 16-MAR-1999 (first entry)  
DT  
XX  
XX Staphylococcus aureus contig SEQ ID #3591.  
XX  
XX Computer readable medium; vaccine; S.aureus infection; immunodetection;  
KW cellulitis; eyelid infection; food poisoning; osteomyelitis; therapy;  
KW skin infection; surgical wound infection; scalded skin syndrome;  
KW toxic shock syndrome; ds.  
XX  
XX Staphylococcus aureus.  
OS  
XX  
XX Key Location/Qualifiers  
FT misc\_feature 361..400  
FT /\*tag= a  
FT /note= "these bases represent a line of missing text in  
FT the sequence listing in the specification. They  
FT are included to maintain the nucleotide numbering  
FT given in the specification for this DNA sequence"  
XX  
XX EF786519-A2.  
PN  
XX  
XX 30-JUL-1997.  
PD  
XX  
XX 07-JAN-1997; 97EP-0100117.  
PF  
XX  
XX 05-JAN-1996; 96US-0009861.  
PR  
XX (HUMA-) HUMAN GENOME SCI INC.  
PA  
XX Barash SC, Choi GH, Dillon PJ, Fannon MR, Kunsch CA;  
PI Rosen CA;  
XX  
XX WPI; 1997-374922/35.  
DR  
XX Polynucleotide(s) and proteins derived from Staphylococcus aureus -  
PT stored on computer readable medium and used in the production of  
PT anti-S.aureus vaccines  
XX  
PS Claim 1; Page 2600; 3271pp; English.  
XX  
XX This sequence represents one of 5191 Staphylococcus aureus DNA sequences  
CC of the invention. The DNA sequences are recorded on a computer readable  
CC medium, preferably selected from a floppy or hard disk, random access  
CC memory (RAM), read-only memory (ROM) or CD-ROM. Homology searches using  
CC the S.aureus DNA sequences allows putative functions to be assigned so  
CC that protein-encoding or regulatory regions of commercial, therapeutic or  
CC industrial importance can be obtained. Specifically, sequences which are  
CC likely to encode antigens have been identified and these polypeptides can  
CC be used in a vaccine composition against S.aureus infection. The  
CC polypeptides can also be used in a kit for the immunodetection of  
CC S.aureus in a sample. S.aureus is implicated in numerous human diseases,  
CC including cellulitis, eyelid infections, food poisoning, osteomyelitis,  
CC skin and surgical wound infections, scalded skin syndrome, toxic shock  
CC syndrome, etc. Organisms transformed with the DNA sequences can be used  
CC for recombinant production of the polypeptides. The new DNA sequences  
CC (and their fragments) are useful as primers or probes for isolating  
CC homologues of any of the S.aureus DNA sequences contained on the  
XX computer readable medium.  
XX  
SQ Sequence 400 BP; 105 A; 82 C; 66 G; 107 T; 40 other;  
Query Match 21.0%; Score 109.4; DB 18; Length 400;  
Best Local Similarity 78.4%; Pred. No. 6.8e-25;  
Matches 145; Conservative 0; Mismatches 36; Indels 4; Gaps 1;

Qy	82	TTATAGTCGTGTA	CTAGCT	AGTTGGTTAG	AGCGCACCCCTG	GATAGAGGTGAGGTCG	CAGCT	141
Db	277	TAATGGGCGCTAT	AGCTCAGCT	CGCTGTTAG	AGCGCACGCGCT	GATAAGCGTGAGGTCG	TGGTT	218
Qy	142	CAATCTGCCAGAC	CTACCAAT	TGCTTGGT	CGACAAGATA	AGGGGCCATAGCT	TCAGCT	201
Db	217	CGAGTCCACTT	AGGCCCGACCAT	TAATTT	----AATACCTAT	TTTGGGGGCTTAGCT	TCAGCT	162
Qy	202	GGGAGAGCGCT	GCCTTGC	CACGAGG	GTCA	GGTTCGATCCGCGCTTGG	CTCCACCAC	261
Db	161	GGGAGAGCGCT	GCCTTGC	CACGAGG	GTCA	GGTTCGATCCGCGCTTGG	CTCCACCAC	102
Qy	262	TCCTCT	266					
Db	101	TATTTT	97					

Search completed: February 1, 2003, 01:33:22  
Job time : 374.136 secs

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OM nucleic - nucleic search, using sw model

Run on: February 1, 2003, 01:17:06 ; Search time 27.0349 Seconds  
(without alignments)  
5898.736 Million cell updates/sec

Title: US-09-931-486-112

Perfect score: 520

Sequence: 1 ATCGAGACATCAGCTTCTT.....CAGATTGCTTGGGTTATAT 520

Scoring table: IDENTITY\_NUC

Gapop 10.0 , Gapext 1.0

Searched: 441362 seqs, 15338381 residues

Total number of hits satisfying chosen parameters: 882724

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Issued Database NA.\*  
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2: /cgn2\_6/ptodata/1/ina/5B\_COMB.seq.\*  
3: /cgn2\_6/ptodata/1/ina/6A\_COMB.seq.\*  
4: /cgn2\_6/ptodata/1/ina/6B\_COMB.seq.\*  
5: /cgn2\_6/ptodata/1/ina/PCTUS\_COMB.seq.\*  
6: /cgn2\_6/ptodata/1/ina/backfiles1.seq.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	520	100.0	520	3	US-08-765-332-112 Sequence 112, App
2	520	100.0	520	4	US-09-448-894-112 Sequence 112, App
3	249	47.9	504	3	US-08-765-332-113 Sequence 113, App
4	249	47.9	504	4	US-09-448-894-113 Sequence 113, App
5	193.2	37.2	499	3	US-08-765-332-114 Sequence 114, App
6	193.2	37.2	499	4	US-09-448-894-114 Sequence 114, App
7	178	34.2	468	3	US-08-765-332-115 Sequence 115, App
8	178	34.2	468	4	US-09-448-894-115 Sequence 115, App
9	174	33.5	471	3	US-08-765-332-111 Sequence 111, App
10	174	33.5	471	4	US-09-448-894-111 Sequence 111, App
11	113.8	21.9	470	3	US-08-765-332-195 Sequence 195, App
12	113.8	21.9	470	4	US-09-448-894-195 Sequence 195, App
13	111	21.3	582	1	US-08-412-614-87 Sequence 87, App1
14	111	21.3	582	2	US-08-635-761-87 Sequence 87, App1
15	111	21.3	582	4	US-09-312-520-87 Sequence 215, App
16	104	20.0	463	3	US-08-765-332-215 Sequence 215, App
17	104	20.0	463	4	US-09-448-894-215 Sequence 215, App
18	104	20.0	475	3	US-08-765-332-214 Sequence 214, App
19	104	20.0	475	4	US-09-448-894-214 Sequence 214, App
20	101.4	19.5	590	1	US-08-412-614-88 Sequence 88, App1
21	101.4	19.5	590	2	US-08-635-761-88 Sequence 88, App1
22	101.4	19.5	590	4	US-09-312-520-88 Sequence 215, App
23	97.8	18.8	363	3	US-08-765-332-119 Sequence 119, App
24	97.8	18.8	363	4	US-09-448-894-119 Sequence 119, App
25	97.4	18.7	808	3	US-08-765-332-131 Sequence 131, App
26	97.4	18.7	808	4	US-09-448-894-131 Sequence 131, App
27	97.4	18.7	808	4	US-09-448-894-131 Sequence 131, App

28 97.4 18.7 808 4 US-09-448-894-132 Sequence 132, App  
29 97.4 18.7 809 3 US-08-765-332-154 Sequence 154, App  
30 97.4 18.7 809 4 US-09-448-894-154 Sequence 154, App  
31 95 18.3 496 3 US-08-765-332-120 Sequence 120, App  
32 95 18.3 496 4 US-09-448-894-120 Sequence 120, App  
33 91.6 17.6 498 3 US-08-765-332-121 Sequence 121, App  
34 91.6 17.6 498 4 US-09-448-894-121 Sequence 121, App  
35 91.6 17.6 603 1 US-08-412-614-85 Sequence 85, App1  
36 91.6 17.6 603 1 US-08-412-614-85 Sequence 85, App1  
37 91.6 17.6 603 2 US-08-635-761-86 Sequence 86, App1  
38 91.6 17.6 603 2 US-08-635-761-86 Sequence 86, App1  
39 91.6 17.6 603 4 US-09-312-520-85 Sequence 85, App1  
40 91.6 17.6 603 4 US-09-312-520-86 Sequence 86, App1  
41 89.2 17.2 664 1 US-08-412-614-89 Sequence 89, App1  
42 82.8 15.9 249 3 US-08-765-332-128 Sequence 128, App  
43 82.8 15.9 249 4 US-09-448-894-128 Sequence 128, App  
44 81.2 15.6 618 4 US-09-703-807-15 Sequence 15, App1  
45 81.2 15.6 619 4 US-09-703-807-13 Sequence 13, App1

#### ALIGNMENTS

RESULT 1  
US-08-765-332-112  
; Sequence 112, Application US/08765332  
; Patent No. 6025132  
; GENERAL INFORMATION:  
; APPLICANT: JANNES, GEERT  
; APPLICANT: ROSSAU, RUDI  
; APPLICANT: VAN HEUVERSWYN, HUGO  
; TITLE OF INVENTION: SIMULTANEOUS DETECTION, IDENTIFICATION  
; TITLE OF INVENTION: AND DIFFERENTIATION OF EUBACTERIAL TAXA USING A  
; TITLE OF INVENTION: HYBRIDIZATION ASSAY  
; NUMBER OF INVENTION: 216  
; NUMBER OF SEQUENCES: 216  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: NIXON & VANDERHYE P.C.  
; STREET: 1100 NORTH GLEBE ROAD, 8TH FLOOR  
; CITY: WASHINGTON  
; STATE: D.C.  
; COUNTRY: USA  
; ZIP: 22201  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/765,332  
; FILING DATE: 23-DEC-1996  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: WO PCT/EP95/02452  
; FILING DATE: 23-JUN-1995  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: EP 95870032.0  
; FILING DATE: 07-APR-1995  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: EP 94870106.5  
; FILING DATE: 24-JUN-1994  
; ATTORNEY/AGENT INFORMATION:  
; NAME: SADOFF, B.J.  
; REGISTRATION NUMBER: 36,663  
; REFERENCE/DOCKET NUMBER: 1487-14  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 703-816-4091  
; TELEFAX: 703-816-4100  
; INFORMATION FOR SEQ ID NO: 112:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 520 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear

; MOLECULE TYPE: CDNA  
; HYPOTHETICAL: NO  
; ANTI-SENSE: NO  
US-08-765-332-112

Query Match 100.0%; Score 520; DB 3; Length 520;  
Best Local Similarity 100.0%; Pred. No. 1.4e-162;  
Matches 520; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATCGAAGACATCAGCTTCTTCAAGTATCCACACAAATTCCTGATTCATATGTCGAACG 60  
Db 1 ATCGAAGACATCAGCTTCTTCAAGTATCCACACAAATTCCTGATTCATATGTCGAACG 60  
QY 61 AATGCTGTAAACGGACCCGCTGTATAGGCTGTAGCTCAGTGGTGTAGAGCGCACCCCTG 120  
Db 61 AATGCTGTAAACGGACCCGCTGTATAGGCTGTAGCTCAGTGGTGTAGAGCGCACCCCTG 120  
QY 121 ATAAGGGTGAGTTCGGCAGTTCAAAATCTCCAGACCTACCAATTCCTTGGTCGAGAAG 180  
Db 121 ATAAGGGTGAGTTCGGCAGTTCAAAATCTCCAGACCTACCAATTCCTTGGTCGAGAAG 180  
QY 181 ATACGGGGCCATAGCTCAGCTGGGAGAGCGCCTGCTTGCACGACGAGGTTCAGCGGTTTC 240  
Db 181 ATACGGGGCCATAGCTCAGCTGGGAGAGCGCCTGCTTGCACGACGAGGTTCAGCGGTTTC 240  
QY 241 GATCCCGCTTGGCTCCACCACTCTCTCGTGTGGCGGTGAGTGTAAAGAGTTTCAGAAATG 300  
Db 241 GATCCCGCTTGGCTCCACCACTCTCTCGTGTGGCGGTGAGTGTAAAGAGTTTCAGAAATG 300  
QY 301 ATCCCGCTTACGTTTGTCTGCTGAGTGTCTGATTCCTGCTTGTGACGAGGTTCAGCGGTTTC 360  
Db 301 ATCCCGCTTACGTTTGTCTGCTGAGTGTCTGATTCCTGCTTGTGACGAGGTTCAGCGGTTTC 360  
QY 361 TCGTCTTTAAATTTGGATATGATAGAGTGTCTGATTCCTGCTTGTGACGAGGTTCAGCGGTTTC 420  
Db 361 TCGTCTTTAAATTTGGATATGATAGAGTGTCTGATTCCTGCTTGTGACGAGGTTCAGCGGTTTC 420  
QY 421 TTGATCTGTCAAGTAAATTTGATGTTCTCAAGACCGCAATTTTCGGCGAATGTCGTC 480  
Db 421 TTGATCTGTCAAGTAAATTTGATGTTCTCAAGACCGCAATTTTCGGCGAATGTCGTC 480  
QY 481 TTCAGATTGAGACAGTAACCAAGATTGCTTGGGGTTTAT 520  
Db 481 TTCAGATTGAGACAGTAACCAAGATTGCTTGGGGTTTAT 520

## RESULT 2

US-09-448-894-112  
; Sequence 112, Application US/09448894  
; Patent No. 6312903

## GENERAL INFORMATION:

APPLICANT: JANNES, GEERT

~~ROSS, KUDI~~

VAN HEUVERSWYN, HUGO

TITLE OF INVENTION: SIMULTANEOUS DETECTION, IDENTIFICATION  
AND DIFFERENTIATION OF EUBACTERIAL TAXA USING A  
HYBRIDIZATION ASSAY

NUMBER OF SEQUENCES: 216

CORRESPONDENCE ADDRESS:

ADDRESSEE: NIXON & VANDERHYE P.C.  
STREET: 1100 NORTH GLEBE ROAD, 8TH FLOOR  
CITY: WASHINGTON  
STATE: D.C.  
COUNTRY: USA  
ZIP: 22201

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA: US/09/448,894  
APPLICATION NUMBER: 6312903-1999  
FILING DATE: 29-No. 6312903-1999

CLASSIFICATION: <Unknown>  
07-APR-1995  
24-JUN-1994

## PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/765,332  
FILING DATE: <Unknown>  
APPLICATION NUMBER: EP 95870032.0  
FILING DATE: 07-APR-1995  
APPLICATION NUMBER: EP 94870106.5  
FILING DATE: 24-JUN-1994

## ATTORNEY/AGENT INFORMATION:

NAME: SADOFF, B.J.  
REGISTRATION NUMBER: 36,663  
REFERENCE/DOCKET NUMBER: 1487-14  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 703-816-4091  
TELEFAX: 703-816-4100

## INFORMATION FOR SEQ ID NO: 112:

SEQUENCE CHARACTERISTICS:  
LENGTH: 520 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: CDNA  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
SEQUENCE DESCRIPTION: SEQ ID NO: 112:  
US-09-448-894-112

Query Match 100.0%; Score 520; DB 4; Length 520;  
Best Local Similarity 100.0%; Pred. No. 1.4e-162;  
Matches 520; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATCGAAGACATCAGCTTCTTCAAGTATCCACACAAATTCCTGATTCATATGTCGAACG 60  
Db 1 ATCGAAGACATCAGCTTCTTCAAGTATCCACACAAATTCCTGATTCATATGTCGAACG 60  
QY 61 AATGCTGTAAACGGACCCGCTGTATAGGCTGTAGCTCAGTGGTGTAGAGCGCACCCCTG 120  
Db 61 AATGCTGTAAACGGACCCGCTGTATAGGCTGTAGCTCAGTGGTGTAGAGCGCACCCCTG 120  
QY 121 ATAAGGGTGAGTTCGGCAGTTCAAAATCTCCAGACCTACCAATTCCTTGGTCGAGAAG 180  
Db 121 ATAAGGGTGAGTTCGGCAGTTCAAAATCTCCAGACCTACCAATTCCTTGGTCGAGAAG 180  
QY 181 ATACGGGGCCATAGCTCAGCTGGGAGAGCGCCTGCTTGCACGACGAGGTTCAGCGGTTTC 240  
Db 181 ATACGGGGCCATAGCTCAGCTGGGAGAGCGCCTGCTTGCACGACGAGGTTCAGCGGTTTC 240  
QY 241 GATCCCGCTTGGCTCCACCACTCTCTCGTGTGGCGGTGAGTGTAAAGAGTTTCAGAAATG 300  
Db 241 GATCCCGCTTGGCTCCACCACTCTCTCGTGTGGCGGTGAGTGTAAAGAGTTTCAGAAATG 300  
QY 301 ATCCCGCTTACGTTTGTCTGCTGAGTGTCTGATTCCTGCTTGTGACGAGGTTCAGCGGTTTC 360  
Db 301 ATCCCGCTTACGTTTGTCTGCTGAGTGTCTGATTCCTGCTTGTGACGAGGTTCAGCGGTTTC 360  
QY 361 TCGTCTTTAAATTTGGATATGATAGAGTGTCTGATTCCTGCTTGTGACGAGGTTCAGCGGTTTC 420  
Db 361 TCGTCTTTAAATTTGGATATGATAGAGTGTCTGATTCCTGCTTGTGACGAGGTTCAGCGGTTTC 420  
QY 421 TTGATCTGTCAAGTAAATTTGATGTTCTCAAGACCGCAATTTTCGGCGAATGTCGTC 480  
Db 421 TTGATCTGTCAAGTAAATTTGATGTTCTCAAGACCGCAATTTTCGGCGAATGTCGTC 480  
QY 481 TTCAGATTGAGACAGTAACCAAGATTGCTTGGGGTTTAT 520  
Db 481 TTCAGATTGAGACAGTAACCAAGATTGCTTGGGGTTTAT 520

## RESULT 3

US-08-765-332-113  
; Sequence 113, Application US/08765332

Patent No. 6025132  
GENERAL INFORMATION:  
APPLICANT: JANNES, GEERT  
APPLICANT: ROSSAU, RUDI  
APPLICANT: VAN HEUVERSWYN, HUGO  
TITLE OF INVENTION: SIMULTANEOUS DETECTION, IDENTIFICATION  
AND DIFFERENTIATION OF EUBACTERIAL TAXA USING A  
HYBRIDIZATION ASSAY  
NUMBER OF SEQUENCES: 216  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: NIXON & VANDERHVE P.C.  
STREET: 1100 NORTH GLEBE ROAD, 8TH FLOOR  
CITY: WASHINGTON  
STATE: D.C.  
COUNTRY: USA  
ZIP: 22201  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent in Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/765,332  
FILING DATE: 23-DEC-1996  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: WO PCT/EP95/02452  
FILING DATE: 23-JUN-1995  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: EP 95870032.0  
FILING DATE: 07-APR-1995  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: EP 94870106.5  
FILING DATE: 24-JUN-1994  
ATTORNEY/AGENT INFORMATION:  
NAME: SADOFF, B.J.  
REGISTRATION NUMBER: 36,663  
REFERENCE/DOCKET NUMBER: 1487-14  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 703-816-4100  
TELEFAX: 703-816-4100  
INFORMATION FOR SEQ ID NO: 113:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 504 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: CDNA  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
US-08-765-332-113  
Query Match 47.9%; Score 249; DB 3; Length 504;  
Best Local Similarity 74.4%; Pred. No. 7.6e-73;  
Matches 392; Conservative 0; Mismatches 105; Indels 30; Gaps 5;  
QY 1 ATCGAAGACATCAGCTTCTTCATAGTATCCACACGAATGCTGTGATTCATAGTCGAAGC 60  
DB 1 ATCGAAGACACCGCTTCTGTCATAGCTCCACACGAATGCTGTGATTCATAGTCGAAGC 60  
QY 61 AATGCTGTAAACGCGCCGCTGTATATATATATATATATATATATATATATATATATATAT 114  
DB 61 GCGATTGGGTTTAGACCGGAGAGTAAGATTGGTCTGTAGCTCAGTTGGTTAGAGCGCA 120  
QY 115 CCCTGTATAGGTAGGTGGGAGTCAATCTGCCAGACCTACCAATGCTTGTGTCG 174  
DB 121 CCCTGTATAGGTAGGTGGGAGTTCGAATCTGCCAGACCTACCAATGCTTGTGTCG 172  
QY 175 AGAAGATACGGGCGCATCAGCTCAGCTGGGAGAGCGCTCCCTTGCACGAGGAGTTCAG 234  
DB 173 -----AAGGGCCATAGCTCAGCTGGGAGAGCGCTCCTTGGACGAGGAGTTCAG 224  
QY 235 CGGTTGATCCCGCTTGGCTCCACCACTCTCTCTGTTGGGTGAGTGTAAAGAGTTC 294

DB 225 CGGTTGATCCCGCTTGGCTCCACCAATTAACCTAGTCCGCAAGACTCAGAAATCAGTGC 284  
QY 295 GAAATGATGCCGCTTTCAGGTTTCTGCTGTGAGTGTGCTGATTTCTGCTTCTTTGACCGGTA 354  
DB 285 TTTACCAGGATGAGGTGATGCTTGGGTTGAACATGATTTCTGGACTTT-----GCG 338  
QY 355 CGAAATCGTCTTTTAAATAATTTGGATATGTATAGTAAGT-GACTGATTAATGCTTTCA 413  
DB 339 CCAGAACTGCTCTTTTAAATAATTTGGGATGTATGATAGAGTAGACCGATGTTGCTTTCA 398  
QY 414 CTGGCAATGATCTGCTCAAGGTAAATTTGTAGTTCTCAAGACGCAAAATTTTCGGCGAA 473  
DB 399 CTGGCAGCATGCTCGCTCAAGGTAAATTTG-CGTGTTCTCTATGCAAAATTTTCGGCGAA 457  
QY 474 TGTGCTTTCACGATTTGACAGACAGTAACACGATGCTTGGGTTATAT 520  
DB 458 TGTGCTTTCACGTTATAGACACAGTAACACGATGCTTGGGTTATAT 504  
RESULT 4  
US-09-448-894-113  
Sequence 113, Application US/09448894  
Patent No. 6312903  
GENERAL INFORMATION:  
APPLICANT: JANNES, GEERT  
APPLICANT: ROSSAU, RUDI  
APPLICANT: VAN HEUVERSWYN, HUGO  
TITLE OF INVENTION: SIMULTANEOUS DETECTION, IDENTIFICATION  
AND DIFFERENTIATION OF EUBACTERIAL TAXA USING A  
HYBRIDIZATION ASSAY  
NUMBER OF SEQUENCES: 216  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: NIXON & VANDERHVE P.C.  
STREET: 1100 NORTH GLEBE ROAD, 8TH FLOOR  
CITY: WASHINGTON  
STATE: D.C.  
COUNTRY: USA  
ZIP: 22201  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent in Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/448,894  
FILING DATE: 29-NOV-1999  
CLASSIFICATION: <Unknown>  
07-APR-1995  
24-JUN-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/765,332  
FILING DATE: <Unknown>  
APPLICATION NUMBER: EP 95870032.0  
FILING DATE: 07-APR-1995  
APPLICATION NUMBER: EP 94870106.5  
FILING DATE: 24-JUN-1994  
ATTORNEY/AGENT INFORMATION:  
NAME: SADOFF, B.J.  
REGISTRATION NUMBER: 36,663  
REFERENCE/DOCKET NUMBER: 1487-14  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 703-816-4091  
TELEFAX: 703-816-4100  
INFORMATION FOR SEQ ID NO: 113:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 504 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: CDNA  
HYPOTHETICAL: NO  
ANTI-SENSE: NO

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SEQUENCE DESCRIPTION: SEQ ID NO: 113;
US-09-448-894-113

Query Match          47.9%; Score 249; DB 4; Length 504;
Best Local Similarity 74.4%; Pred. No. 7.6e-73;
Matches 392; Conservative 0; Mismatches 105; Indels 30; Gaps 5;

QY 1 ATCGAAGACATCAGCTCTTTCATAGTATCCACACGAAATTCCTGATTCATAGTCGAAACG 60
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1 ATCGAAGACACCGCTTCGTATAGCTCCACACGAAATTCCTGATTCATAGTCGAAACG 60
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

QY 61 AATGCTGTAAACGACCGCTTTATA-----GGTCTGTAGCTAGTGGTTAGAGCGCA 114
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Db 61 GCGATTTGGTTAGACCGGAGAGTAACGATTGGCTGTAGCTAGTGGTTAGAGCGCA 120
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

QY 115 CCCCTGATAAGGTTGAGTCCGAGTTCGAAATCTGCCAGACCTACCAATTCCTTGGTCG 174
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 121 CCCCTGATAAGGTTGAGTCCGAGTTCGAAATCTGCCAGACCTACCAATTCCTTGGTCG 174
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

QY 175 AGAAGATACGGGGCCATAGCTAGCTGGGAGAGCGCTGCTTGCACGACGAGGTCAG 234
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 173 -----AAGGGCCATAGCTAGCTGGGAGAGCGCTGCTTGCACGACGAGGTCAG 224
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

QY 235 CGGTTCCGATCCGCTGGCTCCACCACTCTCTGTTGGGTGAGTGTAAAGAGTTCA 294
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 225 CGGTTCCGATCCGCTGGCTCCACCACTCTCTGTTGGGTGAGTGTAAAGAGTTCA 284
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

QY 295 GAAATGATGCGGCTTACAGGTTGTCCTTGAAGTCTGATTCGCTGCTTGGACCGTA 354
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 285 TTTACAGGATGAGTTGATTCGCTGGTGAACATGATTCGCTGCTTGGACCTTT-----GCG 338
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

QY 355 CGAAATCGTCTTTAAAAATTTGGATATGTGATAGAGT-GACTGATTAATTCCTTCA 413
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 339 CGAAATCGTCTTTAAAAATTTGGATATGTGATAGAGTAGACCGGATGTGCTTCA 398
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

QY 414 CTGCAATTCATCTGTCAGGTAAGTAAATTTGATGTTCTCAAGACGCAAAATTTCCGGCGAA 473
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 399 CTGCGACATGTCGCTCAAGGTAAGTAAATTTG-CGTGTTCTCTATGCAAAATTTTCGGCGAA 457
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

QY 474 TGTGCTTCCAGGATGAGACAGTAACCAAGATTGCTTGGGGTTATAT 520
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 458 TGTGCTTCCAGGATGAGACAGTAACCAAGATTGCTTGGGGTTATAT 504
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

RESULT 5
US-08-765-332-114
; Sequence 114, Application US/08765332
; Patent No. 6025132
; GENERAL INFORMATION:
; APPLICANT: JANNES, GEERT
; APPLICANT: ROSSAU, RUDI
; APPLICANT: VAN HEUVERSWYN, HUGO
; TITLE OF INVENTION: SIMULTANEOUS DETECTION, IDENTIFICATION
; TITLE OF INVENTION: AND DIFFERENTIATION OF EUBACTERIAL TAXA USING A
; NUMBER OF SEQUENCES: 216
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: NIXON & VANDERHUYE P.C.
; STREET: 1100 NORTH GLEBE ROAD, 8TH FLOOR
; CITY: WASHINGTON
; STATE: D.C.
; COUNTRY: USA
; ZIP: 22201
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08765,332
; FILING DATE: 23-DEC-1996
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICANT: JANNES, GEERT
```



ROSSAU, RUDI  
VAN HEUVERSWEYN, HUGO  
TITLE OF INVENTION: SIMULTANEOUS DETECTION, IDENTIFICATION  
AND DIFFERENTIATION OF EUBACTERIAL TAXA USING A  
HYBRIDIZATION ASSAY  
NUMBER OF SEQUENCES: 216  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: NIXON & VANDERHYE P.C.  
STREET: 1100 NORTH GLEBE ROAD, 8TH FLOOR  
CITY: WASHINGTON  
STATE: D.C.  
COUNTRY: USA  
ZIP: 22201  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/448,894  
FILING DATE: 29-Nov-1999  
CLASSIFICATION: <Unknown>  
07-APR-1995  
24-JUN-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/765,332  
FILING DATE: <Unknown>  
APPLICATION NUMBER: EP 95870032.0  
FILING DATE: 07-APR-1995  
APPLICATION NUMBER: EP 94870106.5  
FILING DATE: 24-JUN-1994  
ATTORNEY/AGENT INFORMATION:  
NAME: SADOFF, B.J.  
REGISTRATION NUMBER: 36,663  
REFERENCE/DOCKET NUMBER: 1487-14  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 703-816-4091  
TELEFAX: 703-816-4100  
INFORMATION FOR SEQ ID NO: 114:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 499 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: CDNA  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
SEQUENCE DESCRIPTION: SEQ ID NO: 114:  
US-09-448-894-114

Query Match 37.2%; Score 193.2; DB 4; Length 499;  
Best Local Similarity 72.8%; Pred. No. 2.3e-54;  
Matches 386; Conservative 0; Mismatches 103; Indels 41; Gaps 9;  
QY 1 ATCGAAGACATCAGCTTCTTCATAGTATCCACACGAATGCTTGATTGATGTCGAAGC 60  
DB 1 ATCGAAGACTCAGCTTCTTCATAGTATCCACACGAATGCTTGATTGATGTCGAAGC 60  
QY 61 ATGCTGTACAGGACCCGCTGTATATA-----GGTCTAGCTCAGTGTGTTAGACGCA 114  
DB 61 GCGATTGGGTTGAGACCCGAGAGTACGATTGGGCTGTAGCTCAGTGTGTTAGACGCA 120  
QY 115 CCCCTGATAGGTTGAGTGGCGAGTCAAACTGCTCCAGACCTACCAATGCTTG--G 171  
DB 121 CCCCTGATAGGTTGAGTGGCGAGTTCGAATCTGCCAGACCCACCAATGTCGGGATG 180  
QY 172 TCAGAGAGATACGGGGCCATAGCTCAGCTGGGAGAGCGCTGCTTGCACGAGGAGGT 231  
DB 181 GCGAGTGTCAATGGGGCCATAGCTCAGCTGGGAGAGCGCTGCTTGCACGAGGAGGT 240  
QY 232 CAGCGGTTGATCCCGCTTGGCTCCACCACTCTCTCGTGTGCGGTGAGTGTAAAGAGT 291  
DB 241 CAGGAGTTCGATCTCTTGGCTCCACCACTCACTCAG-----ATCGCTGAAGC 291

QY 292 TCAGAAATGATGCGCTTCAGGTTTCTGCTGTTGAGTCTGCTGATTCTCTGTTGACCG 351  
DB 292 TCAGAAATGA-----ACATGTTGATGTTCAATGTTGATTTCTGTTCTTT----- 334  
QY 352 GTAGGAAATCGTTCTTTTAAATAATTTGATATGTGATAGAGTACTGATTAAATGCTTT 411  
DB 335 GCGCAGAACTGTTCTTTTAAATAATTTGGGTATGTATAGAACTGACTAACACGCTG-TTT 393  
QY 412 CACTGGCAATGATCTGCTCAAGGTAAATAATTTGATTTCTCAAGACGCAAAATTTTCGCG 471  
DB 394 CACTGCACGTTG--TTAATCAAGGCANAATTG--CGAGTTCAAGCGGAATTTTCGCG 449  
QY 472 AATGTCGCTTTCACGAT-TGACACAGATTAACACAGATTGCTTGGGGTTATAT 520  
DB 450 AATGTCGCTTTCACGATTAACACAGATTGCTTGGGGTTATAT 499  
RESULT 7  
US-08-765-332-115  
; Sequence 115, Application US/08765332  
; Patent No. 6025132  
; GENERAL INFORMATION:  
; APPLICANT: JANNES, GEERT  
; APPLICANT: ROSSAU, RUDI  
; APPLICANT: VAN HEUVERSWEYN, HUGO  
; TITLE OF INVENTION: SIMULTANEOUS DETECTION, IDENTIFICATION  
; TITLE OF INVENTION: AND DIFFERENTIATION OF EUBACTERIAL TAXA USING A  
; TITLE OF INVENTION: HYBRIDIZATION ASSAY  
; NUMBER OF SEQUENCES: 216  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: NIXON & VANDERHYE P.C.  
; STREET: 1100 NORTH GLEBE ROAD, 8TH FLOOR  
; CITY: WASHINGTON  
; STATE: D.C.  
; COUNTRY: USA  
; ZIP: 22201  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/765,332  
; FILING DATE: 23-DEC-1996  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: WO PCT/EP95/02452  
; FILING DATE: 23-JUN-1995  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: EP 95870032.0  
; FILING DATE: 07-APR-1995  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: EP 94870106.5  
; FILING DATE: 24-JUN-1994  
; ATTORNEY/AGENT INFORMATION:  
; NAME: SADOFF, B.J.  
; REGISTRATION NUMBER: 36,663  
; REFERENCE/DOCKET NUMBER: 1487-14  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 703-816-4091  
; TELEFAX: 703-816-4100  
; INFORMATION FOR SEQ ID NO: 115:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 468 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: CDNA  
; HYPOTHETICAL: NO  
; ANTI-SENSE: NO  
; US-08-765-332-115

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Query Match      34.2%  Score 178;  DB 3;  Length 468;
Best Local Similarity 71.1%;  Pred. No. 2.4e-49;
Matches 371;  Conservative 0;  Mismatches 95;  Indels 56;  Gaps 8;

QY  1 ATCGAGACATCAGCTTCTTCATAGTATCCACAGCAATGCTTGAATCATAGTCAAGC 60
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db  1 ATCGAGACATCAGCTTCTTCATAGTATCCACAGCAATGCTTGAATCATAGTCAAGC 60
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

QY  61 AATGCTGTAAAGCGGCGGCTGTATAGTCTGTAGCTCAGTGTGGTGTAGAGCGCACCCCTG 120
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db  61 CGATTAGGTAGCAACCTTCGAT-TGGGCTGTAGCTCAGTGTGGTGTAGAGCGCACCCCTG 119
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

QY  121 ATAAGGTTAGGTGCGGAGTCAATCTGCCAGACCTACCAATGCTTGTGTCGAGAAGA 180
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db  120 ATAAGGTTAGGTGCGGAGTCAATCTGCCAGACCTACCAATGCTTGTGTCGAGAAGA 180
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

QY  181 ATACGGGCCATAGCTCAGCTGGGAGAGCGCTGCTTGCACGAGGAGTCAAGGTTTC 240
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db  169 ----GGGGCCATAGCTCAGCTGGGAGAGCGCTGCTTGCACGAGGAGTCAAGGTTTC 224
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

QY  241 GATCCCGCTTGGCTCCACCACTCTCTCGTGTGGGTTGAGTGTAAAGAGTTCAGAAATG 300
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db  225 GATCCCGCTTGGCTCCACCACTCTCTCGTGTGGGTTGAGTGTAAAGAGTTCAGAAATG 277
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

QY  301 ATGCCGCTTCAAGTGTTCCTGCTGTAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 360
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db  278 A-----ATATTCGCGTGAATATGATTTCTGAACCTT-----TATCAGAA 317
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

QY  361 TCGTTCCTTTAAAAATTTGGATATGTATAGAGTGAAGTGAATGCTTGAATGCTTCACTGC 418
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db  318 TCGTTCCTTTAAAAATTTGGATATGTATAGAGTGAAGTGAATGCTTGAATGCTTCACTGC 377
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

QY  419 AATTGATCTGGTCAAGTAAATTTGTAGTCTCAAGACGCAAAATTTTCGCGCAATGTCG 478
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db  378 GTGTGTTCAAGCTAAGTAAATTTGTAGTCTCAAGACGCAAAATTTTCGCGCAATGTCG 433
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

QY  479 TCTTCAGGATTGAGACAGTAACCAAGATGCTTGGGTTATAT 520
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db  434 TCTTCAC-----AGTATACCAAGATGCTTGGGTTATAT 468
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

RESULT 9
US-09-448-894-115
; Sequence 115, Application US/08765332
; Patent No. 6025132
; GENERAL INFORMATION:
; APPLICANT: JANNES, GEERT
; APPLICANT: ROSSAU, RUDI
; APPLICANT: VAN HEUVERSWYN, HUGO
```

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Query Match      34.2%  Score 178;  DB 4;  Length 468;
Best Local Similarity 71.1%;  Pred. No. 2.4e-49;
Matches 371;  Conservative 0;  Mismatches 95;  Indels 56;  Gaps 8;

QY  1 ATCGAGACATCAGCTTCTTCATAGTATCCACAGCAATGCTTGAATCATAGTCAAGC 60
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db  1 ATCGAGACATCAGCTTCTTCATAGTATCCACAGCAATGCTTGAATCATAGTCAAGC 60
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

QY  61 AATGCTGTAAAGCGGCGGCTGTATAGTCTGTAGCTCAGTGTGGTGTAGAGCGCACCCCTG 120
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db  61 CGATTAGGTAGCAACCTTCGAT-TGGGCTGTAGCTCAGTGTGGTGTAGAGCGCACCCCTG 119
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

QY  121 ATAAGGTTAGGTGCGGAGTCAATCTGCCAGACCTACCAATGCTTGTGTCGAGAAGA 180
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db  120 ATAAGGTTAGGTGCGGAGTCAATCTGCCAGACCTACCAATGCTTGTGTCGAGAAGA 180
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

QY  181 ATACGGGCCATAGCTCAGCTGGGAGAGCGCTGCTTGCACGAGGAGTCAAGGTTTC 240
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db  169 ----GGGGCCATAGCTCAGCTGGGAGAGCGCTGCTTGCACGAGGAGTCAAGGTTTC 224
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

QY  241 GATCCCGCTTGGCTCCACCACTCTCTCGTGTGGGTTGAGTGTAAAGAGTTCAGAAATG 300
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db  225 GATCCCGCTTGGCTCCACCACTCTCTCGTGTGGGTTGAGTGTAAAGAGTTCAGAAATG 277
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

QY  301 ATGCCGCTTCAAGTGTTCCTGCTGTAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 360
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db  278 A-----ATATTCGCGTGAATATGATTTCTGAACCTT-----TATCAGAA 317
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

QY  361 TCGTTCCTTTAAAAATTTGGATATGTATAGAGTGAAGTGAATGCTTGAATGCTTCACTGC 418
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db  318 TCGTTCCTTTAAAAATTTGGATATGTATAGAGTGAAGTGAATGCTTGAATGCTTCACTGC 377
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

QY  419 AATTGATCTGGTCAAGTAAATTTGTAGTCTCAAGACGCAAAATTTTCGCGCAATGTCG 478
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db  378 GTGTGTTCAAGCTAAGTAAATTTGTAGTCTCAAGACGCAAAATTTTCGCGCAATGTCG 433
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

QY  479 TCTTCAGGATTGAGACAGTAACCAAGATGCTTGGGTTATAT 520
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db  434 TCTTCAC-----AGTATACCAAGATGCTTGGGTTATAT 468
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

RESULT 8
US-09-448-894-115
; Sequence 115, Application US/09448894
; Patent No. 6312903
; GENERAL INFORMATION:
; APPLICANT: JANNES, GEERT
; APPLICANT: ROSSAU, RUDI
; APPLICANT: VAN HEUVERSWYN, HUGO

TITLE OF INVENTION: SIMULTANEOUS DETECTION, IDENTIFICATION AND DIFFERENTIATION OF EUBACTERIAL TAXA USING A HYBRIDIZATION ASSAY

NUMBER OF SEQUENCES: 216
CORRESPONDENCE ADDRESS:
ADDRESSEE: NIXON & VANDERHVE P.C.
STREET: 1100 NORTH GLEBE ROAD, 8TH FLOOR
CITY: WASHINGTON
STATE: D.C.
COUNTRY: USA
ZIP: 22201

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/448,894
FILING DATE: 29-No. 6312903-1999
CLASSIFICATION: <Unknown>
07-APR-1995
24-JUN-1994

PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/765,332
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; APPLICATION NUMBER: 08/765,332
; FILING DATE: <Unknown>
; APPLICATION NUMBER: EP 95870032.0
; FILING DATE: 07-APR-1995
; APPLICATION NUMBER: EP 94870106.5
; FILING DATE: 24-JUN-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: SADOFF, B.J.
; REGISTRATION NUMBER: 36,663
; REFERENCE/DOCKET NUMBER: 1487-14
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 703-816-4091
; TELEFAX: 703-816-4100
; INFORMATION FOR SEQ ID NO: 195:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 470 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cdna
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; SEQUENCE DESCRIPTION: SEQ ID NO: 195:
US-09-448-894-195

Query Match 21.9%; Score 113.8; DB 4; Length 470;
Best Local Similarity 77.1%; Pred. No. 4.4e-28;
Matches 158; Conservative 0; Mismatches 32; Indels 15; Gaps 1;

QY 82 TTATAGGCTGTAGCTACGTTGGTTAGAGCGCACCCCTGATAAGGTTGAGTGGCAGTT 141
DB 72 TTATAGGCTGTAGCTACGTTGGTTAGAGCGCACCCCTGATAAGGTTGAGTGGTGGT 131
QY 142 CAAATCTGCCAGACCTACCAATTCCTTGGTGCAGAGAAATAC-----GG 186
DB 132 CAAGTCCACTCAGGCTACCACTTCTCGAAGTGGAAAGGTAAGTACGCTGATGG 191
QY 187 GGCATAGTCTAGCTGGAGAGCGCTCCCTTGCACGAGAGTGCAGCGTTGATGCC 246
DB 192 GGCATAGTCTAGCTGGAGAGCGCTCCCTTGCACGAGAGTGCAGCGTTGATGCC 251
QY 247 GCTTGGCTCCACCACTCTCTCTGTGT 271
DB 252 GCTTGGCTCCACCACTCTCTCTGTGT 276

RESULT 13
US-08-614-87
; Sequence 87, Application US/08412614
; Patent No. 5536638
; GENERAL INFORMATION:
; APPLICANT: Rossau, Rudl
; APPLICANT: Van Heuverswyn, Hugo
; TITLE OF INVENTION: Hybridization Probes Derived from the
; TITLE OF INVENTION: Spacer Region Between the 16S and 23S rRNA Genes for the
; TITLE OF INVENTION: Detection of No. 5536638-Viral Microorganisms
; NUMBER OF SEQUENCES: 104
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Merchant & Gould
; STREET: 3100 No. 5536638west Center
; CITY: Minneapolis
; STATE: MN
; COUNTRY: USA
; ZIP: 55402-4131
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette 3.5 inch, 1.44 mb capacity
; COMPUTER: IBM PC compatible (Compaq Deskpro 286e)
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: Wordperfect Version #5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/412,614
; FILING DATE:
; CLASSIFICATION: 435

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; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/965,394
; FILING DATE: 17-DEC-1992
; APPLICATION NUMBER: PCT/EP91/00743
; FILING DATE: 18-APR-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB/90901054.3
; FILING DATE: 18-APR-1990
; ATTORNEY/AGENT INFORMATION:
; NAME: Hillson, Randall A.
; REGISTRATION NUMBER: 31,838
; REFERENCE/DOCKET NUMBER: 8076.75-USWO
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 612-332-5300
; TELEFAX: 612-332-9081
; INFORMATION FOR SEQ ID NO: 87:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 582 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; ORGANISM: Bordetella pertussis
; STRAIN: ATCC 10380
; US-08-412-614-87

Query Match 21.3%; Score 111; DB 1; Length 582;
Best Local Similarity 63.8%; Pred. No. 4.1e-27;
Matches 199; Conservative 0; Mismatches 108; Indels 5; Gaps 2;

QY 72 GCACACCGCTTTATAGTCTGTAGCTGAGTGTAGAGCGCACCCCTGATAAGGTTGAG 131
DB 84 GAGAAAGGTTTCGCGGCTGTGTAGCTGAGTGTAGAGCGCACCCCTGATAAGGTTGAG 143
QY 132 GTCCGCGAGTTCAATTCGCCAGACCTACCAATTCGTTGTCGAGAGAAATACGGGGCCA 191
DB 144 GTCGTTGGTTGGAATCCACACAGACCCACCAA--GGTTTCCTGAGAGGAAATGGGGGTG 201
QY 192 TAGCTAGCTGGGAGAGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 251
DB 202 TAGCTAGCTGGGAGAGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 261
QY 252 GCTCCACCACTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 311
DB 262 CTTCCACCAAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 321
QY 312 GGTGTTGCTCTG---TTGAGTGTCTGATTTCTGCTGCTGCTGCTGCTGCTGCTGCTG 368
DB 322 GGTGTTGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 381

RESULT 14
US-08-635-761-87
; Sequence 87, Application US/08635761
; Patent No. 5945282
; GENERAL INFORMATION:
; APPLICANT: Rossau, Rudl
; APPLICANT: Rossau, Rudl
; TITLE OF INVENTION: HYBRIDIZATION PROBES DERIVED FROM THE SPACER REGION BE
; NUMBER OF SEQUENCES: 104
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Merchant, Gould, Smith, Edell, Welter & Schmidt
; STREET: 3100 No. 5945282west Center, 90 S. 7th Street
; CITY: Minneapolis
; STATE: MN
; COUNTRY: U.S.A.
; ZIP: 55402

```

```

RESULT 15
US-09-312-520-87
; Sequence 87, Application US/09312520
; Patent No. 6277577
; GENERAL INFORMATION:
; APPLICANT: ROSSAU, Rudi
; TITLE OF INVENTION: HYBRIDIZATION PROBES DERIVED FROM THE SPACER REGION BE
; NUMBER OF SEQUENCES: 104
; CORRESPONDENCE ADDRESS:

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2:

Search completed: February 1, 2003, 04:24:14  
Job time : 29.0349 secs



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QY 326 AGTGCTGA 333
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Db 275872 ATTCTTA 275879

RESULT 2
US-09-863-086-87
; Sequence 87, Application US/09863086
; Patent No. US20020048762A1
; GENERAL INFORMATION:
; APPLICANT: Rossau, Rudi
; TITLE OF INVENTION: HYBRIDIZATION PROBES DERIVED FROM THE SPACER
; REGION BETWEEN THE 16S A
; NUMBER OF SEQUENCES: 104
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Merchant, Gould, Smith, Edell, Welter & Schmidt
; STREET: 3100 No. US20020048762A1west Center, 90 S. 7th Street
; CITY: Minneapolis
; STATE: MN
; COUNTRY: U.S.A.
; ZIP: 55402
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq Version 1.5
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/863,086
; FILING DATE: 22-May-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/312,520
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Hillson, Randall A
; REGISTRATION NUMBER: 31,838
; REFERENCE/DOCKET NUMBER: 8076.75USC1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 612/332-5300
; TELEFAX: 612/332-9081
; TELEX: <Unknown>
; INFORMATION FOR SEQ ID NO: 87:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 582 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: Genomic DNA
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FRAGMENT TYPE: <Unknown>
; ORIGINAL SOURCE:
; SEQUENCE DESCRIPTION: SEQ ID NO: 87:
US-09-863-086-87

Query Match 21.3%; Score 111; DB 10; Length 582;
Best Local Similarity 63.8%; Pred. No. 3e-26;
Matches 199; Conservative 0; Mismatches 108; Indels 5; Gaps 2;

QY 72 GGCACCCGTTATAGGTCGTAGCTCAGTTGGTTAGAGCGCACCCCTGATAGAGGTGAG 131
| | | | |
Db 84 GAGAAAGGTTTCGCGGTTCTGTAGCTCAGTCGGTTAGAGCACCGTCTTGATAGGCGGGG 143

QY 132 GTCGGCAGTTCRAATGTCGCCACCTACCATTGCTGTCGAGAGATACGGGCGCA 191
| | | | |
Db 144 GTCGTTGGTTCGAATCCAAACAGACCCACCAA--GGTTTCCTGAGAGGAAATGGGGGTG 201

QY 192 TAGCTCAGCTGGGAGAGCGCCTGCCTTGGCAGCAGGAGGTTCAGCGGTTCCGATCCCGCTTG 251
| | | | |
Db 202 TAGCTCAGCTGGGAGAGCGCCTGCTTTGCAAGCAGGATGTCATCGGTTCCGATCCCGTTCA 261
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QY 252 GCTCCACCACCTCTCTCTGTTGCGGTGAGTTTAAAGAGTTTCAAGAAATGATGCCGCTTCA 311
| | | | |
Db 262 CTTCCACCAAAAGCCTGTCCAGAGGATGGGTGTGNNNGAGACCAGCAAGGCGAGAGACAA 321

QY 312 GGTTCGTCCTG---TTGAGTGCCTGATTTCTGGTCTTTTGTACCGGTACGAAATCGTTCTT 368
| | | | |
Db 322 CGTTAGTGTGCGAGTCAGTGTAAAGCGTTGGGTTTGGCCGACAGCTATATATGTTCTT 381

QY 369 TAAATAATTTGGA 380
| | | | |
Db 382 TAACAATTTGGA 393

RESULT 3
US-09-863-086-88
; Sequence 88, Application US/09863086
; Patent No. US20020048762A1
; GENERAL INFORMATION:
; APPLICANT: Rossau, Rudi
; TITLE OF INVENTION: HYBRIDIZATION PROBES DERIVED FROM THE SPACER
; REGION BETWEEN THE 16S A
; NUMBER OF SEQUENCES: 104
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Merchant, Gould, Smith, Edell, Welter & Schmidt
; STREET: 3100 No. US20020048762A1west Center, 90 S. 7th Street
; CITY: Minneapolis
; STATE: MN
; COUNTRY: U.S.A.
; ZIP: 55402
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq Version 1.5
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/863,086
; FILING DATE: 22-May-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/312,520
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Hillson, Randall A
; REGISTRATION NUMBER: 31,838
; REFERENCE/DOCKET NUMBER: 8076.75USC1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 612/332-5300
; TELEFAX: 612/332-9081
; TELEX: <Unknown>
; INFORMATION FOR SEQ ID NO: 88:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 590 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: Genomic DNA
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FRAGMENT TYPE: <Unknown>
; ORIGINAL SOURCE:
; SEQUENCE DESCRIPTION: SEQ ID NO: 88:
US-09-863-086-88

Query Match 19.5%; Score 101.4; DB 10; Length 590;
Best Local Similarity 74.6%; Pred. No. 4e-23;
Matches 141; Conservative 0; Mismatches 46; Indels 2; Gaps 1;

QY 72 GGCACCCGTTATAGGTCGTAGCTCAGTTGGTTAGAGCGCACCCCTGATAGAGGTGAG 131
| | | | |
Db 84 GAGAAAGGTTTCGCGGTTCTGTAGCTCAGTCGGTTAGAGCACCGTCTTGATAGGCGGGG 143
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QY 132 GTCGGCAGTCAAAATGCCCCAGACCTACCAATTCCTGTCGAGAAATACGGGGCCA 191  
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||  
Db 144 GTCGTTGGTTCGAATCCAAACAGACCCACCAA--GGTTTCCTGAGAGGAAATGGGGTG 201  
QY 192 TAGCTCAGCTGGAGAGCGCTGCTTGACGACGAGGAGTTCAGCGGTTTCGATCCGGCTTG 251  
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||  
Db 202 TAGCTCAGCTGGAGAGCGCTGCTTTCGAAGCAGGATGTCATCGGTTTCGATCCGGTCA 261  
QY 252 GCTCCACCA 260  
|||||  
Db 262 CCTCCACCA 270

RESULT 4  
US-09-815-242-1358/c  
; Sequence 1358, Application US/09815242  
; Patent No. US20020061569A1  
; GENERAL INFORMATION:  
; APPLICANT: Haselbeck, Robert  
; APPLICANT: Ohlsen, Kari L.  
; APPLICANT: Zyskind, Judith W.  
; APPLICANT: Wall, Daniel  
; APPLICANT: Trawick, John D.  
; APPLICANT: Carr, Grant J.  
; APPLICANT: Yamamoto, Robert T.  
; APPLICANT: Xu, H. Howard  
; TITLE OF INVENTION: Identification of Essential Genes in  
; FILE REFERENCE: ELITRA.011A  
; CURRENT APPLICATION NUMBER: US/09/815,242  
; PRIOR FILING DATE: 2001-03-21  
; PRIOR APPLICATION NUMBER: 60/191,078  
; PRIOR FILING DATE: 2000-03-21  
; PRIOR APPLICATION NUMBER: 60/206,848  
; PRIOR FILING DATE: 2000-05-23  
; PRIOR APPLICATION NUMBER: 60/207,727  
; PRIOR FILING DATE: 2000-05-26  
; PRIOR APPLICATION NUMBER: 60/242,578  
; PRIOR FILING DATE: 2000-10-23  
; PRIOR APPLICATION NUMBER: 60/253,625  
; PRIOR FILING DATE: 2000-11-27  
; PRIOR APPLICATION NUMBER: 60/257,931  
; PRIOR FILING DATE: 2000-12-22  
; PRIOR APPLICATION NUMBER: 60/269,308  
; PRIOR FILING DATE: 2001-02-16  
; NUMBER OF SEQ ID NOS: 14110  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 1358  
; LENGTH: 243  
; TYPE: DNA  
; ORGANISM: Staphylococcus aureus  
; FEATURE:  
; NAME/KEY: misc\_feature  
; LOCATION: (1)...(243)  
; OTHER INFORMATION: n = A,T,C or G  
US-09-815-242-1358

Query Match 18.5%; Score 96; DB 10; Length 243;  
Best Local Similarity 78.5%; Pred. No. 1.4e-21;  
Matches 128; Conservative 0; Mismatches 31; Indels 4; Gaps 1;  
QY 82 TTATAGGTCCTAGCTCAGTTCAGTTCAGCGCACCCCTGATAGGTTGAGTTCGGCAGTT 141  
Db 159 TAATGGGCTATAGCTCAGCTGTTAGAGCGCACCGCTGATAGCGTTCGGTGGTT 100  
QY 142 CAAATCTGCCAGACCTACCAATTCGTTGTCGAGAGAAATACGGGGCCATAGCTCAGCT 201  
Db 99 CGAGTCCNCTTAGGCCACCAATTAATTT----AATACCTATTTCGGGGCTTAGCTCAGCT 44  
QY 202 GGGAGAGCGCCTGCCTTCGACGACGAGGTCAGCGGTTTCGATC 244  
Db 43 GGGAGAGCGCCTGCTTTCGACGACGAGGTCAGCGGTTTCGATC 1

RESULT 5  
US-09-815-242-1377/c  
; Sequence 1377, Application US/09815242  
; Patent No. US20020061569A1  
; GENERAL INFORMATION:  
; APPLICANT: Haselbeck, Robert  
; APPLICANT: Ohlsen, Kari L.  
; APPLICANT: Zyskind, Judith W.  
; APPLICANT: Wall, Daniel  
; APPLICANT: Trawick, John D.  
; APPLICANT: Carr, Grant J.  
; APPLICANT: Yamamoto, Robert T.  
; APPLICANT: Xu, H. Howard  
; TITLE OF INVENTION: Identification of Essential Genes in  
; FILE REFERENCE: ELITRA.011A  
; CURRENT APPLICATION NUMBER: US/09/815,242  
; PRIOR FILING DATE: 2001-03-21  
; PRIOR APPLICATION NUMBER: 60/191,078  
; PRIOR FILING DATE: 2000-03-21  
; PRIOR APPLICATION NUMBER: 60/206,848  
; PRIOR FILING DATE: 2000-05-23  
; PRIOR APPLICATION NUMBER: 60/207,727  
; PRIOR FILING DATE: 2000-05-26  
; PRIOR APPLICATION NUMBER: 60/242,578  
; PRIOR FILING DATE: 2000-10-23  
; PRIOR APPLICATION NUMBER: 60/253,625  
; PRIOR FILING DATE: 2000-11-27  
; PRIOR APPLICATION NUMBER: 60/257,931  
; PRIOR FILING DATE: 2000-12-22  
; PRIOR APPLICATION NUMBER: 60/269,308  
; PRIOR FILING DATE: 2001-02-16  
; NUMBER OF SEQ ID NOS: 14110  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 1377  
; LENGTH: 255  
; TYPE: DNA  
; ORGANISM: Staphylococcus aureus  
US-09-815-242-1377

Query Match 18.3%; Score 95.4; DB 10; Length 255;  
Best Local Similarity 78.5%; Pred. No. 2.3e-21;  
Matches 128; Conservative 0; Mismatches 31; Indels 4; Gaps 1;  
QY 82 TTATAGGTCCTAGCTCAGTTCAGTTCAGCGCACCCCTGATAGGTTGAGTTCGGCAGTT 141  
Db 159 TAATGGGCTATAGCTCAGCTGTTAGAGCGCACCGCTGATAGCGTTCGGTGGTT 100  
QY 142 CAAATCTGCCAGACCTACCAATTCGTTGTCGAGAGAAATACGGGGCCATAGCTCAGCT 201  
Db 99 CGAGTCCNCTTAGGCCACCAATTAATTT----AATACCTATTTCGGGGCTTAGCTCAGCT 44  
QY 202 GGGAGAGCGCCTGCCTTCGACGACGAGGTCAGCGGTTTCGATC 244  
Db 43 GGGAGAGCGCCTGCTTTCGACGACGAGGTCAGCGGTTTCGATC 1

RESULT 6  
US-09-815-242-1402/c  
; Sequence 1402, Application US/09815242  
; Patent No. US20020061569A1  
; GENERAL INFORMATION:  
; APPLICANT: Haselbeck, Robert  
; APPLICANT: Ohlsen, Kari L.  
; APPLICANT: Zyskind, Judith W.  
; APPLICANT: Wall, Daniel  
; APPLICANT: Trawick, John D.  
; APPLICANT: Carr, Grant J.  
; APPLICANT: Yamamoto, Robert T.  
; APPLICANT: Xu, H. Howard  
; TITLE OF INVENTION: Identification of Essential Genes in

; TITLE OF INVENTION: Prokaryotes  
; FILE REFERENCE: ELITRA.011A  
; CURRENT APPLICATION NUMBER: US/09/815,242  
; CURRENT FILING DATE: 2001-03-21  
; PRIOR APPLICATION NUMBER: 60/191,078  
; PRIOR FILING DATE: 2000-03-21  
; PRIOR APPLICATION NUMBER: 60/206,848  
; PRIOR FILING DATE: 2000-05-23  
; PRIOR APPLICATION NUMBER: 60/207,727  
; PRIOR FILING DATE: 2000-05-26  
; PRIOR APPLICATION NUMBER: 60/242,578  
; PRIOR FILING DATE: 2000-10-23  
; PRIOR APPLICATION NUMBER: 60/253,625  
; PRIOR FILING DATE: 2000-11-27  
; PRIOR APPLICATION NUMBER: 60/257,931  
; PRIOR FILING DATE: 2000-12-22  
; PRIOR APPLICATION NUMBER: 60/269,308  
; PRIOR FILING DATE: 2001-02-16  
; NUMBER OF SEQ ID NOS: 14110  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 1402  
; LENGTH: 255  
; TYPE: DNA  
; ORGANISM: Staphylococcus aureus  
US-09-815-242-1402

Query Match 18.3%; Score 95.4; DB 10; Length 255;  
Best Local Similarity 78.5%; Pred. No. 2.3e-21;  
Matches 128; Conservative 0; Mismatches 31; Indels 4; Gaps 1;  
  
QY 82 TTATAGTCTGTAGCTAGCTAGCTAGCGCCACCCCTGATAGGGTTCAGGTCGGCAGTT 141  
Db 159 TAATGGCCCTATAGCTAGCTAGCTAGCGCCACCCCTGATAGGGTTCAGGTCGGTGGTT 100  
  
QY 142 CAAATCTGCCAGACCTACCAATTTGCTTGGTCGAGAGAAATACGGGCCATAGCTCAGCT 201  
Db 99 CGAGTCACCTTAGCGCCACCAATTAATTT---AATACCTATTGGGGCTTAGCTCAGCT 44  
  
QY 202 GGGAGAGCGCCCTGCTTGGTCAGCGAGGTCAGCGGTTCGATC 244  
Db 43 GGGAGAGCGCCCTGCTTGGTCAGCGAGGTCAGCGGTTCGATC 1

RESULT 7  
US-09-815-242-1415/c  
; Sequence 1415, Application US/09815242  
; Patent No. US20020061569A1  
; GENERAL INFORMATION:  
; APPLICANT: Haselbeck, Robert  
; APPLICANT: Ohlsen, Kari L.  
; APPLICANT: Zyskind, Judith W.  
; APPLICANT: Wall, Daniel  
; APPLICANT: Trawick, John D.  
; APPLICANT: Carr, Grant J.  
; APPLICANT: Yamamoto, Robert T.  
; APPLICANT: Xu, H. Howard  
; TITLE OF INVENTION: Identification of Essential Genes in  
; FILE REFERENCE: ELITRA.011A  
; CURRENT APPLICATION NUMBER: US/09/815,242  
; CURRENT FILING DATE: 2001-03-21  
; PRIOR APPLICATION NUMBER: 60/191,078  
; PRIOR FILING DATE: 2000-03-21  
; PRIOR APPLICATION NUMBER: 60/206,848  
; PRIOR FILING DATE: 2000-05-23  
; PRIOR APPLICATION NUMBER: 60/207,727  
; PRIOR FILING DATE: 2000-05-26  
; PRIOR APPLICATION NUMBER: 60/242,578  
; PRIOR FILING DATE: 2000-10-23  
; PRIOR APPLICATION NUMBER: 60/253,625  
; PRIOR FILING DATE: 2000-11-27  
; PRIOR APPLICATION NUMBER: 60/257,931  
; PRIOR FILING DATE: 2000-12-22  
; NUMBER OF SEQ ID NOS: 14110  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 1402  
; LENGTH: 255  
; TYPE: DNA  
; ORGANISM: Staphylococcus aureus  
US-09-815-242-1402

; PRIOR APPLICATION NUMBER: 60/269,308  
; PRIOR FILING DATE: 2001-02-16  
; NUMBER OF SEQ ID NOS: 14110  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 1415  
; LENGTH: 255  
; TYPE: DNA  
; ORGANISM: Staphylococcus aureus  
US-09-815-242-1415  
  
Query Match 18.3%; Score 95.4; DB 10; Length 255;  
Best Local Similarity 78.5%; Pred. No. 2.3e-21;  
Matches 128; Conservative 0; Mismatches 31; Indels 4; Gaps 1;  
  
QY 82 TTATAGTCTGTAGCTAGCTAGCTAGCGCCACCCCTGATAGGGTTCAGGTCGGCAGTT 141  
Db 159 TAATGGCCCTATAGCTAGCTAGCTAGCGCCACCCCTGATAGGGTTCAGGTCGGTGGTT 100  
  
QY 142 CAAATCTGCCAGACCTACCAATTTGCTTGGTCGAGAGAAATACGGGCCATAGCTCAGCT 201  
Db 99 CGAGTCACCTTAGCGCCACCAATTAATTT---AATACCTATTGGGGCTTAGCTCAGCT 44  
  
QY 202 GGGAGAGCGCCCTGCTTGGTCAGCGAGGTCAGCGGTTCGATC 244  
Db 43 GGGAGAGCGCCCTGCTTGGTCAGCGAGGTCAGCGGTTCGATC 1

RESULT 8  
US-09-815-242-1423/c  
; Sequence 1423, Application US/09815242  
; Patent No. US20020061569A1  
; GENERAL INFORMATION:  
; APPLICANT: Haselbeck, Robert  
; APPLICANT: Ohlsen, Kari L.  
; APPLICANT: Zyskind, Judith W.  
; APPLICANT: Wall, Daniel  
; APPLICANT: Trawick, John D.  
; APPLICANT: Carr, Grant J.  
; APPLICANT: Yamamoto, Robert T.  
; APPLICANT: Xu, H. Howard  
; TITLE OF INVENTION: Identification of Essential Genes in  
; FILE REFERENCE: ELITRA.011A  
; CURRENT APPLICATION NUMBER: US/09/815,242  
; CURRENT FILING DATE: 2001-03-21  
; PRIOR APPLICATION NUMBER: 60/191,078  
; PRIOR FILING DATE: 2000-03-21  
; PRIOR APPLICATION NUMBER: 60/206,848  
; PRIOR FILING DATE: 2000-05-23  
; PRIOR APPLICATION NUMBER: 60/207,727  
; PRIOR FILING DATE: 2000-05-26  
; PRIOR APPLICATION NUMBER: 60/242,578  
; PRIOR FILING DATE: 2000-10-23  
; PRIOR APPLICATION NUMBER: 60/253,625  
; PRIOR FILING DATE: 2000-11-27  
; PRIOR APPLICATION NUMBER: 60/257,931  
; PRIOR FILING DATE: 2000-12-22  
; PRIOR APPLICATION NUMBER: 60/269,308  
; PRIOR FILING DATE: 2001-02-16  
; NUMBER OF SEQ ID NOS: 14110  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 1423  
; LENGTH: 255  
; TYPE: DNA  
; ORGANISM: Staphylococcus aureus  
US-09-815-242-1423

Query Match 18.3%; Score 95.4; DB 10; Length 255;  
Best Local Similarity 78.5%; Pred. No. 2.3e-21;  
Matches 128; Conservative 0; Mismatches 31; Indels 4; Gaps 1;  
  
QY 82 TTATAGTCTGTAGCTAGCTAGCTAGCGCCACCCCTGATAGGGTTCAGGTCGGCAGTT 141  
Db 159 TAATGGCCCTATAGCTAGCTAGCTAGCGCCACCCCTGATAGGGTTCAGGTCGGTGGTT 100

Db 159 TAATGGCCCTAGCTAGCTGGTTAGAGCGCACGCCCTGATAAGCGTGAGGTCGGTGGTT 100  
QY 142 CAATCTGCCAGACCTACCAATTGCTGGTCGAGAGATAACGGGCCATAGCTCAGCT 201  
Db 99 CGAGTCCACTTAGGCCACCAATTAATTT----AATACCTATTGGGGGCTTAGCTCAGCT 44  
QY 202 GGGAGAGCGCCCTGCTTGCACGACGAGGTGACGCGGTTTCGATC 244  
Db 43 GGGAGAGCGCCCTGCTTGCACGACGAGGTGACGCGGTTTCGATC 1

## RESULT 9

US-09-815-242-1431/c

; Sequence 1431, Application US/09815242

; Patent No. US20020061569A1

; GENERAL INFORMATION:

; APPLICANT: Haselbeck, Robert

; APPLICANT: Ohlsen, Kari L.

; APPLICANT: Zyskind, Judith W.

; APPLICANT: Wall, Daniel

; APPLICANT: Trawick, John D.

; APPLICANT: Carr, Grant J.

; APPLICANT: Yamamoto, Robert T.

; APPLICANT: Xu, H. Howard

; TITLE OF INVENTION: Identification of Essential Genes in

; FILE REFERENCE: ELITRA.011A

; CURRENT APPLICATION NUMBER: US/09/815,242

; PRIOR FILING DATE: 2001-03-21

; PRIOR APPLICATION NUMBER: 60/191,078

; PRIOR FILING DATE: 2000-03-21

; PRIOR APPLICATION NUMBER: 60/206,848

; PRIOR FILING DATE: 2000-05-23

; PRIOR APPLICATION NUMBER: 60/207,727

; PRIOR FILING DATE: 2000-05-26

; PRIOR APPLICATION NUMBER: 60/242,578

; PRIOR FILING DATE: 2000-10-23

; PRIOR APPLICATION NUMBER: 60/253,625

; PRIOR FILING DATE: 2000-11-27

; PRIOR APPLICATION NUMBER: 60/257,931

; PRIOR FILING DATE: 2000-12-22

; PRIOR APPLICATION NUMBER: 60/269,308

; PRIOR FILING DATE: 2001-02-16

; NUMBER OF SEQ ID NOS: 14110

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 1431

; LENGTH: 255

; TYPE: DNA

; ORGANISM: Staphylococcus aureus

US-09-815-242-1431

Query Match 18.3%; Score 95.4; DB 10; Length 255;  
Best Local Similarity 78.5%; Pred. No. 2.3e-21;  
Matches 128; Conservative 0; Mismatches 31; Indels 4; Gaps 1;

QY 82 TTATAGGCTGTAGCTAGCTAGTGGTTAGAGCGCACGCCCTGATAAGCGTGAGGTCGGCAGTT 141  
Db 159 TAATGGCCCTAGCTAGCTAGCTGGTTAGAGCGCACGCCCTGATAAGCGTGAGGTCGGTGGTT 100  
QY 142 CAATCTGCCAGACCTACCAATTGCTGGTCGAGAGATAACGGGCCATAGCTCAGCT 201  
Db 99 CGAGTCCACTTAGGCCACCAATTAATTT----AATACCTATTGGGGGCTTAGCTCAGCT 44  
QY 202 GGGAGAGCGCCCTGCTTGCACGACGAGGTGACGCGGTTTCGATC 244  
Db 43 GGGAGAGCGCCCTGCTTGCACGACGAGGTGACGCGGTTTCGATC 1

## RESULT 10

US-09-815-242-1454/c

; Sequence 1454, Application US/09815242

; Patent No. US20020061569A1

; GENERAL INFORMATION:

; APPLICANT: Haselbeck, Robert  
; APPLICANT: Ohlsen, Kari L.  
; APPLICANT: Zyskind, Judith W.  
; APPLICANT: Wall, Daniel  
; APPLICANT: Trawick, John D.  
; APPLICANT: Carr, Grant J.  
; APPLICANT: Yamamoto, Robert T.  
; APPLICANT: Xu, H. Howard  
; TITLE OF INVENTION: Identification of Essential Genes in  
; FILE REFERENCE: ELITRA.011A  
; CURRENT APPLICATION NUMBER: US/09/815,242  
; PRIOR FILING DATE: 2001-03-21  
; PRIOR APPLICATION NUMBER: 60/191,078  
; PRIOR FILING DATE: 2000-03-21  
; PRIOR APPLICATION NUMBER: 60/206,848  
; PRIOR FILING DATE: 2000-05-23  
; PRIOR APPLICATION NUMBER: 60/207,727  
; PRIOR FILING DATE: 2000-05-26  
; PRIOR APPLICATION NUMBER: 60/242,578  
; PRIOR FILING DATE: 2000-10-23  
; PRIOR APPLICATION NUMBER: 60/253,625  
; PRIOR FILING DATE: 2000-11-27  
; PRIOR APPLICATION NUMBER: 60/257,931  
; PRIOR FILING DATE: 2000-12-22  
; PRIOR APPLICATION NUMBER: 60/269,308  
; PRIOR FILING DATE: 2001-02-16  
; NUMBER OF SEQ ID NOS: 14110  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 1454  
; LENGTH: 255  
; TYPE: DNA  
; ORGANISM: Staphylococcus aureus  
US-09-815-242-1454

Query Match 18.3%; Score 95.4; DB 10; Length 255;  
Best Local Similarity 78.5%; Pred. No. 2.3e-21;  
Matches 128; Conservative 0; Mismatches 31; Indels 4; Gaps 1;

QY 82 TTATAGGCTGTAGCTAGCTAGTGGTTAGAGCGCACGCCCTGATAAGCGTGAGGTCGGCAGTT 141  
Db 159 TAATGGCCCTAGCTAGCTAGCTGGTTAGAGCGCACGCCCTGATAAGCGTGAGGTCGGTGGTT 100  
QY 142 CAATCTGCCAGACCTACCAATTGCTGGTCGAGAGATAACGGGCCATAGCTCAGCT 201  
Db 99 CGAGTCCACTTAGGCCACCAATTAATTT----AATACCTATTGGGGGCTTAGCTCAGCT 44  
QY 202 GGGAGAGCGCCCTGCTTGCACGACGAGGTGACGCGGTTTCGATC 244  
Db 43 GGGAGAGCGCCCTGCTTGCACGACGAGGTGACGCGGTTTCGATC 1

## RESULT 11

US-09-815-242-1459/c

; Sequence 1459, Application US/09815242

; Patent No. US20020061569A1

; GENERAL INFORMATION:

; APPLICANT: Haselbeck, Robert

; APPLICANT: Ohlsen, Kari L.

; APPLICANT: Zyskind, Judith W.

; APPLICANT: Wall, Daniel

; APPLICANT: Trawick, John D.

; APPLICANT: Carr, Grant J.

; APPLICANT: Yamamoto, Robert T.

; APPLICANT: Xu, H. Howard

; TITLE OF INVENTION: Identification of Essential Genes in

; FILE REFERENCE: ELITRA.011A

; CURRENT APPLICATION NUMBER: US/09/815,242

; CURRENT FILING DATE: 2001-03-21

; PRIOR APPLICATION NUMBER: 60/191,078

; PRIOR FILING DATE: 2000-03-21

; PRIOR APPLICATION NUMBER: 60/206,848

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; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; NUMBER OF SEQ ID NOS: 1410
; SOFTWARE: fastseq for Windows Version 4.0
; SEQ ID NO 1459
; LENGTH: 255
; TYPE: DNA
; ORGANISM: Staphylococcus aureus
US-09-815-242-1459

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	Query Match	18.3%	Score 95.4;	DB 10;	Length 255;
	Best Local Similarity	78.5%;	Pred. No. 2.3e-21;		
	Matches 128;	Conservative	0;	Mismatches 31;	Indels 4;
				Gaps 1;	
QY	82	TTATAGTCTGTAGCTCAGTTGGTTAGAGCGCACCCCTGTATAAGGGTCAGCTCGCACGTT	141		
Db	159	TAATGGGCCCTATAGCTCAGCTGGTTAGAGCGCACCGCCTGTATAAGCGTCAGCTCGGTGGTT	100		
QY	142	CAAACTCTGCCACAGACCTTACCAATTCGTTGGTCGAGAGAATAACGGGGCCATAGCTCAGCT	201		
Db	99	CGACTCCACTTAGGCCCCACCATTAAATTT----	ATACTATTGGGGCTTAGCTCAGCT	44	
QY	202	GGGAGAGCGGCTGCTTTGCACGACGAGAGGTACGCGGTTTCGATC	244		
Db	43	GGGAGACGGCTGCTTTGCACGACGAGAGGTACGCGGTTTCGATC	1		

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RESULT 12
US-09-815-242-1473/c
Sequence 1473, Application US/09815242
Patent No. US20020061569A1
GENERAL INFORMATION:
APPLICANT: Haselbeck, Robert
APPLICANT: Ohlsen, Karl L.
APPLICANT: Zyskind, Judith W.
APPLICANT: Wall, Daniel
APPLICANT: Trawick, John D.
APPLICANT: Carr, Grant J.
APPLICANT: Yamamoto, Robert T.
APPLICANT: Xu, H. Howard
TITLE OF INVENTION: Identification of Essential Genes in
TITLE OF INVENTION: Prokaryotes
FILE REFERENCE: ELITRA.011A
CURRENT APPLICATION NUMBER: US/09/815,242
CURRENT FILING DATE: 2001-03-21
PRIORITY APPLICATION NUMBER: 60/191,078
PRIORITY FILING DATE: 2000-03-21
PRIORITY APPLICATION NUMBER: 60/206,848
PRIORITY FILING DATE: 2000-05-23
PRIORITY APPLICATION NUMBER: 60/207,727
PRIORITY FILING DATE: 2000-05-26
PRIORITY APPLICATION NUMBER: 60/242,578
PRIORITY FILING DATE: 2000-10-23
PRIORITY APPLICATION NUMBER: 60/253,625
PRIORITY FILING DATE: 2000-11-27
PRIORITY APPLICATION NUMBER: 60/257,931
PRIORITY FILING DATE: 2000-12-22
PRIORITY APPLICATION NUMBER: 60/269,308
PRIORITY FILING DATE: 2001-02-16
NUMBER OF SEQ ID NOS: 14110
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 1473
LENGTH: 255
TYPE: DNA

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	Query Match	18.3%	Score 95.4;	DB 10;	Length 255;
	Best Local Similarity	78.5%;	Pred. No. 2.3e-21;		
	Matches 128;	Conservative	0;	Mismatches 31;	Indels 4; Gaps 1;
Qy	82	TTATAGGTCTCTACTCAGTTCGTTTAGAGCCACCCCCTGATAAGGGTCAGTCGCAGTT	141		
Db	159	TAAATGGGCCATATAGCTCAGCTCGTGGTTAGAGCCAGCCCTGATAAGCGTGAGTCGGTGTT	100		
Qy	142	CARAATCTGCCAGACCTTACCATTGCTTGGTCGAGAAGATACGGGGCCATAGCTCAGCT	201		
Db	99	CGAATCACTTAGGCCACCACTTAATTT-----AATACCTATTGGGGGCTTAGCTCAGCT	44		
Qy	202	GGGAGAGCGCCTGCTTTCAGCGAGGAGGTTCAGCGGTTTCGATC	244		

Db 43 GGGAGAGCGCTGCTTTGCACGAGGAGTCAAGCGGTTCGATC 1  
|||||

## RESULT 14

US-09-815-242-1544/c  
; Sequence 1544, Application US/09815242  
; Patent No. US20020061569A1  
; GENERAL INFORMATION:  
; APPLICANT: Haselbeck, Robert  
; APPLICANT: Ohlsen, Karl L.  
; APPLICANT: Zyskind, Judith W.  
; APPLICANT: Wall, Daniel  
; APPLICANT: Trawick, John D.  
; APPLICANT: Carr, Grant J.  
; APPLICANT: Yamamoto, Robert T.  
; APPLICANT: Xu, H. Howard

; TITLE OF INVENTION: Identification of Essential Genes in  
; FILE OF INVENTION: Prokaryotes  
; FILE REFERENCE: ELITRA.011A

; CURRENT APPLICATION NUMBER: US/09/815,242

; PRIOR FILING DATE: 2001-03-21

; PRIOR APPLICATION NUMBER: 60/191,078

; PRIOR FILING DATE: 2000-03-21

; PRIOR APPLICATION NUMBER: 60/206,848

; PRIOR FILING DATE: 2000-05-23

; PRIOR APPLICATION NUMBER: 60/207,727

; PRIOR FILING DATE: 2000-05-26

; PRIOR APPLICATION NUMBER: 60/242,578

; PRIOR FILING DATE: 2000-10-23

; PRIOR APPLICATION NUMBER: 60/253,625

; PRIOR FILING DATE: 2000-11-27

; PRIOR APPLICATION NUMBER: 60/257,931

; PRIOR FILING DATE: 2000-12-22

; PRIOR APPLICATION NUMBER: 60/269,308

; PRIOR FILING DATE: 2001-02-16

; NUMBER OF SEQ ID NOS: 14110

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 1544

; LENGTH: 255

; TYPE: DNA

; ORGANISM: Staphylococcus aureus

US-09-815-242-1544

Query Match 18.3%; Score 95.4; DB 10; Length 255;  
Best Local Similarity 78.5%; Pred. No. 2.3e-21;  
Matches 128; Conservative 0; Mismatches 31; Indels 4; Gaps 1;

QY 82 TTATAGTCTGTAGCTCAGTGGTTAGAGCGCACCCCTGATAAGGTTGAGGTGCGCAGTT 141

Db 159 TAATGGCCCTATAGCTCAGCTGAGTGGTTAGAGCGCACCCCTGATAAGCGTGAAGTGGTGGTT 100

QY 142 CAAATCTGCCAGACCTACCAATTCGTTGTCGAGAAGATACGGGGCCATAGCTCAGCT 201

Db 99 CGAGTCCACTTAGGCCACCATTAAATTT----AATACCTATTGGGGGCTTAGCTCAGCT 44

QY 202 GGGAGAGCGCGCTGCTTTGCACGAGGAGTCAAGCGGTTCGATC 244

Db 43 GGGAGAGCGCGCTGCTTTGCACGAGGAGTCAAGCGGTTCGATC 1

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Search completed: February 1, 2003, 06:51:14

Job time : 248.936 secs

## RESULT 15

US-09-815-242-1638/c

; Sequence 1638, Application US/09815242

; Patent No. US20020061569A1

; GENERAL INFORMATION:

; APPLICANT: Haselbeck, Robert

; APPLICANT: Ohlsen, Karl L.

; APPLICANT: Zyskind, Judith W.

; APPLICANT: Wall, Daniel

; APPLICANT: Trawick, John D.

; APPLICANT: Carr, Grant J.

; APPLICANT: Yamamoto, Robert T.



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OM nucleic - nucleic search, using sw model

Run on: February 1, 2003, 01:09:56 ; Search time 970.301 Seconds  
(without alignments)  
8679.427 Million cell updates/sec

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Perfect score: 520  
Sequence: 1 ATCGAAGACATCAGCTTCTT.....CAGATTGCTGGGGTTATAT 520

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 16154066 seqs, 8097743376 residues  
Total number of hits satisfying chosen parameters: 32308132

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

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EST:\*  
1: em\_estba:\*  
2: em\_esthum:\*  
3: em\_estin:\*  
4: em\_estmu:\*  
5: em\_estov:\*  
6: em\_estpl:\*  
7: em\_estro:\*  
8: em\_htc:\*  
9: gb\_est1:\*  
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11: gb\_htc:\*  
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14: gb\_est5:\*  
15: em\_estfun:\*  
16: em\_estcom:\*  
17: gb\_gss:\*  
18: em\_gss\_hum:\*  
19: em\_gss\_inv:\*  
20: em\_gss\_pln:\*  
21: em\_gss\_vrt:\*  
22: em\_gss\_fun:\*  
23: em\_gss\_mam:\*  
24: em\_gss\_mus:\*  
25: em\_gss\_other:\*  
26: em\_gss\_pro:\*  
27: em\_gss\_rod:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
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c 2	175.4	33.7	629	17	BH201541 Sml-57P13
c 3	170.8	32.8	639	17	AQ509640 nbxb0096P
c 4	124.4	23.9	319	10	BE092111 IL2-BT073
c 5	77	14.8	754	17	BH405252 AG-ND-127
c 6	73	14.0	593	17	BH400944 AG-ND-158

c 7	73	14.0	760	17	BH393190
c 8	69.4	13.3	619	9	AA680996
c 9	69.4	13.3	6499	17	BH771024
c 10	67.8	13.0	497	13	BI544108
c 11	67.8	13.0	548	13	BI544155
c 12	66.8	12.8	577	17	BH819575
c 13	66.2	12.7	539	13	BI544086
c 14	63.8	12.3	287	17	BH614410
c 15	62.6	12.0	191	17	AZ578476
c 16	62.6	12.0	712	17	BH397037
c 17	58.6	11.3	579	17	BH375975
c 18	57.2	11.0	608	17	BH375641
c 19	54.6	10.5	696	17	BH383241
c 20	53.6	10.3	679	13	BI263958
c 21	52.6	10.1	541	17	BH387664
c 22	52.6	10.1	774	12	BG354849
c 23	52.4	10.1	617	9	AI526132
c 24	51.8	10.0	713	13	BH096963
c 25	50.6	9.7	2149	17	AQ012191
c 26	49.6	9.5	551	10	BE092053
c 27	49.4	9.5	612	17	AQ989869
c 28	49.2	9.5	653	13	BH318992
c 29	48.2	9.3	501	13	BH313245
c 30	48	9.2	372	10	BE092243
c 31	47.6	9.2	1258	17	BH770957
c 32	47.6	9.2	3268	17	BH770998
c 33	46.6	9.0	938	17	AZ683938
c 34	46.4	8.9	461	17	BH644007
c 35	45.8	8.8	874	17	CNS066SM
c 36	45.6	8.8	904	17	BH159957
c 37	45.4	8.7	715	17	BH375497
c 38	45.2	8.7	907	17	CNS06N2C
c 39	45	8.7	876	17	CNS06T5R
c 40	45	8.7	902	17	CNS06M5P
c 41	45	8.7	1047	17	CNS06XDL
c 42	44.8	8.6	197	17	BH855109
c 43	44.8	8.6	216	17	BH169234
c 44	44.8	8.6	330	14	BQ205940
c 45	44.4	8.5	432	13	BI941477

## ALIGNMENTS

RESULT 1  
BH200120/c  
LOCUS  
Sml-57J2.TF Sml Schistosoma mansoni genomic clone Sml-57J2, DNA  
DEFINITION  
sequence.  
ACCESSION  
BH200120  
VERSION  
BH200120.1 GI:16370164  
KEYWORDS  
GSS.  
SOURCE  
Schistosoma mansoni.  
ORGANISM  
Schistosoma mansoni  
Eukaryota; Metazoa; Platyhelminthes; Trematoda; Digenea;  
Strigeidida; Schistosomatoidea; Schistosomatidae; Schistosoma.  
REFERENCE  
1 (bases 1 to 507)  
AUTHORS  
Shetty,J., Simpson,A., Malek,J., Koo,H., LoVerde,P.T. and El-Sayed,N.M.  
TITLE  
Use of end sequences from Schistosoma mansoni (Puerto Rico strain) Sml BAC library for gene discovery and map construction  
JOURNAL  
Unpublished (2001)  
COMMENT  
Other\_GSSs: Sml-57J2.TR  
Contact: Najib M. El-Sayed  
Department of Eukaryotic Genomics  
The Institute for Genomic Research  
9712 Medical Center Dr., Rockville, MD 20850, USA  
Tel: 301 838 0200  
Fax: 301 838 0208  
Email: nelsayed@tigr.org  
lo.edu).  
Seq primer: M13 For  
Class: BAC ends.

FEATURES  
source

Location/Qualifiers  
1. .507  
/organism="Schistosoma mansoni"  
/strain="Puerto Rico"  
/db\_xref="taxon:6183"  
/clone\_lib="Sml-57P13"  
/clone\_lib="Sml"  
/note="Vector: pBelOBAC11; Site\_1: Hin dIII; Constructed in the laboratory of Dr. Denis Le Paslier at the Fondation Jean Dausset, CEPH, Paris, France. Briefly, Schistosoma mansoni agarose embedded DNA was partially digested with Hin dIII. High molecular weight fragments were ligated in pBelOBAC11 digested with Hin dIII. The average insert size is 100 kb. Total clone coverage: approx. 7.95 x the haploid genome. Further information can be found in Le Paslier et al. (2000) Construction and characterization of a Schistosoma mansoni bacterial artificial chromosome library. Genomics 65: 87-94."

BASE COUNT 136 a 129 c 117 g 125 t

Query Match 34.3%; Score 178.6; DB 17; Length 507;  
Best Local Similarity 72.0%; Pred. No. 2e-44;  
Matches 358; Conservative 0; Mismatches 99; Indels 40; Gaps 8;

QY 1 ATCGAAGACATCAGCTTCTTCATAGTATCCACAGAAATGCTTGATTCATAGTCGAACG 60  
DB 485 ATCAAGACCTCAGCTTCTTCATAGTATCCACAGAAATGCTTGATTCATAGTCGAACG 426  
QY 61 AATGCTGTAAACCGACCGCGTGTATA-----GGTCTGTAGCTCAGTTGGTTAGAGCGCA 114  
DB 425 GCGATTGGTTGAGACCCGAGAGTACGATTGGTCTGTAGCTCAGTTGGTTAGAGCGCA 366  
QY 115 CCCCTGATAAGGTCGAGTCGCGAGTCAAAATCGCCAGACCTACCAATTCGTTG 171  
DB 365 CCCCTGATAAGGTCGAGTCGCGAGTCAAAATCGCCAGACCTACCAATTCGTTG 171  
QY 172 TCAGAGAATATAGCTGGTCAAGTAAATTTAGTTCTCAAGACGCAAAATTTTCGGCG 471  
DB 92 CACTGCGACGTTG--TTAATCAAGGCAAAATTTG--CGAGTTCAAGCGGCAATTTTCGGCG 37  
QY 472 AATGCTGCTTTCAGAT 488  
DB 36 AATGCTGCTTCAGTT 20

RESULT 2  
BH201541/c  
LOCUS  
DEFINITION Sml-57P13.TF Sml Schistosoma mansoni genomic clone Sml-57P13, DNA sequence.  
ACCESSION BH201541  
VERSION BH201541.1 GI:16373041  
KEYWORDS  
SOURCE Schistosoma mansoni.  
ORGANISM Schistosoma mansoni.  
Eukaryota; Metazoa; Platyhelminthes; Trematoda; Digenea;

REFERENCE  
AUTHORS

TITLE  
JOURNAL  
COMMENT

Strigeidida; Schistosomatoidea; Schistosomatidae; Schistosoma.  
1 (bases 1 to 629)  
Shetty,J., Simpson,A., Malek,J., Koo,H., Loverde,P.T. and El-Sayed,N.M.  
Use of end sequences from Schistosoma mansoni (Puerto Rico strain) Sml BAC library for gene discovery and map construction  
Unpublished (2001)  
Other\_GSSs: Sml-57P13.TR  
Contact: Najib M. El-Sayed  
Department of Eukaryotic Genomics  
The Institute for Genomic Research  
9712 Medical Center Dr., Rockville, MD 20850, USA  
Tel: 301 838 0200  
Fax: 301 838 0208  
Email: nelsayed@tigr.org  
lo.edu).

Seq primer: M13 For  
Class: BAC ends.

FEATURES  
source

Location/Qualifiers  
1. .629

/organism="Schistosoma mansoni"  
/strain="Puerto Rico"  
/db\_xref="taxon:6183"  
/clone\_lib="Sml-57P13"  
/clone\_lib="Sml"

/note="Vector: pBelOBAC11; Site\_1: Hin dIII; Constructed in the laboratory of Dr. Denis Le Paslier at the Fondation Jean Dausset, CEPH, Paris, France. Briefly, Schistosoma mansoni agarose embedded DNA was partially digested with Hin dIII. High molecular weight fragments were ligated in pBelOBAC11 digested with Hin dIII. The average insert size is 100 kb. Total clone coverage: approx. 7.95 x the haploid genome. Further information can be found in Le Paslier et al. (2000) Construction and characterization of a Schistosoma mansoni bacterial artificial chromosome library. Genomics 65: 87-94."

BASE COUNT 157 a 172 c 146 g 154 t

Query Match 33.7%; Score 175.4; DB 17; Length 629;  
Best Local Similarity 71.6%; Pred. No. 2.3e-43;  
Matches 356; Conservative 0; Mismatches 101; Indels 40; Gaps 8;

QY 1 ATCGAAGACATCAGCTTCTTCATAGTATCCACAGAAATGCTTGATTCATAGTCGAACG 60  
DB 485 ATCGAAGACATCAGCTTCTTCATAGTATCCACAGAAATGCTTGATTCATAGTCGAACG 426  
QY 61 AATGCTGTAAACCGACCGCGTGTATA-----GGTCTGTAGCTCAGTTGGTTAGAGCGCA 114  
DB 425 GCGATTGGTTGAGACCCGAGAGTACGATTGGTCTGTAGCTCAGTTGGTTAGAGCGCA 366  
QY 115 CCCCTGATAAGGTCGAGTCGCGAGTCAAAATCGCCAGACCTACCAATTCGTTG 171  
DB 365 CCCCTGATAAGGTCGAGTCGCGAGTCAAAATCGCCAGACCTACCAATTCGTTG 171  
QY 172 TCAGAGAATATAGCTGGGCGCATAGCTAGCTGGGAGAGCGCTCGCTTCGACGCGAGGAGT 231  
DB 305 GCGAGTGTCAAATGGGCGCATAGCTAGCTGGGAGAGCGCTCGCTTCGACGCGAGGAGT 246  
QY 232 CAGCGGTTGATCCCGCTTGGCTCCACCACTCTCTCGTGTGGCGGTGAGTGTAAAGAGT 291  
DB 245 CAGGAGTGTGATCCTCTTGGCTCCACCACTCACTCAG-----ATCGCTGAAGAGC 195  
QY 292 TCAGAAATGATCCCGCTTCAGGTTTGTCTCTGTCAGTGTCTTCTGCTTCTTGTGACCG 351  
DB 194 TCAGAAATGA-----ACATTTGGTAGTTCAATGTTGATTTCTTGGTCTTT----- 152  
QY 352 GTACGAAATCGTCTTTTAAATAATTTGGATATGTGATAGAGTACGATTAATTCGTTT 411  
DB 151 GCGCCAGAACTGTCTTTTAAATAATTTGGGATGTGATAGAGTACGATTAACGCGTG-TTT 93  
QY 412 CACTGGCAATTCATCTGGTCAAGGTAATAATTTCTAGTCTTCAAGACCAATTTTCGGCG 471





into the pUC 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."

```
BASE COUNT      73 a      62 c      91 g      93 t
ORIGIN

Query Match      23.9%; Score 124.4; DB 10; Length 319;
Best Local Similarity 68.0%; Pred. No. 1.2e-27;
Matches 208; Conservative 0; Mismatches 86; Indels 12; Gaps 2;

QY 99 AGTTGGTTAGAGCCACCCCTGATAGAGGTGAGTGCAGTCAAAATCTGCCAGACCT 158
Db 1 AGTTGGTTAGAGCCACCCCTTGTATAGAGGTGAGTGCAGTCAAAATCTGCCAGACCC 60
QY 159 ACCAATTGCTGTGTCGAGAAG-----AATACGGGGCCATAGCTACGCTGGGAGAGCG 210
Db 61 ACCAATTGCTGTGCGGGAAGCCCTGTAGAAATACGGGGCCATAGCTACGCTGGGAGAGCG 120
QY 211 CTTGCTTGTGACGAGAGGTGACGGTTCGATCCCGGTTGGCTCCACCACTCTCTCGTG 270
Db 121 CTTGCTTGTGACGAGAGGTCAACGGTTCGATCCCGGTTGGCTCCACCACTTACGTTGT 180
QY 271 TTGCGGTGAGTGTAAAG-----AGTTCAGAAATGATGCCGCTTCAGGTTTGCCTGTGA 326
Db 181 GATGGTGTGCTGTAGTTCCTCTCGGTTAGAGTTAGAAATGAGCAATCCATCATGC 240
QY 327 GTGCTGATTTCTGCTTTTACCGGTACGAAATCTTCTTTAAAAATTTGGATATGTG 386
Db 241 GATGGTGAATGTTGATTTCTAGTCTTTGATTAGATCGTCTTTACAAATTTGGGTATGTG 300
QY 387 ATAGAA 392
Db 301 ATAGAA 306

RESULT 5
BH405252/c
LOCUS
DEFINITION AG-ND-127K13.TR ND-TAM Anopheles gambiae genomic clone AG-ND-127K13
ACCESSION BH405252
VERSION BH405252.1 GI:17351468
KEYWORDS GSS.
SOURCE African malaria mosquito.
ORGANISM Anopheles gambiae
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea; Anopheles.
REFERENCE 1 (bases 1 to 754)
AUTHORS Shetty,J., Malek,J., Koo,H., Collins,F., Gardner,M. and Loftus,B.J.
TITLE Direct Submission of BAC-end sequences from Anopheles gambiae
JOURNAL Unpublished (2001)
COMMENT Contact: Brendan J Loftus
Department of Eukaryotic Genomics
9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 0208
Fax: 301 838 3543
Email: bjoftus@tigr.org
This clone is from an A. gambiae BAC library (ND-TAM) provided by F.H. Collins and sequenced by The Institute for Genomic Research (TIGR). The BAC library was generated from A. gambiae PEST strain DNA. All DNA was extracted from newly hatched first instar larvae to minimize the inclusion of DNA from microorganisms that inhabit the gut. The DNA is derived from mixed sexes of larvae. The BAC library was constructed at Texas A&M University BAC Center University, College Station, Texas 77843-2123, USA using a HindIII partial digest.
Seq primer: M13 Rev
Class: BAC ends.
Location/Qualifiers
1..754
/organism="Anopheles gambiae"

BASE COUNT      180 a      199 c      167 g      208 t
ORIGIN

Query Match      14.8%; Score 77; DB 17; Length 754;
Best Local Similarity 64.9%; Pred. No. 1.2e-12;
Matches 150; Conservative 0; Mismatches 70; Indels 11; Gaps 2;

QY 78 CTTGTTATAGTCTGTAGCTCAGTTGGTTAGAGCCACCCCTGATAGGGTGCAGTCCGC 137
Db 645 CTTGGACTGGTCTGTAGCTCAGCTGGTTAGAGCACCGTCTTGTATAGGCGGGTCTGT 586
QY 138 AGTTCAAAATCTGCCAGACCTACCA-----TTGCTTGGTCAGAGAATACAGGG 187
Db 585 GGTTCGAGGCCAACTAGACCCACCAAGATTCCAAATGCTGTGTTGTCGAGGATCCCGGG 526
QY 188 GCATAGCTCAGC-TGGGAGAGCGCTTGCCTTGCACGACGAGGTGCAGCGTTGCATCCC 246
Db 525 GGATTAAGCTCAGCTTGGGAGAGCACCTGCTTTGCAACGAGGGGTGCTCGGTTGATCCC 466
QY 247 GCTTGCTCCACCACTCTCTCGTGTTCGCTGAGTGTAAAGAGCTTCAGAA 297
Db 465 GTCATCTCCACCAAGATCGCTGGTGGCAACAAGAGAGCTTGCAGGA 415

RESULT 6
BH400944/c
LOCUS
DEFINITION AG-ND-158022.TF ND-TAM Anopheles gambiae genomic clone AG-ND-158022
ACCESSION BH400944
VERSION BH400944.1 GI:17347147
KEYWORDS GSS.
SOURCE African malaria mosquito.
ORGANISM Anopheles gambiae
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea; Anopheles.
REFERENCE 1 (bases 1 to 593)
AUTHORS Shetty,J., Malek,J., Koo,H., Collins,F., Gardner,M. and Loftus,B.J.
TITLE Direct Submission of BAC-end sequences from Anopheles gambiae
JOURNAL Unpublished (2001)
COMMENT Other_GSSs: AG-ND-158022.TR
Contact: Brendan J Loftus
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 0208
Fax: 301 838 3543
Email: bjoftus@tigr.org
This clone is from an A. gambiae BAC library (ND-TAM) provided by F.H. Collins and sequenced by The Institute for Genomic Research (TIGR). The BAC library was generated from A. gambiae PEST strain DNA. All DNA was extracted from newly hatched first instar larvae to minimize the inclusion of DNA from microorganisms that inhabit the gut. The DNA is derived from mixed sexes of larvae. The BAC library was constructed at Texas A&M University BAC Center University, College Station, Texas 77843-2123, USA using a HindIII partial digest.
Seq primer: M13 For
Class: BAC ends.
Location/Qualifiers
1..593
/organism="Anopheles gambiae"
/strain="PEST"
/db_xref="taxon:7165"
/clone="AG-ND-158022"
/clone_lib="ND-TAM"
/note="Vector: pECBAC1; Site_1: HindIII"
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Matches 130; Conservative 0; Mismatches 34; Indels 22; Gaps 2;
QY 97 TCAGTTGGTAGAGCGCACCCCTGATAGAGGTGAGGTGGCAGTTCAAATCTGCCAGAC 156
    ||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 518 TCAGTGGTTAGAGCGCACCCCTGATAGAGGTGAGGTGGTTCAGTCCACTCAGGC 459
    ||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 157 CTACCAATT-----GCTTGGTCGAGAAGATACGGGCCCATAGCT 196
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 458 CTACCAATTTGCACGGCAAAATTTGAAGAGGTTTTAACTACATGCTATGGGTTATAGCT 399
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 197 CAGCTGGGAGAGCGCTCCCTTGA--CGCAGGAGTACGGGTTGCTATCCGCTGGCT 254
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 398 CAGCTGGGAGAGCGCTCTTTGTCATCGCAGGAGGTCNCCGGTTTGATCCCGCNTNGCT 339
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 255 CCACCA 260
    |||||
Db 338 CCACCA 333

RESULT 9
BH771024
LOCUS
DEFINITION
    BH771024 6499 bp DNA linear GSS 01-MAY-2002
    LMGtag746 MGI363 Random Sequence Tag Library Lactococcus lactis
    subsp. cremoris genomic, DNA sequence.
ACCESSION
    BH771024
VERSION
    BH771024.1 GI:20373981
KEYWORDS
    GSS.
SOURCE
    Lactococcus lactis subsp. cremoris.
ORGANISM
    Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
    Lactococcus.
REFERENCE
    1 (bases 1 to 6499)
    Bolotin,A., Ehrlich,S.D. and Sorokin,A.
    Studies of genomes of dairy bacteria Lactococcus lactis
    Sci. Aliments, (2002) In press
    Contact: Sorokin A
    Genetique Microbienne
    INRA
    CRJ INRA, Domaine de Vilvert, 78352 Jouy en Josas cedex, France
    Tel: 33 1 34 65 25 16
    Fax: 33 1 34 65 25 21
    Email: sorokine@jouy.inra.fr
    best homologue in strain IL1403 is ywgA (78%)
    Class: shotgun
    High quality sequence start: 30
    High quality sequence stop: 6471.
FEATURES
    source
    1..6499
    /organism="Lactococcus lactis subsp. cremoris"
    /strain="MGI363"
    /db_xref="taxon:1359"
    /clone_lib="MGI363 Random Sequence Tag Library"
    /notes="Vector: pSGM02; Site_1: SmaI; Library of
    chromosomal fragments of L.lactis strain MGI363 was
    prepared by partial AluI digestion or by sonication."
BASE COUNT
    1946 a 1228 c 1683 g 1642 t
ORIGIN
    Query Match 13.3%; Score 69.4; DB 17; Length 6499;
    Best Local Similarity 92.4%; Pred. No. 1.2e-09;
    Matches 73; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 179 GAATACGGGGCCATAGCTACGTGGGAGAGCGCTGCTGTCACGAGGAGGTAGCGGT 238
    ||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 2159 GATGTGGGGCCCTAGCTAGCTGGGAGAGCGCTGCTGTTGTCACGAGGAGGTAGCGGT 2218
    ||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 239 TCATCCCGCTGGCTCCA 257
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 2219 TCATCCCGCTAGGCTCCA 2237

RESULT 10
BI544108

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LOCUS
DEFINITION
    BI544108 497 bp mRNA linear EST 01-MAR-2002
    S071 Gracilaria lemneiformis gametophyte cDNA library Gracilaria
    lemneiformis cDNA 5', mRNA sequence.
ACCESSION
    BI544108
VERSION
    BI544108.1 GI:19033790
KEYWORDS
    EST.
SOURCE
    Gracilaria lemneiformis.
ORGANISM
    Gracilaria lemneiformis.
    Eukaryota; Rhodophyta; Florideophyceae; Gracilariaceae; Gracilariaceae; Gracilaria.
    1 (bases 1 to 497)
    Sun,X., Yang,G.P., Mao,Y.X. and Zhang,X.C.
    Analysis of expressed sequence tags of a marine red alga,
    Gracilaria lemneiformis
    Unpublished (2001)
    Contact: Sun, X.; Zhang, X. C.
    College of Marine Life Sciences
    Ocean University of Qingdao
    Yushan Road 5, Qingdao, 266003, Shandong, China
    Tel: +86-0532-2032789
    Fax: +86-0532-2032276
    Email: xczhang@ouqd.edu.cn
    PCR Primers
    FORWARD: 5' -CGTGATACATGCTCTAGAGT-3'
    BACKWARD: 5' -CTGATCTAGACCTCAGGCTC-3'
    Seq primer: 5' -CGTGGTACCATGCTCTAGAGT-3'
    POLYA-No.
FEATURES
    source
    1..497
    /organism="Gracilaria lemneiformis"
    /db_xref="taxon:2778"
    /clone_lib="Gracilaria lemneiformis gametophyte cDNA
    library"
    /tissue_type="gametophyte thalli"
    /note="Vector: pMD 18-T; Site_1: EcoR V with a T hang;
    Wild type Gracilaria lemneiformis were harvested from
    Zhanshan Bay, Qingdao (China). After rinsed with boiled
    seawater, younger thalli was cut and washed every 3-4
    days until 1 month. Then thalli was cultivated in
    Provasoli medium. Total RNA was isolated from thalli of
    gametophyte algae, using UNIQ-10 Trizol total RNA
    Preparation Kit(Sangon Inc., Shanghai, China). The cDNA
    was synthesized, amplified and cloned using cDNA
    Synthesis Kit, cDNA PCR Library Kit and pMD 18-T vector
    (Takara Biotechnology Co., Ltd., Dalian, China),
    respectively."
BASE COUNT
    151 a 77 c 103 g 166 t
ORIGIN
    Query Match 13.0%; Score 67.8; DB 13; Length 497;
    Best Local Similarity 69.1%; Pred. No. 6.8e-10;
    Matches 114; Conservative 0; Mismatches 37; Indels 14; Gaps 1;

QY 93 TAGCTCAGTTGGTTAGAGCGCACCCCTGTATAGGGTGAGTGGCAGTTCAAATCTGCC 152
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 232 TAGCTCAGTTGGTTAGAGCGCACCCCTGTATAGGGTGAGTGGCTTCAAATCCAGGA 291
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 153 ACACCTACCAATTGCTTGGTCGAGAAGATACGGGGCCATAGCTCAGCTGGGAGAGCGCC 212
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 292 TAGCCACCATGA-----ATAAGGGGGTATAGCTCAGCTGGTAGAGCGCT 337
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 213 TGCCTTGACCGCAGGAGGTGAGCGGTTCGATCCGCTTGGCTCCA 257
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 338 GCTTTTGCAAGCAGATGTCAGCGGTTCAAATCCGCTTATCTCCA 382
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

RESULT 11
BI544155
LOCUS
DEFINITION
    BI544155 548 bp mRNA linear EST 01-MAR-2002
    S129 Gracilaria lemneiformis gametophyte cDNA library Gracilaria
    lemneiformis cDNA 5', mRNA sequence.
ACCESSION
    BI544155
VERSION
    BI544155.1 GI:19033837

```



/note="Vector: pMD 18-T; Site\_1: EcoR V with a T hang; Wild type Gracilaria lemaneiformis were harvested from Zhanshan Bay, Qingdao (China). After rinsed with boiled seawater, younger thalli was cut and washed every 3-4 days until 1 month. Then thalli was cultivated in Provasoli medium. Total RNA was isolated from thalli of gametophyte algae, using UNIQ-10 Trizol Total RNA Preparation Kit (Sangon Inc., Shanghai, China). The cDNA was synthesized, amplified and cloned using cDNA Synthesis Kit, cDNA PCR Library Kit and pMD 18-T vector (Takara Biotechnology Co., Ltd., Dalian, China), respectively.

BASE COUNT 179 a 89 c 109 g 162 t  
ORIGIN

Query Match 12.7%; Score 66.2; DB 13; Length 539;  
Best Local Similarity 68.5%; Pred. No. 2.3e-09;  
Matches 113; Conservative 0; Mismatches 38; Indels 14; Gaps 1;

QY 93 TAGCTCAGTGGTTAGAGCGCCCTGATAGAGGTGAGGTGCGCAGTTCAAATCTGCC 152  
|||||  
DB 73 TAGCTCAGTGGTTAGAGCGCCCTGATAGAGGTGAGGTGCGCAGTTCAAATCTGCC 132  
|||||

QY 153 AGACCTACCAATGCTGTGTCGAGAGATACGGGCCCATAGCTCAGCTGGGAGAGCC 212  
|||||  
DB 133 TAGCCCCACATGA-----ATAAGGGGGGTATAGCTCAGCTGGTGTAGAGTGCT 178  
|||||

QY 213 TGCCTTGCAGCAGGAGGTGAGGTGCTGATCCCGCTGGCTCCA 257  
|||||  
DB 179 GCTTTTGAAGCAGATGTCAGCGGTTCAAATCCGGTTATCTCCA 223  
|||||

RESULT 14  
BH614410 287 bp DNA linear GSS 07-JAN-2002  
LOCUS

DEFINITION 1C22AG2 Subclones from overlapping BAC clones spanning the hrp cluster of Erwinia carotovora subsp. atroseptica Pectobacterium carotovorum subsp. atrosepticum genomic, DNA sequence.

ACCESSION BH614410  
VERSION BH614410.1 GI:18078210  
KEYWORDS GSS.  
SOURCE Pectobacterium carotovorum subsp. atrosepticum.  
ORGANISM Pectobacterium carotovorum subsp. atrosepticum.  
Bacteria: Proteobacteria; gamma subdivision; Enterobacteriaceae; Pectobacterium.

REFERENCE 1 (bases 1 to 287)  
Bell, K.S., Avrova, A.O., Holvea, M.C., Cardle, L., Morris, W., De Jong, W., Toth, I.K., Waugh, R., Bryan, G.J., and Birch, P.R.J.  
TITLE Sample sequencing of a selected region of the genome of Erwinia carotovora subsp. atroseptica reveal candidate phytopathogenicity genes and allows comparison with Escherichia coli

JOURNAL Unpublished (2002)  
COMMENT Contact: Bell KS  
Scottish Crop Research Institute  
Invergowrie, Dundee, United Kingdom, DD2 5DA  
Email: kbells@scri.sari.ac.uk  
Class: BAC subclone.

FEATURES Location/Qualifiers  
source 1..287  
/organism="Pectobacterium carotovorum subsp. atrosepticum"  
/strain="SCRI1039"  
/db\_xref="taxon:29471"  
/clone\_lib="Subclones from overlapping BAC clones spanning the hrp cluster of Erwinia carotovora subsp. atroseptica"  
/note="Vector: pGEM 3zf; DNA from BAC clones Eca2B8 and EcalC22 was nebulised and cloned into pGEM 3zf and sequenced with SP6 or T7 primers"  
BASE COUNT 74 a 62 c 78 g 73 t  
ORIGIN

Query Match 12.3%; Score 63.8; DB 17; Length 287;  
Best Local Similarity 85.5%; Pred. No. 8.4e-09;  
Matches 71; Conservative 0; Mismatches 12; Indels 0; Gaps 0;

QY 83 TATAGGCTGTAGCTCAGTGGTTAGAGCGCCCTGATAGAGGTGAGGTGCGCAGTTC 142  
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DB 170 TACAGGCTGTAGCTCAGTGGTTAGAGCGCCCTGATAGAGGTGAGGTGCGTGGTTC 229  
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QY 143 AAATCTGCCAGACCTACCAATT 165  
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DB 230 AAGTCCACTCAGCGCTACCAAT 252  
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RESULT 15  
AZ578476/c 191 bp DNA linear GSS 08-DEC-2000  
LOCUS

DEFINITION 23h03 Shot-gun genomic library of Rhizobium strain ANU265 Rhizobium sp. NGR234 genomic clone 23h03, DNA sequence.

ACCESSION AZ578476  
VERSION AZ578476.1 GI:11605796  
KEYWORDS GSS.  
SOURCE Rhizobium sp. NGR234.  
ORGANISM Rhizobium sp. NGR234.  
Bacteria: Proteobacteria; Alphaproteobacteria; Rhizobiales;

REFERENCE 1 (bases 1 to 191)  
Viprey, V., Rosenthal, A., Broughton, W.J. and Perret, X.  
TITLE Genetic snapshots of the Rhizobium species NGR234 genome  
JOURNAL Genome Biol. 1 (6), RESEARCH0014 (2000)  
MEDLINE 21114532  
COMMENT Contact: Virginie Viprey  
Laboratoire de Biologie Molculaire des Plantes Supérieures  
University of Geneva  
1 Chemin de l'Imperatrice, Chambesy/Geneva 1292, Switzerland  
Tel: +44(0)1603450000  
Fax: +44(0)1603450045  
Email: virginie.viprey@bbrc.ac.uk  
Class: shotgun.

FEATURES Location/Qualifiers  
source 1..191  
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BASE COUNT 47 a 62 c 44 g 37 t 1 others  
ORIGIN

Query Match 12.0%; Score 62.6; DB 17; Length 191;  
Best Local Similarity 87.2%; Pred. No. 1.5e-08;  
Matches 68; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

QY 185 GGGCCCATAGCTCAGCTGGGAGAGCGCTGCTTCAGCGCAGGAGGTTCAGCGTTCGATC 244  
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DB 111 GGGCTGTAGCTCAGCTGGGAGAGCACNTGCTTTCAGACGAGGGGTTCAGCGTTCGATC 52  
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QY 245 CCGCTTGGCTCCCACT 262  
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DB 51 CCGCTCAGCTCCCACT 34  
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Search completed: February 1, 2003, 04:21:54  
Job time : 976.301 secs

GenCore version 5.1.3  
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: February 1, 2003, 01:06:21 : Search time 1037.68 Seconds  
(without alignments)  
14135.156 Million cell updates/sec

Title:

US-09-931-486-113

Perfect score: 504

Sequence: 1 ATCGAAGACACCGGCTTCGT.....CAGATTGCTGGGGTTATAT 504

Scoring table: IDENTITY\_NUC

Gapop 10.0 , Gapext 1.0

Searched: 2054640 seqs, 14551402878 residues

Total number of hits satisfying chosen parameters: 4109280

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

GenEmbl.\*

1: gb\_ba.\*  
2: gb\_htg.\*  
3: gb\_in.\*  
4: gb\_om.\*  
5: gb\_ov.\*  
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7: gb\_ph.\*  
8: gb\_pl.\*  
9: gb\_pr.\*  
10: gb\_ro.\*  
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13: gb\_un.\*  
14: gb\_vi.\*  
15: em\_ba.\*  
16: em\_fun.\*  
17: em\_hum.\*  
18: em\_in.\*  
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21: em\_or.\*  
22: em\_ov.\*  
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27: em\_sts.\*  
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29: em\_vi.\*  
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33: em\_htg\_mus.\*  
34: em\_htg\_pln.\*  
35: em\_htg\_rtd.\*  
36: em\_htg\_mam.\*  
37: em\_htg\_vrt.\*  
38: em\_sy.\*  
39: em\_htgo\_hum.\*  
40: em\_htgo\_mus.\*  
41: em\_htgo\_other.\*

score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Match	Length	DB	ID	Description
1	504	100.0	504	6	A48046	A48046 Sequence 11
2	504	100.0	504	6	AX177091	AX177091 Sequence
3	504	100.0	504	6	AX191054	AX191054 Sequence
4	504	100.0	505	1	PST251910	PST251910 Pseudomon
5	502.4	99.7	505	1	PST390584	PST390584 Pseudomon
6	500.4	99.3	505	1	PST390585	PST390585 Pseudomon
7	500	99.2	505	1	PST390582	PST390582 Pseudomon
8	499.2	99.0	505	1	PST390583	PST390583 Pseudomon
9	489.6	97.1	505	1	PST251900	PST251900 Pseudomon
10	486.6	96.5	506	1	PST251908	PST251908 Pseudomon
11	483.4	95.9	506	1	PST390588	PST390588 Pseudomon
12	345.4	68.5	528	1	PST251903	PST251903 Pseudomon
13	344.2	68.3	528	1	PST251905	PST251905 Pseudomon
14	342.6	68.0	528	1	PST390589	PST390589 Pseudomon
15	341.6	67.8	529	1	PST251904	PST251904 Pseudomon
16	341.6	67.8	529	1	PST390587	PST390587 Pseudomon
17	307.6	61.0	530	1	PST251907	PST251907 Pseudomon
18	306	60.7	530	1	PST251906	PST251906 Pseudomon
19	305.2	60.6	560	1	AF356514	AF356514 Pseudomon
20	287	56.9	529	1	PST251901	PST251901 Pseudomon
21	287	56.9	529	1	PST251902	PST251902 Pseudomon
22	284.2	56.4	529	1	PST390590	PST390590 Pseudomon
23	268.6	53.3	5785	1	PSU65012	U65012 Pseudomonas
24	265.4	52.7	499	6	A48047	A48047 Sequence 11
25	265.4	52.7	499	6	AR177092	AR177092 Sequence
26	265.4	52.7	499	6	AX191055	AX191055 Sequence
27	264	52.4	523	1	PST390581	PST390581 Pseudomon
28	249	49.4	520	6	A48045	A48045 Sequence 11
29	249	49.4	520	6	AR177090	AR177090 Sequence
30	249	49.4	520	6	AX191053	AX191053 Sequence
31	228.6	45.4	616	1	AF422492	AF422492 Unculture
32	225.8	44.8	471	6	A48044	A48044 Sequence 11
33	225.8	44.8	471	6	AR177089	AR177089 Sequence
34	225.8	44.8	471	6	AX191052	AX191052 Sequence
35	222.4	44.1	707	1	PSEDFO	L28162 Pseudomonas
36	221	43.8	528	1	PAE439391	AJ439391 Pseudomon
C 37	221	43.8	11176	1	AE004949	AE004949 Pseudomon
C 38	221	43.8	12065	1	AE004883	AE004883 Pseudomon
39	217.6	43.2	705	1	PSEDFM	L28160 Pseudomonas
40	214.4	42.5	705	1	PSEDFN	L28161 Pseudomonas
41	213.2	42.3	498	1	PAE439392	AJ439392 Pseudomon
42	212.2	42.1	521	1	PAE439389	AJ439389 Pseudomon
43	212	42.1	544	1	AF083211	AF083211 Azotobact
44	210.8	41.8	533	1	AF079808	AF079808 Azotobact
45	209	41.5	531	1	PAE439388	AJ439388 Pseudomon

# ALIGNMENTS

RESULT 1  
A48046  
LOCUS A48046  
DEFINITION Sequence 113 from Patent WO9600298.  
ACCESSION A48046  
VERSION A48046.1 GI:2301908  
SOURCE  
KEYWORDS  
ORGANISM  
unidentified.  
unidentified.  
unclassified.  
REFERENCE  
AUTHORS  
TITLE  
JAMES G. ROSSAU R and VAL H. H.  
SIMULTANEOUS DETECTION, IDENTIFICATION AND DIFFERENTIATION OF  
EUBACTERIAL TAXA USING A HYBRIDIZATION ASSAY  
Patent: WO 9600298-A 113 04-JAN-1996;  
JOURNAL  
Pred. No. is the number of results predicted by chance to have a



INNOGENETICS NV (BE)  
Other publication AU 2924695 960119.

FEATURES  
source  
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/organism="unidentified"  
/db\_xref="taxon:32644"

BASE COUNT 119 a 111 c 137 g 137 t

ORIGIN

Query Match 100.0%; Score 504; DB 6; Length 504;

Best Local Similarity 100.0%; Pred. No. 5.1e-140;

Matches 504; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATCGAAGACACCGGCTTCGTCATAAGCTCCACACGAAATTCGTCATTCACCTTGGGAAAG 60

Db 1 ATCGAAGACACCGGCTTCGTCATAAGCTCCACACGAAATTCGTCATTCACCTTGGGAAAG 60

QY 61 GCGATTGGGTTTAGACCCGAGAGTAACGATTGGGTCTGTAGCTCAGTTCAGTTAGAGCGCA 120

Db 61 GCGATTGGGTTTAGACCCGAGAGTAACGATTGGGTCTGTAGCTCAGTTCAGTTAGAGCGCA 120

QY 121 CCCTGATAAGGGTGGAGTGGCGATTCGAAATCTGCCAGACCCACCAATCGAAGGGCC 180

Db 121 CCCTGATAAGGGTGGAGTGGCGATTCGAAATCTGCCAGACCCACCAATCGAAGGGCC 180

QY 181 ATAGCTCAGCTGGGAGAGCGCCTCTTTCACGAGGAGGTTCAGCGGTTCGATCCCGCTT 240

Db 181 ATAGCTCAGCTGGGAGAGCGCCTCTTTCACGAGGAGGTTCAGCGGTTCGATCCCGCTT 240

QY 241 GGCTCCACCATTAACCTAGTTCGCGGAAAGCTCAGAAATGAGTGTTCACGAGGATGAGGT 300

Db 241 GGCTCCACCATTAACCTAGTTCGCGGAAAGCTCAGAAATGAGTGTTCACGAGGATGAGGT 300

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Db 301 TGATTGCTGGGTTGAACATTGATTTCTGGACTTTGCCGGAAGCTCAGAAATGAGTGTTCACGAGGATGAGGT 360

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QY 481 TAACAGATTGCTTGGGTTATAT 504

Db 481 TAACAGATTGCTTGGGTTATAT 504

RESULT 2

AR177091

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

FEATURES

source

BASE COUNT

ORIGIN

Query Match

Best Local Similarity

Matches 504;

Conservative 0;

Mismatches 0;

Indels 0;

Gaps 0;

AR177091 504 bp DNA linear PAT 17-DEC-2001

Sequence 113 from patent US 6312903.

AR177091

AR177091.1 GI:17919446

Unknown.

Unclassified.

1 (bases 1 to 504)

James G., Rossau, R. and Van Heuverswyn, H.

Simultaneous detection, identification and differentiation of

subcellular taxa using a hybridization assay

Patent: US 6312903-A 113 06-NOV-2001;

Location/Qualifiers

1..504

/organism="unknown"

BASE COUNT 119 a 111 c 137 g 137 t

ORIGIN

Query Match

Best Local Similarity

Matches 504;

Conservative 0;

Mismatches 0;

Indels 0;

Gaps 0;

Matches 504; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 61 GCGATTGGGTTTAGACCCGAGAGTAACGATTGGGTCTGTAGCTCAGTTCAGTTAGAGCGCA 120

QY 121 CCCTGATAAGGGTGGAGTGGCGATTCGAAATCTGCCAGACCCACCAATCGAAGGGCC 180

Db 121 CCCTGATAAGGGTGGAGTGGCGATTCGAAATCTGCCAGACCCACCAATCGAAGGGCC 180

QY 181 ATAGCTCAGCTGGGAGAGCGCCTCTTTCACGAGGAGGTTCAGCGGTTCGATCCCGCTT 240

Db 181 ATAGCTCAGCTGGGAGAGCGCCTCTTTCACGAGGAGGTTCAGCGGTTCGATCCCGCTT 240

QY 241 GGCTCCACCATTAACCTAGTTCGCGGAAAGCTCAGAAATGAGTGTTCACGAGGATGAGGT 300

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RESULT 3

AX191054

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

FEATURES

source

BASE COUNT

ORIGIN

Query Match

Best Local Similarity

Matches 504;

Conservative 0;

Mismatches 0;

Indels 0;

Gaps 0;

AX191054 504 bp DNA linear PAT 10-AUG-2001

Sequence 113 from Patent EP1091004.

AX191054

AX191054.1 GI:15149699

unidentified.

unidentified.

unclassified.

1 (bases 1 to 504)

James G., Rossau, R. and van Heuverswyn, H.

Simultaneous detection, identification and differentiation of

subcellular taxa using a hybridization assay

Patent: EP 1091004-A 113 11-APR-2001;

INNOGENETICS N.V. (BE)

Location/Qualifiers

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/organism="unidentified"

/db\_xref="taxon:32644"

BASE COUNT 119 a 111 c 137 g 137 t

ORIGIN

Query Match 100.0%; Score 504; DB 6; Length 504;

Best Local Similarity 100.0%; Pred. No. 5.1e-140;

Matches 504; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 61 GCGATTGGGTTTAGACCCGAGAGTAACGATTGGGTCTGTAGCTCAGTTCAGTTAGAGCGCA 120

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Db 421 TAAAAATTTGCGTGTCTCTATGCAAAATTTTCGGCGAATGTCGCTTCACGTTATAGACAG 480
QY 481 TAACCAAGATTGCTGGGGTTATAT 504
Db 481 TAACCAAGATTGCTGGGGTTATAT 504

RESULT 4
PST251910
LOCUS
DEFINITION
Pseudomonas stutzeri internal transcribed spacer 1 (ITS1), trna-Ile
and trna-Ala, strain CCUG 11256-T.
ACCESSION
AJ251910
VERSION
AJ251910.1 GI:9844598
KEYWORDS
RNA-Ile; trna-Ala; trna-Ile.
SOURCE
Pseudomonas stutzeri.
ORGANISM
Bacteria; Proteobacteria; gamma subdivision; Pseudomonadaceae;
Pseudomonas.
REFERENCE
1 (bases 1 to 505)
Guasp, C., Moore, E.R., Lalucat, J. and Bannas, A.
Utility of internally transcribed 16S-23S rDNA spacer regions for
the definition of Pseudomonas stutzeri genomovars and other
Pseudomonas species
Int. J. Syst. Evol. Microbiol. 50 Pt 4, 1629-1639 (2000)
20393664
PUBMED
10939670
Bannas, A.
Direct Submission
Submitted (14-DEC-1999) Bannas, A., Division of Microbiology,
National Research Centre for Biotechnology, Mascheroder Weg 1,
D-38124 Braunschweig, GERMANY
Location/Qualifiers
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/db_xref="taxon:316"
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93. .169
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177. .251
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BASE COUNT 120 a 111 c 137 g 137 t  
ORIGIN

Query Match 100.0%; Score 504; DB 1; Length 505;  
Best Local Similarity 100.0%; Pred. No. 5.1e-140;  
Matches 504; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 482 TAACCAAGATTGCTGGGGTTATAT 505

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RESULT 5  
PST390584  
LOCUS  
DEFINITION  
Pseudomonas stutzeri intergenic spacer, trna-Ile and trna-Ala  
genes, strain SD93936.  
ACCESSION  
AJ390584  
VERSION  
AJ390584.1 GI:9844624  
KEYWORDS  
IGS; intergenic spacer; transfer RNA Ile; transfer RNA-Ala;  
trna-Ala gene; trna-Ile gene.  
SOURCE  
Pseudomonas stutzeri.  
ORGANISM  
Bacteria; Proteobacteria; gamma subdivision; Pseudomonadaceae;  
Pseudomonas.  
REFERENCE  
1 (bases 1 to 505)  
Guasp, C., Moore, E.R., Lalucat, J. and Bannas, A.  
Utility of internally transcribed 16S-23S rDNA spacer regions for  
the definition of Pseudomonas stutzeri genomovars and other  
Pseudomonas species  
Int. J. Syst. Evol. Microbiol. 50 Pt 4, 1629-1639 (2000)  
20393664  
PUBMED  
10939670  
Bannas, A.  
Direct Submission  
Submitted (15-DEC-1999) Bannas, A., Division of Microbiology,  
National Research Centre for Biotechnology, Mascheroder Weg 1,  
D-38124 Braunschweig, GERMANY  
Location/Qualifiers  
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source

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177..251  
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120 a 112 c 137 g 136 t

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Db 482 TAACAGATTCCTGGGGTTATAT 505

RESULT 6  
PST390585  
LOCUS  
DEFINITION Pseudomonas stutzeri intergenic spacer, trna-ile and trna-Ala  
genes, strain AER2.5.  
ACCESSION AJ390585  
VERSION AJ390585.1 GI:9844625  
KEYWORDS IGS: intergenic spacer; transfer RNA Ile; transfer RNA-Ala;  
trna-Ala gene; trna-ile gene.  
SOURCE Pseudomonas stutzeri  
ORGANISM Pseudomonas stutzeri  
Bacteria; Proteobacteria; gamma subdivision; Pseudomonadaceae;  
Pseudomonas.  
REFERENCE 1 (bases 1 to 505)  
AUTHORS Guasp,C., Moore,E.R., Lalucat,J. and Bannasar,A.  
TITLE Utility of internally transcribed 16S-23S rDNA spacer regions for

the definition of Pseudomonas stutzeri genomovars and other  
Pseudomonas species  
Int. J. Syst. Evol. Microbiol. 50 Pt 4, 1629-1639 (2000)  
20393664  
PUBMED 10939670  
REFERENCE 2 (bases 1 to 505)  
AUTHORS Bannasar,A.  
TITLE Direct Submission  
SUBMITTED (15-DEC-1999) Bannasar A., Division of Microbiology,  
National Research Centre for Biotechnology, Mascheroder Weg 1,  
D-38124 Braunschweig, GERMANY  
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/anticodon=(pos:127..129,aa:Ile)  
177..251  
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120 a 112 c 136 g 136 t 1 others

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Best Local Similarity 99.4%; Pred. No. 6.1e-139;  
Matches 501; Conservative 1; Mismatches 2; Indels 0; Gaps 0;  
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Db 62 GCGATTGGGTTAGACCCGAGAGTAACGATTGGGTCTGTAGCTCAGTTCAGTTAGACGCA 121  
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QY 421 TAAATTTGCGTGTCTCTATGCAAAATTTTCGGCGAAATGCTCTTCACGTTATAGACAG 480  
Db 422 TAAATTTGCGTGTCTCTATGCAAAATTTTCGGCGAAATGCTCTTCACGTTATAGACAG 481  
QY 481 TAACAGATTCCTGGGGTTATAT 504  
Db 482 TAACAGATTCCTGGGGTTATAT 505  
RESULT 7  
PST390582  
LOCUS  
PST390582 505 bp DNA linear BCT 16-AUG-2000

DEFINITION Pseudomonas stutzeri intergenic spacer, tRNA-Ile and tRNA-Ala  
 genes, strain SADN19.  
 ACCESSION AJ390582  
 VERSION AJ390582.1 GI:9844622  
 KEYWORDS IGS; intergenic spacer; transfer RNA Ile; transfer RNA-Ala;  
 tRNA-Ala gene; tRNA-Ile gene.  
 SOURCE Pseudomonas stutzeri.  
 ORGANISM Pseudomonas stutzeri.  
 Bacteria; Proteobacteria; gamma subdivision; Pseudomonadaceae;  
 Pseudomonas.  
 1 (bases 1 to 505)  
 Guasp,C., Moore,E.R., Lalucat,J. and Bennisar,A.  
 Utility of internally transcribed 16S-23S rDNA spacer regions for  
 the definition of Pseudomonas stutzeri genomovars and other  
 Pseudomonas species  
 Int. J. Syst. Evol. Microbiol. 50 Pt 4, 1629-1639 (2000)  
 JOURNAL MEDLINE  
 PUBMED 20393664  
 REFERENCE 10939670  
 2 (bases 1 to 505)  
 Bennisar,A.  
 Direct Submission  
 Submitted (15-DEC-1999) Bennisar A., Division of Microbiology,  
 National Research Centre for Biotechnology, Mascheroder Weg 1,  
 D-38124 Braunschweig, GERMANY  
 JOURNAL  
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Query Match 99.2%; Score 500; DB 1; Length 505;  
 Best Local Similarity 99.2%; Pred. No. 8e-139;  
 Matches 500; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 ATCGAAGACACCGGCTTCGTCATAGCTCCACAGTAACGATTGGGTCCTAGCTCAGTTGGTTAGAGCGCA 60  
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QY 421 TAAATTTCCGTTGTTCTCTATGCAAAATTTCCGCGAATTCGTTCTTACGTTATAGACAG 480  
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 QY 481 TAACCAGATTGCTGGGGTTATAT 504  
 DB 482 TAACCAGATTGCTGGGGTTATAT 505

RESULT 8  
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 LOCUS Pseudomonas stutzeri intergenic spacer, tRNA-Ile and tRNA-Ala  
 DEFINITION genes, strain SD55473.  
 ACCESSION AJ390583  
 VERSION AJ390583.1 GI:9844623  
 KEYWORDS IGS; intergenic spacer; transfer RNA Ile; transfer RNA-Ala;  
 tRNA-Ala gene; tRNA-Ile gene.  
 SOURCE Pseudomonas stutzeri.  
 ORGANISM Pseudomonas stutzeri.  
 Bacteria; Proteobacteria; gamma subdivision; Pseudomonadaceae;  
 Pseudomonas.  
 1 (bases 1 to 505)  
 Guasp,C., Moore,E.R., Lalucat,J. and Bennisar,A.  
 Utility of internally transcribed 16S-23S rDNA spacer regions for  
 the definition of Pseudomonas stutzeri genomovars and other  
 Pseudomonas species  
 Int. J. Syst. Evol. Microbiol. 50 Pt 4, 1629-1639 (2000)  
 JOURNAL MEDLINE  
 PUBMED 20393664  
 REFERENCE 10939670  
 2 (bases 1 to 505)  
 Bennisar,A.  
 Direct Submission  
 Submitted (15-DEC-1999) Bennisar A., Division of Microbiology,  
 National Research Centre for Biotechnology, Mascheroder Weg 1,  
 D-38124 Braunschweig, GERMANY  
 JOURNAL  
 FEATURES  
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 /anticodon=(pos:127..129,aa:Ile)  
 177..251  
 /product="tRNA-Ala"  
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 /anticodon=(pos:204..206,aa:Ala)  
 BASE COUNT 121 a 113 c 135 g 136 t  
 ORIGIN

Query Match 99.0%; Score 499.2; DB 1; Length 505;  
 Best Local Similarity 99.4%; Pred. No. 1.4e-138;  
 Matches 501; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

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 QY 61 GCGATTGGGTTTAGACCGGAGAGTAACGATTGGGTCCTAGCTCAGTTGGTTAGAGCGCA 120  
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 QY 121 CCCCTGATAGGGTTCGAGTCGGCAGTTCGAATCTGCCAGACCCACCAATCGAAGGGGCC 180  
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Db 422 TAAATTTGCGTGTCTCTATGCAAAATTTTCGGCGAATGTCGTTCTCACGTTATAGACAG 481
QY 481 TAACAGATTGCTTGGGTTATAT 504
Db 482 TAACAGATTGCTTGGGTTATAT 505

RESULT 9
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LOCUS Pseudomonas stutzeri internal transcribed spacer 1 (ITS1), tRNA-Ile
DEFINITION gene, and tRNA-Ala gene, strain ATCC 17594.
ACCESSION AJ251900
VERSION AJ251900.1 GI:9844588
KEYWORDS internal transcribed spacer 1; ITS1; transfer RNA-Ala; transfer
Pseudomonas stutzeri.
SOURCE Pseudomonas stutzeri.
ORGANISM Bacteria; Proteobacteria; gamma subdivision; Pseudomonadaceae;
Pseudomonas.
REFERENCE 1 (bases 1 to 505)
AUTHORS Guasp,C., Moore,E.R., Lalucat,J. and Bannasar,A.
TITLE Utility of internally transcribed 16S-23S rDNA spacer regions for
the definition of Pseudomonas stutzeri genomovars and other
Pseudomonas species
JOURNAL Int. J. Syst. Evol. Microbiol. 50 Pt 4, 1629-1639 (2000)
MEDLINE 20393664
PUBMED 10939670
REFERENCE 2 (bases 1 to 505)
AUTHORS Bannasar,A.
TITLE Direct Submission
JOURNAL Submitted (14-DEC-1999) Bannasar A., Division of Microbiology,
National Research Centre for Biotechnology, Mascheroder Weg 1,
D-38124 Braunschweig, GERMANY
FEATURES
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/anticodon=(pos:127..129,aa:Ile)
177..251
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/anticodon=(pos:204..206,aa:Ala)
134 g 136 t

BASE COUNT 121 a 114 c 134 g 136 t
ORIGIN

Query Match 97.1%; Score 489.6; DB 1; Length 505;
Best Local Similarity 98.2%; Pred. No. 1.1e-135;
Matches 495; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

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Db 422 TAAATTTGCGTGTCTCTATGCAAAATTTTCGGCGAATGTCGTTCTCACGTTATAGACAG 481
QY 481 TAACAGATTGCTTGGGTTATAT 504
Db 482 TAACAGATTGCTTGGGTTATAT 505

RESULT 10
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LOCUS Pseudomonas stutzeri internal transcribed spacer 1 (ITS1), tRNA-Ile
DEFINITION and tRNA-Ala, strain DNSP21.
ACCESSION AJ251908
VERSION AJ251908.1 GI:9844596
KEYWORDS internal transcribed spacer 1; ITS1; transfer RNA-Ala; transfer
RNA-Ile; tRNA-Ala; tRNA-Ile.
SOURCE Pseudomonas stutzeri.
ORGANISM Bacteria; Proteobacteria; gamma subdivision; Pseudomonadaceae;
Pseudomonas.
REFERENCE 1 (bases 1 to 506)
AUTHORS Guasp,C., Moore,E.R., Lalucat,J. and Bannasar,A.
TITLE Utility of internally transcribed 16S-23S rDNA spacer regions for
the definition of Pseudomonas stutzeri genomovars and other
Pseudomonas species
JOURNAL Int. J. Syst. Evol. Microbiol. 50 Pt 4, 1629-1639 (2000)
MEDLINE 20393664
PUBMED 10939670
REFERENCE 2 (bases 1 to 506)
AUTHORS Bannasar,A.
TITLE Direct Submission
JOURNAL Submitted (14-DEC-1999) Bannasar A., Division of Microbiology,
National Research Centre for Biotechnology, Mascheroder Weg 1,
D-38124 Braunschweig, GERMANY
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/anticodon=(pos:127..129,aa:ile)  
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121 a 113 c 136 g 136 t

BASE COUNT 121 a 113 c 136 g 136 t  
ORIGIN

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Best Local Similarity 99.0%; Pred. No. 8.4e-135;  
Matches 500; Conservative 0; Mismatches 4; Indels 1; Gaps 1;

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62 GCGATTGGGTTTAGACCCGAGAGTAACGATTGGGTCTGTAGCTCAGTTGGTTAGAGCGCA 121  
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480 GTAAACAGATTGCTGGGTTTATAT 504  
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RESULT 11  
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LOCUS  
DEFINITION  
Pseudomonas stutzeri intergenic spacer, trna-ile and trna-ala  
genes, strain JDA.  
AJ390588  
VERSION  
IGS; intergenic spacer; transfer RNA ile; transfer RNA-ala;  
trna-ala gene; trna-ile gene.  
Pseudomonas stutzeri.  
SOURCE  
Pseudomonas stutzeri  
Bacteria; Proteobacteria; gamma subdivision; Pseudomonadaceae;  
Pseudomonas.  
REFERENCE  
1 (bases 1 to 506)  
Guasp, C., Moore, E.R., Lalucat, J. and Bannas, A.  
Utility of internally transcribed 16S-23S rDNA spacer regions for  
the definition of Pseudomonas stutzeri genomovars and other  
Pseudomonas species  
Int. J. Syst. Evol. Microbiol. 50 Pt 4, 1629-1639 (2000)  
JOURNAL  
MEDLINE  
PUBMED  
20393664  
10939670  
REFERENCE  
2 (bases 1 to 506)

AUTHORS Bannas, A.  
TITLE Direct Submission  
JOURNAL Submitted (15-DEC-1999) Bannas, A., Division of Microbiology,  
National Research Centre for Biotechnology, Mascheroder Weg 1,  
D-38124 Braunschweig, GERMANY  
FEATURES  
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177..251  
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122 a 113 c 136 g 135 t

BASE COUNT 122 a 113 c 136 g 135 t  
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Query Match 95.9%; Score 483.4; DB 1; Length 506;  
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Matches 498; Conservative 0; Mismatches 6; Indels 1; Gaps 1;

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480 GTAAACAGATTGCTGGGTTTATAT 504  
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482 GTAAACAGATTGCTGGGTTTATAT 506  
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RESULT 12  
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LOCUS  
DEFINITION  
Pseudomonas stutzeri internal transcribed spacer 1 (ITS1), trna-ile  
and trna-ala, strain AN11.  
AJ390588  
VERSION  
AJ390588.1 GI:9844593  
INTERNAL TRANSCRIBED SPACER 1; ITS1; transfer RNA-ala; transfer  
RNA-ile; trna-ala; trna-ile.

SOURCE Pseudomonas stutzeri.  
ORGANISM Pseudomonas stutzeri  
Bacteria; Proteobacteria; gamma subdivision; Pseudomonadaceae;  
Pseudomonas  
REFERENCE 1 (bases 1 to 528)  
AUTHORS Guasp,C., Moore,E.R., Lalucat,J. and Bannasar,A.  
TITLE Utility of internally transcribed 16S-23S rDNA spacer regions for  
the definition of Pseudomonas stutzeri genomovars and other  
Pseudomonas species  
JOURNAL Int. J. Syst. Evol. Microbiol. 50 Pt 4, 1629-1639 (2000)  
MEDLINE 20393664  
PUBMED 10939670  
REFERENCE 2 (bases 1 to 528)  
AUTHORS Bannasar,A.  
TITLE Direct Submission  
JOURNAL Submitted (14-DEC-1999) Bannasar A., Division of Microbiology,  
National Research Centre for Biotechnology, Mascheroder Weg 1,  
D-38124 Braunschweig, GERMANY  
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QY 217 GAGGTGAGGTTTCATCCCGCTTGGCTCCACCATTAACTCGAAATCGCTGAAAGCTCA 274  
DB 242 GAGGTGAGGTTTCATCCCGCTTGGCTCCACCATTAACTCGAAATCGCTGAAAGCTCA 301  
QY 275 GAAATCAGTGTTCACCAAGATGAGTTGATGGCTGGGTTGACATTCATTTCTGGACTT 334  
DB 302 GAAATCAGTGTTCACCAAGATGAGTTGATGGCTGGGTTGACATTCATTTCTGGACTT 357  
QY 335 TGGCCGAGAACTGTTCTTTAAAAATTTGGGTATGTGATAGAAGTGA-CCGATGTGTGC 393  
DB 358 TGGCCGAGAACTGTTCTTTAAAAATTTGGGTATGTGATAGAAGTGAATTCAGTGGTCA 417  
QY 394 TTTCACTGCGAGATGTCGCGTCAAGTAAATTTGCGTGTCTCTATGCAAAATTTTCGG 453  
DB 418 TTTCACTGCGATTAATCAAGTCAAGTAAATTTGCGTGTCTCTATGCAAAATTTTCGG 477

QY 454 CGAATGTCGCTTCACGTTATAGACAGTAACACAGATTGCTTGGGGTTATAT 504  
DB 478 CGAATGTCGCTTCACGTTATAGACAGTAACACAGATTGCTTGGGGTTATAT 528  
PST251903 528 bp DNA linear BCT 16-AUG-2000  
Pseudomonas stutzeri internal transcribed spacer 1 (ITS1), rRNA-Ile  
and trna-Ala, strain DSM 50227.  
AJ251903  
AJ251903.1 GI:9844591  
internal transcribed spacer 1; ITS1; transfer RNA-Ala; transfer  
RNA-Ile; trna-Ala; trna-Ile.  
Pseudomonas stutzeri.  
Bacteria; Proteobacteria; gamma subdivision; Pseudomonadaceae;  
Pseudomonas.  
REFERENCE 1 (bases 1 to 528)  
AUTHORS Guasp,C., Moore,E.R., Lalucat,J. and Bannasar,A.  
TITLE Utility of internally transcribed 16S-23S rDNA spacer regions for  
the definition of Pseudomonas stutzeri genomovars and other  
Pseudomonas species  
JOURNAL Int. J. Syst. Evol. Microbiol. 50 Pt 4, 1629-1639 (2000)  
MEDLINE 20393664  
PUBMED 10939670  
REFERENCE 2 (bases 1 to 528)  
AUTHORS Bannasar,A.  
TITLE Direct Submission  
JOURNAL Submitted (14-DEC-1999) Bannasar A., Division of Microbiology,  
National Research Centre for Biotechnology, Mascheroder Weg 1,  
D-38124 Braunschweig, GERMANY  
FEATURES  
source  
1. .528  
/organism="Pseudomonas stutzeri"  
/strain="DSM 50227"  
/db\_xref="taxon:316"  
/note="PCR-amplified rDNA"  
misc\_feature  
1. .528  
/notes="internal transcribed spacer 1, ITS1"  
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93. .169  
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BASE COUNT 124 a 111 c 143 g 150 t  
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Best Local Similarity 84.2%; Pred. No. 4.2e-92;  
Matches 447; Conservative 0; Mismatches 53; Indels 31; Gaps 4;  
QY 1 ATCGAAGACCGCGCTTCGTATAGCTCCACAGCAATTCCTGATTCACCTGCGAAAG 60  
DB 2 ATCGAAGACTTCAGCTTCCTATAGCTCCACAGCAATTCCTGATTCACCTGCGAAAG 61  
QY 61 GCGATTGGGTTTACGCCGAGAGTACGATTGGGCTCTGTAGCTCAGTTGGTTAGAGCGCA 120  
DB 62 GCGATTGGGTTTACGCCGAGAGAGAGATGGGCTCTGTAGCTCAGTTGGTTAGAGCGCA 121  
QY 121 CCCCTGATAGGTTGAGTGGCGAGTTCGAATCTGCCAGACCCACCAAA----- 169  
DB 122 CCCCTGATAGGTTGAGTGGCGAGTTCGAATCTGCCAGACCCACCAATTCATGGGA 181  
QY 170 -----TCGAAGGGCCATAGCTCAGTGGGAGAGCGCTTGGCAGCAG 216  
DB 182 TGTGGCGGATCTAGATGGGCGCATAGCTCAGTGGGAGAGCGCTTGGCAGCAG 241  
QY 217 GAGGTGAGGTTTCATCCCGCTTGGCTCCACCATTAACTC--TAGTCGCGGAAAGCTCA 274

Db 242 GAGGTCAGCGGTTGATCCCGCTTGGCTCCACCATTAACCTGCAAAATCGCTGAAAGCTCA 301  
QY 275 GAAATGAGTGTGTTACCAAGATGAGTTGATTCGCTGGGTTGAAACATGATTCTTGGACTT 334  
Db 302 GAAATGAGTGTGTTGCGCATCCCTGATGTGTGAGGCT---ATTGATTCTTGGTCTT 357  
QY 335 TCGCCGAGAACTGTTCTTTAAATAATTTGGGTATGTATGATAGAGTAGA-CCGATGTGTTC 393  
Db 358 TCGCCGAGAACTGTTCTTTAAATAATTTGGGTATGTATGATAGAGTAGAATTGAGTGGTCAC 417  
QY 394 TTTCACTGGCAGCATGTCGCTCAAGGTAAATTTGGGTATGTATGATAGAGTAGA-CCGATGTGTTC 453  
Db 418 TTTCACTGGTGTATTTCAAGTCAAGGTAAATTTGGGTATGTATGATAGAGTAGA-CCGATGTGTTC 477  
QY 454 CGAATGTCGCTTTCACGTTATAGACAGTAACCAAGATTGCTTGGGTTTATAT 504  
Db 478 CGAATGTCGCTTTCACGTTATAGACAGTAACCAAGATTGCTTGGGTTTATAT 528

RESULT 14  
PST390589  
LOCUS PST390589 528 bp DNA linear BCT 16-AUG-2000  
DEFINITION Pseudomonas stutzeri intergenic spacer, tRNA-Ile and tRNA-Ala genes, strain P111.  
ACCESSION AJ390589  
VERSION 1  
PUBMED 10939670  
KEYWORDS IGS; intergenic spacer; transfer RNA Ile; transfer RNA-Ala; tRNA-Ala gene; tRNA-Ile gene.  
SOURCE Pseudomonas stutzeri.  
ORGANISM Pseudomonas stutzeri.  
Bacteria; Proteobacteria; gamma subdivision; Pseudomonadaceae; Pseudomonas.

REFERENCE 1 (bases 1 to 528)  
AUTHORS Guasp,C., Moore,E.R., Lalucat,J. and Bannasar,A.  
TITLE Utility of internally transcribed 16S-23S rDNA spacer regions for the definition of Pseudomonas stutzeri genomovars and other Pseudomonas species  
JOURNAL Int. J. Syst. Evol. Microbiol. 50 Pt 4, 1629-1639 (2000)  
MEDLINE 20393664  
PUBMED 10939670  
REFERENCE 2 (bases 1 to 528)  
AUTHORS Bannasar,A.  
TITLE Direct Submission  
JOURNAL Submitted (15-DEC-1999) Bannasar A., Division of Microbiology, National Research Centre for Biotechnology, Mascheroder Weg 1, D-38124 Braunschweig, GERMANY

FEATURES  
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1. .528  
/organism="Pseudomonas stutzeri"  
/strain="P111"  
/db\_xref="taxon:316"  
misc\_feature 1. .528  
/note="intergenic spacer"  
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/anticodon="(pos:127..129,aa:Ile)"  
trna 201..275  
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/anticodon="(pos:228..230,aa:Ala)"  
BASE COUNT 127 a 109 c 140 g 152 t  
ORIGIN

Query Match 68.0%; Score 342.6; DB 1; Length 528;  
Best Local Similarity 84.0%; Pred. No. 1.3e-91;  
Matches 446; Conservative 0; Mismatches 54; Indels 31; Gaps 4;

QY 1 ATCGAAGACACCGGTTGCTATAGAGTCCACGATTCGCTGATTCACCTGCGAAG 60  
Db 2 ATCGAAGACCTCAGCTTCTTATAGCTCCACGATTCGCTGATTCACCTAGCGAAA 61  
QY 61 GCGATTGGGTTTAGACCCGAGAGTAACGATTGGGCTGTAGCTCAGTTGGTTAGACGCA 120

Db 62 GCATTTGGTTTACCCGAGAGACGATTTGGGCTCTGTAGCTCAGTTGTTAGACGCA 121  
QY 121 CCCTGATTAAGGTGAGTGGGAGTTCGATTCGATTCGCCAGACCCACCA----- 169  
Db 122 CCCTGATTAAGGTGAGTGGGAGTTCGATTCGATTCGCCAGACCCACCAATTGTCATGGGA 181  
QY 170 -----TCGAAAGGGGCATAGCTCAGCTGAGGAGCGCTGCTTTCACGACGAG 216  
Db 182 TGTGGCCGATCTGTAGATGGGCCATAGCTCAGCTGAGGAGCGCTGCTTTCACGACGAG 241  
QY 217 GAGTTCAGCGGTTGATTCGCGCTTGGGTCCACCATTTAACTC---TAGTCGCGGAAAGCTCA 274  
Db 242 GAGTTCAGCGGTTGATTCGCGCTTGGGTCCACCATTTAACTC---TAGTCGCGGAAAGCTCA 301  
QY 275 GAAATGAGTGTGTTACCAAGGATGAGTTGATTCGCTGGGTTGAAACATGATTCTTGGACTT 334  
Db 302 GAAATGAGTGTGTTACCAAGGATGAGTTGATTCGCTGGGTTGAAACATGATTCTTGGACTT 357  
QY 335 TCGCCGAGAACTGTTCTTTAAATAATTTGGGTATGTATGATAGAGTAGA-CCGATGTGTTC 393  
Db 358 TCGCCGAGAACTGTTCTTTAAATAATTTGGGTATGTATGATAGAGTAGAATTGAGTGGTCAC 417  
QY 394 TTTCACTGGCAGCATGTCGCTCAAGGTAAATTTGGGTATGTATGATAGAGTAGA-CCGATGTGTTC 453  
Db 418 TTTCACTGGTGTATTTCAAGTCAAGGTAAATTTGGGTATGTATGATAGAGTAGA-CCGATGTGTTC 477  
QY 454 CGAATGTCGCTTTCACGTTATAGACAGTAACCAAGATTGCTTGGGTTTATAT 504  
Db 478 CGAATGTCGCTTTCACGTTATAGACAGTAACCAAGATTGCTTGGGTTTATAT 528

RESULT 15  
PST251904  
LOCUS PST251904 529 bp DNA linear BCT 16-AUG-2000  
DEFINITION Pseudomonas stutzeri internal transcribed spacer 1 (ITS1), tRNA-Ile and tRNA-Ala, strain AN10.  
ACCESSION AJ251904.1 GI:9844592  
VERSION 1  
PUBMED 10939670  
KEYWORDS Internal transcribed spacer 1; ITS1; transfer RNA-Ala; transfer RNA-Ile; tRNA-Ala; tRNA-Ile.  
SOURCE Pseudomonas stutzeri.  
ORGANISM Pseudomonas stutzeri.  
Bacteria; Proteobacteria; gamma subdivision; Pseudomonadaceae; Pseudomonas.

REFERENCE 1 (bases 1 to 529)  
AUTHORS Guasp,C., Moore,E.R., Lalucat,J. and Bannasar,A.  
TITLE Utility of internally transcribed 16S-23S rDNA spacer regions for the definition of Pseudomonas stutzeri genomovars and other Pseudomonas species  
JOURNAL Int. J. Syst. Evol. Microbiol. 50 Pt 4, 1629-1639 (2000)  
MEDLINE 20393664  
PUBMED 10939670  
REFERENCE 2 (bases 1 to 529)  
AUTHORS Bannasar,A.  
TITLE Direct Submission  
JOURNAL Submitted (14-DEC-1999) Bannasar A., Division of Microbiology, National Research Centre for Biotechnology, Mascheroder Weg 1, D-38124 Braunschweig, GERMANY

FEATURES  
source  
1. .529  
/organism="Pseudomonas stutzeri"  
/strain="AN10"  
/db\_xref="taxon:316"  
/note="PCR-amplified rDNA"  
misc\_feature 1. .529  
/note="internal transcribed spacer 1, ITS1"  
trna 93. .169  
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/note="codon recognized: AUC"  
/anticodon="(pos:127..129,aa:Ile)"  
trna 201..275  
/product="tRNA-Ala"







GenCore version 5.1.3  
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OM nucleic - nucleic search, using sw model

Run on: January 31, 2003, 19:23:36 ; Search time 119.347 Seconds  
(without alignments)  
9510.154 Million cell updates/sec

Title: US-09-931-486-113  
Perfect score: 504  
Sequence: 1 ATCGAAGACACCGCTTCGT.....CAGATTGCTGGGTATAT 504

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 2185239 seqs, 1125999159 residues

Total number of hits satisfying chosen parameters: 4370478

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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- 2: /SID22/gcgdata/geneseq/geneseqn-emb1/NA1981.DAT.\*
- 3: /SID22/gcgdata/geneseq/geneseqn-emb1/NA1982.DAT.\*
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- 23: /SID22/gcgdata/geneseq/geneseqn-emb1/NA2001B.DAT.\*
- 24: /SID22/gcgdata/geneseq/geneseqn-emb1/NA2002.DAT.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	504	100.0	504	17	AAT11844
2	265.4	52.7	499	17	AAT11845
3	249	49.4	520	17	AAT11843
4	225.8	44.8	471	17	AAT11842
5	205.2	40.7	468	17	AAT11846
6	184.4	36.6	588	22	AAI69774
7	117.2	23.3	664	12	AAQ14106
8	110.6	21.9	1396	22	AAH55089
9	110.6	21.9	2839	22	AAH54998

10	110.6	21.9	3444	22	AAH54992
11	110.6	21.9	4429	22	AAH54300
12	109.8	21.8	400	18	AAV78022
13	108.6	21.5	603	12	AAQ14102
14	108.6	21.5	640681	24	ABA92787
15	108.4	21.5	20844	21	AAAB1460
16	108.4	21.5	172325	21	AAF21613
17	108.4	21.5	349980	21	AAF21544
18	108.4	21.5	349980	21	AAF21607
19	108.4	21.5	349980	21	AAF21611
20	108.4	21.5	349980	21	AAF21612
21	108.4	21.5	837096	21	AAAB1489
22	108.4	21.5	1437668	21	AAAB1490
23	108.2	21.5	400	18	AAV77902
24	108.2	21.5	1311	18	AAV77852
25	107.2	21.3	400	18	AAV77984
26	107	21.2	335	12	AAQ14103
27	102.8	20.4	808	17	AAT11889
28	102.8	20.4	808	17	AAT11890
29	102.8	20.4	809	17	AAT11891
30	102.6	20.4	351	18	AAV78405
31	97.8	19.4	549	12	AAQ14109
32	97	19.2	498	12	AAQ14107
33	97	19.2	269223	22	AAF28554
34	95	18.8	349980	22	AAH64966
35	94.2	18.7	343	18	AAV78492
36	93.6	18.6	400	18	AAV77919
37	91.8	18.2	243	23	AAAS48781
38	91.4	18.1	470	17	AAT11898
39	91.2	18.1	255	23	AAAS48800
40	91.2	18.1	255	23	AAAS48825
41	91.2	18.1	255	23	AAAS48838
42	91.2	18.1	255	23	AAAS48846
43	91.2	18.1	255	23	AAAS48854
44	91.2	18.1	255	23	AAAS48877
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## ALIGNMENTS

RESULT 1  
AAT11844  
ID AAT11844 standard; DNA; 504 BP.  
XX AAT11844;  
AC AAT11844;  
XX  
DT 03-SEP-1996 (first entry)  
XX  
DE P. stutzeri LMG 2333 16S-23S rRNA spacer region.  
XX  
KW Probe; detection; identification; microorganism; amplify;  
16S-23S rRNA spacer region; respiratory tract; universal;  
KW species-specific; ss.  
XX  
OS Pseudomonas stutzeri.  
XX  
PN WO9600298-A1.  
XX  
PD 04-JAN-1996.  
XX  
PF 23-JUN-1995; 95WO-EP02452.  
XX  
PR 07-APR-1995; 95EP-0870032.  
XX  
PR 24-JUN-1994; 94EP-0870106.  
XX  
PA (INNO-) INNOGENETICS NV.  
XX  
PI Jannes G, Rossau R, Van Heuverswyn H;  
XX WPT; 1996-068882/07.  
XX  
PT Novel hybridisation assay for the detection of eubacteria - esp

S. epidermidis gen  
S. epidermidis gen  
Staphylococcus aur  
N.gonorrhoeae stra  
Buchnera sp. genom  
N. meningitidis pa  
Neisseria meningit  
Neisseria meningit  
Neisseria meningit  
Neisseria meningit  
N. meningitidis pa  
N. meningitidis B  
Staphylococcus aur  
Staphylococcus aur  
Staphylococcus aur  
N.gonorrhoeae stra  
Brucella melitensi  
Brucella suis NIDO  
Brucella abortus  
Staphylococcus aur  
M.nonliquefaciens  
B.catarhalis stra  
Genomic fragment #  
C glutamicum codin  
Staphylococcus aur  
Staphylococcus aur  
Staphylococcus aur  
Yersinia enterocol  
Staphylococcus aur  
Staphylococcus aur  
Staphylococcus aur  
Staphylococcus aur  
Staphylococcus aur  
Staphylococcus aur

PT Mycobacterium, comprises amplifying the 16S-23S rRNA spacer region  
 XX  
 PS  
 XX Claim 2; Fig 38; 248pp; English.  
 CC The sequences given in AAT11791-857 represent the 16S-23S rRNA spacer  
 CC regions derived from various microorganisms. These sequences were  
 CC used in the method of the invention for the detection and identification  
 CC of at least one or more microorganisms. The method comprises amplifying  
 CC the 16S-23S rRNA spacer region and hybridising one or more of the probes  
 CC given in AAT3401.1-77 to the amplified sequence. These probes were  
 CC specifically used to detect microorganisms in samples originating from  
 CC the respiratory tract. This spacer region is derived from *Pseudomonas*  
 CC *stutzeri* LMG 2333.  
 XX  
 SQ Sequence 504 BP; 119 A; 111 C; 137 G; 137 T; 0 other;  
 Query Match 100.0%; Score 504; DB 17; Length 504;  
 Best Local Similarity 100.0%; Pred. No. 1.7e-163;  
 Matches 504; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
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 DB 1 ATCGAAGACACCGGCTTCGTCATAGCTCCACACGAATTCGTTGATTCACCTTCGGAAG 60  
 QY 61 GCGATTGGGTTAGACCCGAGAGTACGATGGGTCTGTAGCTCAGTTGGTTAGAGCGCA 120  
 DB 61 GCGATTGGGTTAGACCCGAGAGTACGATGGGTCTGTAGCTCAGTTGGTTAGAGCGCA 120  
 QY 121 CCCCTGATAGGGTGAGGTGGCGAGTTCGATCTGCCAGACCCACCAATCGAAGGGCC 180  
 DB 121 CCCCTGATAGGGTGAGGTGGCGAGTTCGATCTGCCAGACCCACCAATCGAAGGGCC 180  
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 DB 181 ATAGCTCAGCTGGGAGAGCGCTCCTTTCGACGAGGAGTTCAGCGGTTGATCCCGCTT 240  
 QY 241 GGCTCCACCAATTAAGTCTAGTTCGCGAAGAGTCTCAGAAATGAGTTTACAGGATGAGGT 300  
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 QY 361 TGGTATGCTGATAGAGTAGACCGATGTTGCTTTTCACTGGCAGCATGTCGCGTCAAGG 420  
 DB 361 TGGTATGCTGATAGAGTAGACCGATGTTGCTTTTCACTGGCAGCATGTCGCGTCAAGG 420  
 QY 421 TAAATTTGCGTGTCTCTATGCAAAATTTTCGGCGAATGTCGTTTACGTTATAGACAG 480  
 DB 421 TAAATTTGCGTGTCTCTATGCAAAATTTTCGGCGAATGTCGTTTACGTTATAGACAG 480  
 QY 481 TAACACGATTCTGGGGTTATAT 504  
 DB 481 TAACACGATTCTGGGGTTATAT 504

## RESULT 2

AAT11845  
 ID AAT11845 standard; DNA; 499 BP.  
 XX  
 AC AAT11845;  
 XX  
 DT 03-SEP-1996 (first entry)  
 XX  
 DE *P. alcaligenes* LMG 1224 16S-23S rRNA spacer region.  
 XX  
 KW Probe; detection; identification; microorganism; amplify;  
 KW 16S-23S rRNA spacer region; respiratory tract; universal;  
 KW species-specific; ss.  
 XX  
 OS *Pseudomonas* *alcaligenes*.  
 XX

PN WO9600298-A1.  
 XX  
 PD 04-JAN-1996.  
 XX  
 PF 23-JUN-1995; 95WO-EP02452.  
 XX  
 PR 07-APR-1995; 95EP-0870032.  
 PR 24-JUN-1994; 94EP-0870106.  
 XX  
 PA (INNO-) INNOGENETICS NV.  
 XX  
 PI Jannes G. Rossau R. Van Heulewyn H.  
 XX  
 DR WPI; 1996-068882/07.  
 XX  
 XX Novel hybridisation assay for the detection of eubacteria - esp  
 PT Mycobacterium, comprises amplifying the 16S-23S rRNA spacer region  
 PT  
 XX Claim 2; Fig 39; 248pp; English.  
 PS  
 XX The sequences given in AAT11791-857 represent the 16S-23S rRNA spacer  
 CC regions derived from various microorganisms. These sequences were  
 CC used in the method of the invention for the detection and identification  
 CC of at least one or more microorganisms. The method comprises amplifying  
 CC the 16S-23S rRNA spacer region and hybridising one or more of the probes  
 CC given in AAT3401.1-77 to the amplified sequence. These probes were  
 CC specifically used to detect microorganisms in samples originating from  
 CC the respiratory tract. This spacer region is derived from *Pseudomonas*  
 CC *alcaligenes* LMG 1224.  
 CC  
 XX Sequence 499 BP; 123 A; 109 C; 130 G; 137 T; 0 other;  
 SQ  
 Query Match 52.7%; Score 265.4; DB 17; Length 499;  
 Best Local Similarity 78.5%; Pred. No. 4.4e-81;  
 Matches 412; Conservative 0; Mismatches 66; Indels 47; Gaps 6;  
 QY 1 ATCGAAGACACCGGCTTCGTCATAGCTCCACACGAATTCGTTGATTCACCTTCGGAAG 60  
 DB 1 ATCGAAGACACCGGCTTCGTCATAGCTCCACACGAATTCGTTGATTCACCTTCGGAAG 60  
 QY 61 GCGATTGGGTTAGACCCGAGAGTACGATGGGTCTGTAGCTCAGTTGGTTAGAGCGCA 120  
 DB 61 GCGATTGGGTTAGACCCGAGAGTACGATGGGTCTGTAGCTCAGTTGGTTAGAGCGCA 120  
 QY 121 CCCCTGATAGGGTGAGGTGGCGAGTTCGAATTCGCCAGACCCACCAATTCGCGGATG 172  
 DB 121 CCCCTGATAGGGTGAGGTGGCGAGTTCGAATTCGCCAGACCCACCAATTCGCGGATG 180  
 QY 173 -----AAGGGCCATAGCTCAGCTGGGAGAGCGCTGCTTTGACCGCAGAGGT 221  
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 QY 222 CAGCGGTTGATCCGCTTGGCTCCACCATTAACCTCTAG-TCGCCGAAGCTCAGAAATG 280  
 DB 241 CAGGATTGATCTCCTTGGCTCCACCATCACTCAGATCGCTGAAGCTCAGAAATG 300  
 QY 281 AGTGTTCACAGGATGAGGTTGATTCGCTGGGTTGAACATGATTTGGAGCTTTGCGCC 340  
 DB 301 AACATT-----GGTAGTCAATGTTGATTTCTGCTTCTGCTTTCGCGCC 339  
 QY 341 AGAAGTGTCTTTAAATAATTTGGGTATGTATAGAGTAGACCGATGTTGCTTTCAC 400  
 DB 340 AGAAGTGTCTTTAAATAATTTGGGTATGTATAGAGTAGACCGATGTTGCTTTCAC 395  
 QY 401 GGCAGATGTCGCGTCAAGGTAATAATTTGCGTGTGTTCTCTATGCAAAATTTTCGGCGAATG 460  
 DB 396 CTGCACGTTGTTAATCAAGGCAAAATTTGCGAGTTC-AAGCGGAATTTTCGGCGAATG 454  
 QY 461 CGCTTTCACGTTA-TAGACAGTAACGATGCTTTGGGGTTATAT 504  
 DB 455 CGCTTTCACGTTACGAATCTATACACAGATGCTTTGGGGTTATAT 499

## RESULT 3

AAT11843  
ID AAT11843 standard; DNA; 520 BP.

XX AC AAT11843;

XX DT 03-SEP-1996 (first entry)

XX DE P. pseudoalcaligenes LMG 1225 16S-23S rRNA spacer region.

XX KW Probe; detection; identification; microorganism; amplify;  
KW 16S-23S rRNA spacer region; respiratory tract; universal;  
KW species-specific; ss.

XX OS Pseudomonas pseudoalcaligenes.

XX PN WO9600298-A1.

XX PD 04-JAN-1996.

XX PF 23-JUN-1995; 95WO-EP02452.

XX PR 07-APR-1995; 95EP-0870032.

XX PR 24-JUN-1994; 94EP-0870106.

XX XX (INNO-) INNOGENETICS NV.

XX PI Jannes G, Rossau R, Van Heuverswyn H.

XX WPI; 1996-068882/07.

XX Novel hybridisation assay for the detection of eubacteria - esp  
XX Mycobacterium, comprises amplifying the 16S-23S rRNA spacer region

XX Claim 2; Fig 37; 248pp; English.

XX The sequences given in AAT11791-857 represent the 16S-23S rRNA spacer  
XX regions derived from various microorganisms. These sequences were  
XX used in the method of the invention for the detection and identification  
XX of at least one or more microorganisms. The method comprises amplifying  
XX the 16S-23S rRNA spacer region and hybridising one or more of the probes  
XX given in AAT34011-77 to the amplified sequence. These probes were  
XX specifically used to detect microorganisms in samples originating from  
XX the respiratory tract. This spacer region is derived from Pseudomonas  
XX pseudoalcaligenes LMG 1225.

XX Sequence 520 BP; 126 A; 109 C; 134 G; 151 T; 0 other;

Query Match 49.4%; Score 249; DB 17; Length 520;

Best Local Similarity 74.4%; Pred. No. 2.1e-75;

Matches 392; Conservative 0; Mismatches 105; Indels 30; Gaps 5;

QY 1 ATCGAAGACACGGGCTTCGTCATAGCTCCACACAGAAATGCTGATTCACCTTGGCAAG 60

DB 1 ATCGAAGACATCAGCTTCTTCATAGTATCCACAGAAATGCTGATTCATAGTGAACG 60

QY 61 CGGATTGGTTAGACCGGAGAGTAACGATGGGTCCTAGCTCAGTGGTTAGAGCGCA 120

DB 61 AATGCTGTAAACGACCGCCGTGTATA-----GGTCTAGCTAGTGGTTAGAGCGCA 114

QY 121 CCCCTGATAAGGGTGAAGTCGGCAGTTCGAATCTGCCAGACCCACCAATCG----- 172

DB 115 CCCCTGATAAGGGTGAAGTCGGCAGTTCGAATCTGCCAGACCTACCAATTCCTTGGTCG 174

QY 173 -----AAGGGCCATAGCTCAGCTGGGAGAGCGCTGCTTTCACGCGAGAGGTGAC 224

DB 175 AGAAGATACGGGGCATAGCTCAGCTGGGAGAGCGCTGCTTTCACGCGAGAGGTGAC 234

QY 225 CGGTTGATCCCGTTGGCTCCACCATTAACCTAGTCGCGCGAAGACTCAGAAATGAGTG 284

DB 235 CGGTTGATCCCGTTGGCTCCACCATTCCTCTCGTGTGGGTGAGGTGTTAAAGAGTCA 294

QY 285 TTACCAGGATGAGGTTGATTGCCTGGGTTGAACATGATTGTTCTGGACTTT-----GCG 338

DB 295 GAATGATGCGCGCTTCAGGTTTCTCTGTGTAGTCTGATTTCTGCTCTTTGACCGTA 354  
QY 339 CCAGAACTGTTCTTTAAATAATTTGGGTATGTCATAGACAGTGTGTTGCTTCA 398  
DB 355 CGAAATCGTTCTTTTAAATAATTTGGATATGTGATAGACT-GACTGATTAATTTGCTTCA 413  
QY 399 CTGGCAGCATGTCGCGTCAAGGTAATAATTTG-CGTGTTCTCTATCAAAATTTTCGCGAA 457  
DB 414 CTGGCAATGATCTGTCAAGGTAATAATTTGATGTTCTCAAGACGCAAAATTTTCGCGAA 473  
QY 458 TGTGCTTCTCAGTTTATACAGTAACCAAGATTTGTTGGGTTATAT 504  
DB 474 TGTGCTTCTCAGGATTGAGACAGTAACCAAGATTTGTTGGGTTATAT 520

## RESULT 4

AAT11842

ID AAT11842 standard; DNA; 471 BP.

XX AC AAT11842;

XX DT 03-SEP-1996 (first entry)

XX DE P. aeruginosa UZG 5669 16S-23S rRNA spacer region.

XX KW Probe; detection; identification; microorganism; amplify;  
KW 16S-23S rRNA spacer region; respiratory tract; universal;  
KW species-specific; ss.

XX OS Pseudomonas aeruginosa.

XX PN WO9600298-A1.

XX PD 04-JAN-1996.

XX PF 23-JUN-1995; 95WO-EP02452.

XX PR 07-APR-1995; 95EP-0870032.

XX PR 24-JUN-1994; 94EP-0870106.

XX PA (INNO-) INNOGENETICS NV.

XX PI Jannes G, Rossau R, Van Heuverswyn H.

XX WPI; 1996-068882/07.

XX Novel hybridisation assay for the detection of eubacteria - esp  
XX Mycobacterium, comprises amplifying the 16S-23S rRNA spacer region

XX Claim 2; Fig 36; 248pp; English.

XX The sequences given in AAT11791-857 represent the 16S-23S rRNA spacer  
XX regions derived from various microorganisms. These sequences were  
XX used in the method of the invention for the detection and identification  
XX of at least one or more microorganisms. The method comprises amplifying  
XX the 16S-23S rRNA spacer region and hybridising one or more of the probes  
XX given in AAT34011-77 to the amplified sequence. These probes were  
XX specifically used to detect microorganisms in samples originating from  
XX the respiratory tract. This spacer region is derived from Pseudomonas  
XX aeruginosa UZG 5669.

XX Sequence 471 BP; 116 A; 103 C; 120 G; 132 T; 0 other;

Query Match 44.8%; Score 225.8; DB 17; Length 471;

Best Local Similarity 75.1%; Pred. No. 2e-67;

Matches 396; Conservative 0; Mismatches 52; Indels 79; Gaps 6;

QY 1 ATCGAAGACACCGGCTTCGTCATAGCTCCACAGAAATGCTGATTCACCTTGGCAAG 60

DB 1 ATCGAAGATCCCGGCTTCTTCATAGCTCCACAGAAATGCTGATTCACCTGTTAG-- 58

QY 61 CGGATTGGTTTAGACCCCGAGAGTAACGATTGGGTCCTGTAGCTCAGTTGTTAGAGCGCA 120

Db 59 -----ACGATTGGGCTGTAGCTCAGTTGGTTAGACGCA 93  
 QY 121 CCCTGATGAAGGTGAGGTGCGCAGTTTGAATCTGCCAGAGCCACCAATCG----- 172  
 Db 94 CCCTGATGAAGGTGAGGTGCGCAGTTTGAATCTGCCAGAGCCACCAATTTGGTGTG 153  
 QY 173 -----AAGGGCCATAGCTCAGCTGGGAGAGCGCCCTGCTTTGCACGAGCA 218  
 Db 154 CTGCGTGATCCGATACGGGGCCATAGCTCAGCTGGGAGAGCGCCCTGCTTTGCACGAGCA 213  
 QY 219 GGTACAGCGGTTCGATCCCGCTTGGCTCCACCAATTAACCTAGTCCGCGAAAGCTCAGAAA 278  
 Db 214 GGTACAGAGTTCGATCCCTTGGCTCCACCAATTAACCAATCGTCCGAAAGCTCAGAAA 273  
 QY 279 TGAGTGTTTTACCAGGATGAGGTGTGATTGCTGGGTTGAACATTTGATTTCTGGACTTTGGC 338  
 Db 274 TGAATGTT-----CGTGGATGAACATTTGATTTCTGGTCTTTGCA 312  
 QY 339 CAGAACTGTTCTTTAAAAATTTGGGTATGTGATAGAAGT-AGACCGATGTGTTGCTTTTC 397  
 Db 313 CAGAACTGTTCTTTAAAAATTTGGGTATGTGATAGAAGTGAAGTGAATGATCTCTTTC 372  
 QY 398 ACTGSCACCATGTCGCGTCAAGGTAAATTTGCGTGTCTCTATGCAAAATTTTCGGCGAA 457  
 Db 373 ACTGCTGATCATCAAGTCAAGGTAAATTTGCGAGTTC-AAGCGCAATTTTCGGCGAA 431  
 QY 458 TGTGCTCTTACGTTATAGACAGTAACACAGATTGCTTGGGTTTATAT 504  
 Db 432 TGTGCTCTTACAGTA-----TAACACAGATTGCTTGGGTTTATAT 471

## RESULT 5

AA11846  
 ID AAT11846 standard; DNA; 468 BP.  
 XX AC AAT11846;  
 XX AC AAT11846;  
 DT 03-SEP-1996 (first entry)  
 XX DE P. putida LMG 2232 16S-23S rRNA spacer region.  
 XX KW Probe; detection; identification; microorganism; amplify;  
 KW 16S-23S rRNA spacer region; respiratory tract; universal;  
 KW species-specific; ss.  
 XX OS Pseudomonas putida.  
 XX PN WO9600298-A1.  
 XX PD 04-JAN-1996.  
 XX PF 23-JUN-1995; 95WO-EP02452.  
 XX PR 07-APR-1995; 95EP-0870032.  
 XX PR 24-JUN-1994; 94EP-0870106.  
 XX XX  
 PA (INNO-) INNOGENETICS NV.  
 XX  
 PI Jannes G, Rossau R, Van Heuverswyn H;  
 XX WPI; 1996-068882/07.  
 XX  
 PT Novel hybridisation assay for the detection of eubacteria - esp  
 PT Mycobacterium, comprises amplifying the 16S-23S rRNA spacer region  
 XX  
 PS Claim 2; Fig 40; 248pp; English.  
 XX  
 CC The sequences given in AAT11791-857 represent the 16S-23S rRNA spacer  
 CC regions derived from various microorganisms. These sequences were  
 CC used in the method of the invention for the detection and identification  
 CC of at least one or more microorganisms. The method comprises amplifying  
 CC the 16S-23S rRNA spacer region and hybridising one or more of the probes

CC given in AAT34011-77 to the amplified sequence. These probes were  
 CC specifically used to detect microorganisms in samples originating from  
 CC the respiratory tract. This spacer region is derived from Pseudomonas  
 CC putida LMG 2232.  
 XX  
 SQ Sequence 468 BP; 117 A; 101 C; 117 G; 133 T; 0 other;

Query Match 40.7%; Score 205.2; DB 17; Length 468;  
 Best Local Similarity 74.7%; Pred. No. 2.7e-60;  
 Matches 378; Conservative 0; Mismatches 88; Indels 40; Gaps 8;

QY 1 ATCTAAGACACACGGCTTCGTCTCATAGCTCCACACCAATTTGTTGATTTCTGTTGCAAG 60  
 Db 1 ATCTGACGACATCAGTGTCTCATAGCTCCACACCAATTTGTTGATTTCTGTTGCAAG 59  
 QY 61 GCGATTGGSTTTAGACCTCCGAGAGTAACGATTGGGTCTGTAGCTCAGTTGTTGATAGCGCA 120  
 Db 60 ACGATTAGGTTAGCAACCTT-----CGATTGGGTCTGTAGCTCAGTTGTTGATAGCGCA 113  
 QY 121 CCCCTGATAAGGTGAGGTGCGGAGTTCGAATCTGCCAGACCCACCAA-TCGAAAGGGC 179  
 Db 114 CCCCTGATAAGGTGAGGTGCGGAGTTCGAATCTGCCAGACCCACCAA-TCGAAAGGGC 173  
 QY 180 CATAGCTCAGCTGGGAGAGCGCTCTTTCACGACGAGGTCACGGGTTCCATCCCGCT 239  
 Db 174 CATAGCTCAGCTGGGAGAGCGCTCTTTCACGACGAGGTCACGGGTTCCATCCCGCT 233  
 QY 240 TGGCTCCACCATTAACCTAGTCTAGTCGCGGAAAGCTCAGAAATGAGTGTTTACCAAGGATGAGG 299  
 Db 234 TGGCTCCACC-----ACCCCGCTTGGCAGTTTGTCAAGCTTAGNA 274  
 QY 300 TTGATTGCTGGGTGAACATTTCTGGACTTTGGCCAGAGAACTGTCTTTAAAAAT 359  
 Db 275 ATGAATATTCGCGTCGAATATTTGATTTCTGAACTTT--ATCAGAATCTGTTCTTTAAAAAT 332  
 QY 360 TTGGTATGTCATAGAACTAGA-CGGATGCTGTGCTTTTCACTGGCAGCATGTCGGGTCAA 418  
 Db 333 TTGGGTATGATAGAAAGATAGACTGGACAGCACTTTTCACTGGTGTGTGTTACGGGTAA 392  
 QY 419 GGTAAAAATTCGCTGTTCTTCTATGCAAAATTTTCGGCGAATGTCGCTCTTCACTGTTATAGAC 478  
 Db 393 GGTAAAAATTCGCTGTTCTTCTATGCAAAATTTTCGGCGAATGTCGCTCTTCACTGTTATAGAC 478  
 QY 479 AGTAACACAGATTGCTTGGGTTATAT 504  
 Db 445 --TAACACAGATTGCTTGGGTTATAT 468

## RESULT 6

AA169774  
 ID AAI69774 standard; DNA; 588 BP.  
 XX AC AAI69774;  
 XX AC AAI69774;  
 DT 13-DEC-2001 (first entry)  
 XX DE 16S/23S rRNA spacer region.  
 XX KW Bacterium detection; 16S/23S rRNA spacer region; ds.  
 XX OS Pseudomonas putida.  
 XX PN JP2001190279-A.  
 XX PD 17-JUL-2001.  
 XX PF 13-JAN-2000; 2000JP-0004160.  
 XX PR 13-JAN-2000; 2000JP-0004160.  
 XX PA (MITO ) MITSUBISHI JUKOGYO KK.  
 XX WPI; 2001-605311/69.



RESULT 9	
AAH54998/c	
ID	AAH54998 standard; DNA; 2839 BP.
XX	
XX	
AC	AAH54998;
XX	
DT	03-SEP-2001 (first entry)
XX	
DE	S. epidermidis genomic polynucleotide sequence SEQ ID NO:4362.
XX	
KW	Staphylococcus epidermidis SRI strain; infection; diagnosis;
KW	vaccination; endocarditis; ds.
XX	
OS	Staphylococcus epidermidis.
XX	
PN	WO200134809-A2.
XX	
PD	17-MAY-2001.
XX	
PF	09-NOV-2000; 2000WO-US30782.
XX	
PR	09-NOV-1999; 99US-0164258.
XX	
PA	(GLAX ) GLAXO GROUP LTD.
XX	
XX	Kimmerly WJ;
PL	
XX	
DR	WPI; 2001-316495/33.
XX	
PT	Nucleic acids encoding polypeptides from Staphylococcus epidermidis,

RESULT 10	
AAH54992	
ID	AAH54992 standard; DNA; 3444 BP.
XX	
XX	
AC	AAH54992;
XX	
DT	03-SEP-2001 (first entry)
XX	
XX	
DE	S. epidermidis genomic polynucleotide sequence SEQ ID NO:4356.
XX	
KW	Staphylococcus epidermidis SRI strain; infection; diagnosis;
KW	vaccination; endocarditis; ds.
XX	
OS	Staphylococcus epidermidis.
XX	
PN	WO200134809-A2.
XX	
PD	17-MAY-2001.
XX	
PF	09-NOV-2000; 2000WO-US30782.
XX	
PR	09-NOV-1999; 99US-0164258.
XX	
PA	(GLAX ) GLAXO GROUP LTD.
XX	
XX	









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XX 07-APR-2000; 2000JP-0107160.
XX (RIKA ) RIKAGAKU KENKYUSHO.
XX WPI; 2002-126043/17.
XX A genomic DNA of cockroach-symbiotic bacterium
XX Claim 1; Page 16-230; 237pp; Japanese.
XX The present invention describes a gene (I) derived from Buchnera sp.
XX containing the DNA (a) or (b), (a) has a fully defined base pair
XX sequence selected from a table of sequences found in the Buchnera sp.
XX genomic DNA of ABA92787 given in the specification or is a DNA selected
XX from complementary DNA sequences, and (b) is a DNA which hybridizes with
XX the DNA (a) and encodes a protein. Also described are: (1) a recombinant
XX vector (II) containing (I); (2) a transformant (III) containing (II);
XX (3) a genomic DNA of Buchnera sp. containing the sequence given in
XX ABA92787; (4) a plasmid derived from Buchnera sp. containing DNA (c) or
XX or ABB92789 and (d) is a plasmid which hybridizes with a DNA; and (5) a
XX method for the preparation of a protein in which (III) is cultured and
XX the expression protein of the object of the invention is collected from the
XX resultant culture. The DNA is useful for developing agricultural
XX chemicals for exterminating cockroaches. The present sequence represents
XX the specifically claimed Buchnera sp. genomic DNA sequence, from the
XX present invention.
XX Sequence 640681 BP; 237522 A; 83822 C; 84757 G; 234580 T; 0 other;
XX
XX Query Match 21.5%; Score 108.6; DB 24; Length 640681;
XX Best Local Similarity 79.6%; Pred. No. 2.9e-25;
XX Matches 144; Conservative 0; Mismatches 29; Indels 8; Gaps 1;
XX
XX QY 80 AGAGTAACGATGGTGTAGCTCAGTGTGGTATAGCGACCCCTCATAGGCTGAGGT 139
XX DB 275628 AAAAAATTGAGGCTGTGATCAGATGTTAGAGCGCACCCCTCATAGGCTGAGGT 275687
XX
XX QY 140 CGGCAGTTCGAATCTGCCAGACCCACCAATCGAA-----GGGGCATAGCTCAGCT 191
XX DB 275688 CGGTGTTCAATTCACCTCAGGCTTACCAATAAAAAATCATCTGGGGCTATAGCTCAGCT 275747
XX
XX QY 192 GGGAGAGCGCTCTTTCAGCAGGAGGTTCAGTCCGCTTGGCTCCACCAT 251
XX DB 275748 GGGAGAGCGCTCTTTCAGCAGGAGGTTCAGTCCGCTTGGCTCCACCAT 275807
XX
XX QY 252 T 252
XX DB 275808 T 275808
XX
XX RESULT 15
XX ID AAA81460 standard; DNA; 20844 BP.
XX AC AAA81460;
XX
XX 04-DEC-2000 (first entry)
XX
XX N. meningitidis partial DNA sequence gnm_8 SEQ ID NO:8.
XX
XX Neisseria meningitidis; Neisseria gonorrhoeae; genome; immunogenic;
XX antigen; vaccine; diagnosis; infection; antibacterial; identification;
XX Meningococcus B; MenB; ds.
XX
XX Neisseria meningitidis.
XX
XX WO200022430-A2.
XX
XX 20-APR-2000.
XX
XX 08-OCT-1999; 99WO-US23573.

```

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XX 09-OCT-1998; 98US-0103794.
XX 30-APR-1999; 99US-0132068.
XX (CHIR ) CHIRON CORP.
XX
XX Frazer CM, Hickey E, Peterson J, Tettelin H, Venter JC;
XX Masignani V, Galeotti C, Mora M, Ratti G, Scarselli M, Scarlato V;
XX Rappuoli R, Pizza M;
XX WPI; 2000-318079/27.
XX
XX Isolated nucleotide sequences of Neisseria meningitidis which can be
XX used in the diagnosis and treatment of N. meningitidis infection and
XX other Neisserial infections, for example, N.gonorrhoea
XX
XX Claim 7; Page 320-326; 1760pp; English.
XX
XX The present invention describes methods of obtaining immunogenic
XX proteins from Neisseria genomic sequences. AAA81453 to AAA82414
XX represent specifically claimed Neisseria meningitidis genomic DNA
XX sequences; AAA81260 to AAA81303 and AAB25620 to AAB25663 represent
XX Neisseria DNA sequences and their corresponding proteins; AAA81254 to
XX AAA81259 and AAA81304 to AAA81321 represent PCR primers used in the
XX isolation of Neisseria meningitidis DNA sequences; and AAA81322 to
XX AAA81452 represent Neisseria meningitidis MenB polynucleotide ORF
XX sequences, which are all used in the exemplification of the present
XX invention. The nucleic acid sequences, protein sequences, and antibodies
XX against them, can be used in the manufacture of a composition. The
XX composition can be used as a medicament (or in the manufacture of a
XX medicament) for treating, preventing or diagnosing infection due to
XX Neisserial bacteria. For example, some of the identified proteins could
XX be components of vaccines against Meningococcus B; against all serotypes;
XX and/or against all pathogenic Neisseriae. Identification of sequences
XX from the bacterium will also facilitate production of biological probes,
XX particularly organism-specific probes. Attempts to make efficacious
XX Meningococcus B vaccines have failed mainly due to antigen tolerance.
XX Multivalent vaccines have also been tried but none have successfully
XX overcome antigenic variability. The provision of further, complete
XX sequences may provide an opportunity to identify secreted or surface
XX exposed proteins that may be presumed targets for the immune system and
XX which are not antigenically variable or at least more conserved than
XX other more variable regions.
XX
XX Sequence 20844 BP; 5244 A; 5005 C; 5645 G; 4949 T; 1 other;
XX
XX Query Match 21.5%; Score 108.4; DB 21; Length 20844;
XX Best Local Similarity 83.3%; Pred. No. 5.5e-26;
XX Matches 135; Conservative 0; Mismatches 26; Indels 1; Gaps 1;
XX
XX QY 92 GGGTCTGTAGCTCAGTGTAGAGCGCACCCCTGATAAGGTTGAGTTCGGCAGTTGCAA 151
XX DB 20552 GGGTTTGTAGCTCAGTGTAGAGCGCACCGCTTGTATAGCGTGGGTTCGAGTTCAAG 20611
XX
XX QY 152 TCTGCCAGACCCACCAATCGAAGGGGCCATAGCTCAGTGGGAGAGCGCTGCTTTCGA 211
XX DB 20612 TCTTCCAGACCCACCA- GAACGGGGGCATAGCTCAGTGGGTAGAGCACCTGCTTGA 20670
XX
XX QY 212 GCGAGGAGGTGAGCGGTTCGATCCCGCTTGGCTCCACCATTA 253
XX DB 20671 AGCAGGGGGTTCATCGGTTCGATCCCGCTTGGCTCCACCATTA 20712
XX
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XX Job time : 358.347 secs

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GenCore version 5.1.3  
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OM nucleic - nucleic search, using sw model

Run on: February 1, 2003, 01:17:06 ; Search time 26.2031 Seconds  
(without alignments)  
5898.736 Million cell updates/sec

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Perfect score: 504  
Sequence: 1 ATCAGACACCGCTTCGT.....CAGATTGCTGGGGTTATAT 504

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 441362 seqs, 153338381 residues

Total number of hits satisfying chosen parameters: 882724

Minimum DB seq length: 0  
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Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

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4: /cgn2\_6/ptodata/1/ina/6B\_COMB.seq: \*  
5: /cgn2\_6/ptodata/1/ina/PTCUS\_COMB.seq: \*  
6: /cgn2\_6/ptodata/1/ina/backfiles1.seq: \*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Match	Length	DB	ID	Description
1	504	100.0	504	3	US-08-765-332-113	Sequence 113, App
2	504	100.0	504	4	US-09-448-894-113	Sequence 113, App
3	265.4	52.7	499	3	US-08-765-332-114	Sequence 114, App
4	265.4	52.7	499	4	US-09-448-894-114	Sequence 114, App
5	249	49.4	520	3	US-08-765-332-112	Sequence 112, App
6	249	49.4	520	4	US-09-448-894-112	Sequence 112, App
7	225.8	44.8	471	3	US-08-765-332-111	Sequence 111, App
8	225.8	44.8	471	4	US-09-448-894-111	Sequence 111, App
9	205.2	40.7	468	3	US-08-765-332-115	Sequence 115, App
10	205.2	40.7	468	4	US-09-448-894-115	Sequence 115, App
11	117.2	23.3	664	1	US-08-412-614-89	Sequence 89, Appl
12	108.6	21.5	603	1	US-08-412-614-85	Sequence 85, Appl
13	108.6	21.5	603	1	US-08-412-614-86	Sequence 86, Appl
14	108.6	21.5	603	2	US-08-635-761-86	Sequence 86, Appl
15	108.6	21.5	603	2	US-08-635-761-85	Sequence 85, Appl
16	108.6	21.5	603	4	US-09-312-520-86	Sequence 86, Appl
17	108.6	21.5	603	4	US-09-312-520-85	Sequence 85, Appl
18	102.8	20.4	808	3	US-08-765-332-131	Sequence 131, App
19	102.8	20.4	808	4	US-09-448-894-131	Sequence 131, App
20	102.8	20.4	808	4	US-09-448-894-132	Sequence 132, App
21	102.8	20.4	809	3	US-08-765-332-154	Sequence 154, App
22	102.8	20.4	809	4	US-09-448-894-154	Sequence 154, App
23	102.8	20.4	654	2	US-08-635-761-89	Sequence 89, Appl
24	99.4	19.7	654	4	US-09-312-520-89	Sequence 89, Appl
25	99.4	19.7	654	4	US-09-312-520-88	Sequence 88, Appl
26	97.8	19.4	549	1	US-08-412-614-92	Sequence 92, Appl
27	97.8	19.4	549	2	US-08-635-761-92	Sequence 92, Appl

Sequence 92, Appl  
Sequence 90, Appl  
Sequence 90, Appl  
Sequence 90, Appl  
Sequence 195, App  
Sequence 195, App  
Sequence 87, Appl  
Sequence 87, Appl  
Sequence 88, Appl  
Sequence 88, Appl  
Sequence 88, Appl  
Sequence 215, App  
Sequence 215, App  
Sequence 214, App  
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Sequence 119, App  
Sequence 119, App

28 97.8 19.4 549 4 US-09-312-520-92  
29 97 19.2 498 1 US-08-412-614-90  
30 97 19.2 498 2 US-08-635-761-90  
31 97 19.2 498 4 US-09-312-520-90  
32 91.4 18.1 470 3 US-08-765-332-195  
33 91.4 18.1 470 4 US-09-448-894-195  
34 88.6 17.6 582 1 US-08-412-614-87  
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36 88.6 17.6 582 4 US-09-312-520-87  
37 88.6 17.6 590 1 US-08-412-614-88  
38 88.6 17.6 590 2 US-08-635-761-88  
39 88.6 17.6 590 4 US-09-312-520-88  
40 88 17.5 463 3 US-08-765-332-215  
41 88 17.5 463 4 US-09-448-894-215  
42 88 17.5 475 3 US-08-765-332-214  
43 88 17.5 475 4 US-09-448-894-214  
44 83 16.5 363 3 US-08-765-332-119  
45 83 16.5 363 4 US-09-448-894-119

## ALIGNMENTS

RESULT 1  
US-08-765-332-113  
Sequence 113, Application US/08765332  
Patent No. 6025132  
GENERAL INFORMATION:  
APPLICANT: JANNES, GEERT  
APPLICANT: ROSSAU, RUDI  
APPLICANT: VAN HEUVESWYN, HUGO  
TITLE OF INVENTION: SIMULTANEOUS DETECTION, IDENTIFICATION  
TITLE OF INVENTION: AND DIFFERENTIATION OF EUBACTERIAL TAXA USING A  
TITLE OF INVENTION: HYBRIDIZATION ASSAY  
NUMBER OF SEQUENCES: 216  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: NIXON & VANDERHIVE P.C.  
STREET: 1100 NORTH GLEBE ROAD, 8TH FLOOR  
CITY: WASHINGTON  
STATE: D.C.  
COUNTRY: USA  
ZIP: 22201  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08765.332  
FILING DATE: 23-DEC-1996  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: WO PCT/EP95/02452  
FILING DATE: 23-JUN-1995  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: EP 95870032.0  
FILING DATE: 07-APR-1995  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: EP 94870106.5  
FILING DATE: 24-JUN-1994  
ATTORNEY/AGENT INFORMATION:  
NAME: SADOFF, B.J.  
REGISTRATION NUMBER: 36,663  
REFERENCE/DOCKET NUMBER: 1487-14  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 703-816-4091  
TELEFAX: 703-816-4100  
INFORMATION FOR SEQ ID NO: 113:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 504 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear

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; MOLECULE TYPE: cDNA
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
US-08-765-332-113

Query Match      100.0%; Score 504; DB 3; Length 504;
Best Local Similarity 100.0%; Pred. No. 7e-168;
Matches 504; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATCGAAGACACCGCTTCGTCATAGCTCCACACGAGTTCGTTGATTCACATTCGCGAAG 60
   |||||||
Db 1 ATCGAAGACACCGCTTCGTCATAGCTCCACACGAGTTCGTTGATTCACATTCGCGAAG 60

QY 61 GCGATTGGGTTAGACCCGAGAGTAAAGATTGGGTCTGTAGCTCAGTTCGTTAGAGCGCA 120
   |||||||
Db 61 GCGATTGGGTTAGACCCGAGAGTAAAGATTGGGTCTGTAGCTCAGTTCGTTAGAGCGCA 120

QY 121 CCCCTGATAAGGGTGAGGTGGCGAGTTCGATTCGATTCGATTCGATTCGATTCGATTCG 180
   |||||||
Db 121 CCCCTGATAAGGGTGAGGTGGCGAGTTCGATTCGATTCGATTCGATTCGATTCGATTCG 180

QY 181 ATAGCTCAGCTGGGAGAGCGCTCTCTTTCGACGAGGAGTTCAGCGGTTGATCCCGCTT 240
   |||||||
Db 181 ATAGCTCAGCTGGGAGAGCGCTCTCTTTCGACGAGGAGTTCAGCGGTTGATCCCGCTT 240

QY 241 GGCTCCACCATTAACCTAGTCCGCGAAGCTCAGAAATGAGTGTTCACGAGGATGAGGT 300
   |||||||
Db 241 GGCTCCACCATTAACCTAGTCCGCGAAGCTCAGAAATGAGTGTTCACGAGGATGAGGT 300

QY 301 TGATTGGCTGGGTTGACATTCGATTCGATTCGATTCGATTCGATTCGATTCGATTCGATTC 360
   |||||||
Db 301 TGATTGGCTGGGTTGACATTCGATTCGATTCGATTCGATTCGATTCGATTCGATTCGATTC 360

QY 361 TGGGTATGTATAGAGTACCGATGCTGCTTTCACGAGGAGTTCGCGTCAAGG 420
   |||||||
Db 361 TGGGTATGTATAGAGTACCGATGCTGCTTTCACGAGGAGTTCGCGTCAAGG 420

QY 421 TAAATTTGGGTTCTCTATGCAAAATTTTCGCGAATGCTGCTTCACGTTATAGACAG 480
   |||||||
Db 421 TAAATTTGGGTTCTCTATGCAAAATTTTCGCGAATGCTGCTTCACGTTATAGACAG 480

QY 481 TAACCAAGATTGCTGGGGTTATAT 504
   |||||||
Db 481 TAACCAAGATTGCTGGGGTTATAT 504

RESULT 2
US-09-448-894-113
; Sequence 113, Application US/09448894
; Patent No. 6312903
; GENERAL INFORMATION:
; APPLICANT: JANNES, GEERT
; ROSSAU, RUDI
; VAN HEUVERSWYN, HUGO
; TITLE OF INVENTION: SIMULTANEOUS DETECTION, IDENTIFICATION
; AND DIFFERENTIATION OF EUBACTERIAL TAXA USING A
; HYBRIDIZATION ASSAY
; NUMBER OF SEQUENCES: 216
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: NIXON & VANDERHUYE P.C.
; STREET: 1100 NORTH GLEBE ROAD, 8TH FLOOR
; CITY: WASHINGTON
; STATE: D.C.
; COUNTRY: USA
; ZIP: 22201
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/448,894
; FILING DATE: 29-No. 6312903-1999
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; CLASSIFICATION: <Unknown>
; 07-APR-1995
; 24-JUN-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/765,332
; FILING DATE: <Unknown>
; APPLICATION NUMBER: EP 95870032.0
; FILING DATE: 07-APR-1995
; APPLICATION NUMBER: EP 94870106.5
; FILING DATE: 24-JUN-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: SADOFF, B.J.
; REGISTRATION NUMBER: 36,663
; REFERENCE/DOCKET NUMBER: 1487-14
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 703-816-4091
; TELEFAX: 703-816-4100
; INFORMATION FOR SEQ ID NO: 113:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 504 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; SEQUENCE DESCRIPTION: SEQ ID NO: 113:
US-09-448-894-113

Query Match      100.0%; Score 504; DB 4; Length 504;
Best Local Similarity 100.0%; Pred. No. 7e-168;
Matches 504; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATCGAAGACACCGCTTCGTCATAGCTCCACACGAAATTCGTTGATTCACATTCGCGAAG 60
   |||||||
Db 1 ATCGAAGACACCGCTTCGTCATAGCTCCACACGAAATTCGTTGATTCACATTCGCGAAG 60

QY 61 GCGATTGGGTTAGACCCGAGAGTAAAGATTGGGTCTGTAGCTCAGTTCGTTAGAGCGCA 120
   |||||||
Db 61 GCGATTGGGTTAGACCCGAGAGTAAAGATTGGGTCTGTAGCTCAGTTCGTTAGAGCGCA 120

QY 121 CCCCTGATAAGGGTGAGGTGGCGAGTTCGAAATCTGCCACAGACCCACCAATCGAAGGGGCC 180
   |||||||
Db 121 CCCCTGATAAGGGTGAGGTGGCGAGTTCGAAATCTGCCACAGACCCACCAATCGAAGGGGCC 180

QY 181 ATAGCTCAGCTGGGAGAGCGCTCTCTTTCGACGAGGAGTTCAGCGGTTGATCCCGCTT 240
   |||||||
Db 181 ATAGCTCAGCTGGGAGAGCGCTCTCTTTCGACGAGGAGTTCAGCGGTTGATCCCGCTT 240

QY 241 GGCTCCACCATTAACCTAGTCCGCGAAGCTCAGAAATGAGTGTTCACGAGGATGAGGT 300
   |||||||
Db 241 GGCTCCACCATTAACCTAGTCCGCGAAGCTCAGAAATGAGTGTTCACGAGGATGAGGT 300

QY 301 TGATTGGCTGGGTTGACATTCGATTCGATTCGATTCGATTCGATTCGATTCGATTCGATTC 360
   |||||||
Db 301 TGATTGGCTGGGTTGACATTCGATTCGATTCGATTCGATTCGATTCGATTCGATTCGATTC 360

QY 361 TGGGTATGTATAGAGTACCGATGCTGCTTTCACGAGGAGTTCGCGTCAAGG 420
   |||||||
Db 361 TGGGTATGTATAGAGTACCGATGCTGCTTTCACGAGGAGTTCGCGTCAAGG 420

QY 421 TAAATTTGGGTTCTCTATGCAAAATTTTCGCGAATGCTGCTTCACGTTATAGACAG 480
   |||||||
Db 421 TAAATTTGGGTTCTCTATGCAAAATTTTCGCGAATGCTGCTTCACGTTATAGACAG 480

QY 481 TAACCAAGATTGCTGGGGTTATAT 504
   |||||||
Db 481 TAACCAAGATTGCTGGGGTTATAT 504

RESULT 3
US-08-765-332-114
; Sequence 114, Application US/08765332
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Patent No. 6025132  
GENERAL INFORMATION:  
APPLICANT: JANNES, GEERT  
APPLICANT: ROSSAU, RUDI  
APPLICANT: VAN HEUVERSWYN, HUGO  
TITLE OF INVENTION: SIMULTANEOUS DETECTION, IDENTIFICATION  
AND DIFFERENTIATION OF EUBACTERIAL TAXA USING A  
TITLE OF INVENTION: HYBRIDIZATION ASSAY  
NUMBER OF SEQUENCES: 216  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: NIXON & VANDERHYE P.C.  
STREET: 1100 NORTH GLEBE ROAD, 8TH FLOOR  
CITY: WASHINGTON  
STATE: D.C.  
COUNTRY: USA  
ZIP: 22201  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/765,332  
FILING DATE: 23-DEC-1996  
CLASSIFICATION: 435  
PRIOR APPLICATION NUMBER: WO PCT/EP95/02452  
FILING DATE: 23-JUN-1995  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: EP 95870032.0  
FILING DATE: 07-APR-1995  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: EP 94870106.5  
FILING DATE: 24-JUN-1994  
ATTORNEY/AGENT INFORMATION:  
NAME: SADOFF, B.J.  
REGISTRATION NUMBER: 36,663  
REFERENCE/DOCKET NUMBER: 1487-14  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 703-816-4091  
TELEFAX: 703-816-4100  
INFORMATION FOR SEQ ID NO: 114:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 499 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
US-08-765-332-114

Query Match 52.7%; Score 265.4; DB 3; Length 499;  
Best Local Similarity 78.5%; Pred. No. 9.2e-84;  
Matches 412; Conservative 0; Mismatches 66; Indels 47; Gaps 6;

QY 1 ATCGAAGACCGGCTCGTCATAGCTCCACAGAAATGCTTATTCACATTCGCAAG 60  
DB 1 ATCGAAGACTTCAGCTTCTTATAAGTTCACAGAAATGCTTATTCACATTCGCAAA 60  
QY 61 GCGATTGGGTTAGACCCGAGAGTAACGATTGGGTCTGTAGCTCAGTTGGTTAGAGCGCA 120  
DB 61 GCGATTGGGTTAGACCCGAGAGTAACGATTGGGTCTGTAGCTCAGTTGGTTAGAGCGCA 120  
QY 121 CCCCTGATAAGGGTGAGGTGCGGAGTCCGAATCTCCAGAGCCACCAATTCG----- 172  
DB 121 CCCCTGATAAGGGTGAGGTGCGGAGTCCGAATCTCCAGAGCCACCAATTCGCGGATG 180  
QY 173 -----AAGGGCCATAGCTCAGCTGGGAGAGGCGCTTTCACCCAGAGGT 221  
DB 181 GCCAGTGTCAATGGGGCCATAGCTCAGCTGGGAGAGGCGCTTTCACCCAGAGGT 240  
QY 222 CAGCGGTTCCGCGCTTGGCTCCACCAATTAACCTCTAG-TCGCCGGAAGCTCAGAAATG 280

DB 241 CAGGAGTTCGATCCTCTGGCTCCACCATCAACTCACGATCGCTGAAAGCTCAGAAATG 300  
QY 281 AGTGTTCACCATGAGGTTGATTCGCTGGGTTGACATTCATTCGACATTCGCGCC 340  
DB 301 AACATT-----GGTAGTTCAATGTTGATTTCTGTTCTGTTCTGCGCC 339  
QY 341 AGAATCTGTTCTTAAATAATTTGGGTATGTATGATAGAGTAGACCGGATGTTGCTTTCAT 400  
DB 340 AGAATCTGTTCTTAAATAATTTGGGTATGTATGATAGAGTAGACCTAACACGCG-----TGTTTCA 395  
QY 401 GGCAGCATGTCGCGTCAAGGTAAATTTGCGTGTCTCTATGCAAAATTTTCGCGCAATGT 460  
DB 396 CTGCACGTTGTTAATCAAGGCAAAATTTGCGAGTTC-AAAGCGGAATTTTCGCGCAATGT 454  
QY 461 CGTCTTCACGTTA-TAGACAGTAACAGATTCGTTGGGCTTATAT 504  
DB 455 CGTCTTCACGTTACGAATCTATAACCAAGATTGCTTGGGGTTATAT 499

RESULT 4  
US-09-448-894-114  
Sequence 114, Application US/09448894  
Patent No. 6312903  
GENERAL INFORMATION:  
APPLICANT: JANNES, GEERT  
APPLICANT: ROSSAU, RUDI  
APPLICANT: VAN HEUVERSWYN, HUGO  
TITLE OF INVENTION: SIMULTANEOUS DETECTION, IDENTIFICATION  
AND DIFFERENTIATION OF EUBACTERIAL TAXA USING A  
HYBRIDIZATION ASSAY  
NUMBER OF SEQUENCES: 216  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: NIXON & VANDERHYE P.C.  
STREET: 1100 NORTH GLEBE ROAD, 8TH FLOOR  
CITY: WASHINGTON  
STATE: D.C.  
COUNTRY: USA  
ZIP: 22201  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/448,894  
FILING DATE: 29-NOV-6312903-1999  
CLASSIFICATION: <Unknown>  
07-APR-1995  
24-JUN-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/765,332  
FILING DATE: <Unknown>  
APPLICATION NUMBER: EP 95870032.0  
FILING DATE: 07-APR-1995  
APPLICATION NUMBER: EP 94870106.5  
FILING DATE: 24-JUN-1994  
ATTORNEY/AGENT INFORMATION:  
NAME: SADOFF, B.J.  
REGISTRATION NUMBER: 36,663  
REFERENCE/DOCKET NUMBER: 1487-14  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 703-816-4091  
TELEFAX: 703-816-4100  
INFORMATION FOR SEQ ID NO: 114:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 499 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA  
HYPOTHETICAL: NO  
ANTI-SENSE: NO

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;
; SEQUENCE DESCRIPTION: SEQ ID NO: 114:
US-09-448-894-114

Query Match          52.7%; Score 265.4; DB 4; Length 499;
Best Local Similarity 78.5%; Pred. No. 9.2e-84;
Matches 412; Conservative 0; Mismatches 66; Indels 47; Gaps 6;

QY 1 ATCGAAGACACCGGCTTCGTCATAAGCTCCACACGAATTCGTTGATTCACCTTCGGAAG 60
   |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
Db 1 ATCGAAGACTTCAGCTTCCTTCATAAGTCCACACGAATTCGTTGATTCACCTTCGGAAG 60

QY 61 GCATTTGGTTTAGACCCGAGAGTACGATGGGTCTGAGTCACTGTTGGTTAGAGCGCA 120
   |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
Db 61 GCATTTGGTTTAGACCCGAGAGTACGATGGGTCTGAGTCACTGTTGGTTAGAGCGCA 120

QY 121 CCCTGATTAAGGTGAGGTGCGGAGTTCGAATCTGCCAGACCCACCAATCG----- 172
   |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
Db 121 CCCTGATTAAGGTGAGGTGCGGAGTTCGAATCTGCCAGACCCACCAATTCGCGGATG 180

QY 173 -----AAGGGGCCATAGCTCAGCTGGGAGAGCGCCTGCTTTGCACGACGAGGT 221
   |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
Db 181 GCCAGTGTCAAAATGGGGCCATAGCTCAGCTGGGAGAGCGCCTGCTTTGCACGACGAGGT 240

QY 222 CAGCGTTTCGATCCCGCTTGGCTCCACCAATTAAGTCTAG--TCGCCGAAAGCTCAGAAATG 280
   |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
Db 241 CAGGAGTTCGATCCCTTGGCTCCACCAATTAAGTCTAG--TCGCCGAAAGCTCAGAAATG 300

QY 281 AGTGTTTTACCAGGATGAGGTGATTGCCCTGGGTTGAACATTTGATTTCTGACTTTTCGCGC 340
   |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
Db 301 ACATTT-----GGTAGTTCATGTTGATTTCTGCTTTTCGCGC 339

QY 341 AGAAGTGTCTTTAAATTTGGGTATGTAGTAGAGTACAGCATGTTGCTTTTCACT 400
   |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
Db 340 AGAAGTGTCTTTAAATTTGGGTATGTAGTAGAGTACAGCATGTTGCTTTTCACT 395

QY 401 GGCAGCATGTCGCTCAAGTAAATTTGCGTGTCTCTATCAAAATTTTCGCGCAATCT 460
   |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
Db 396 CTGACGTTGTTAATCAGGCAAAATTTGCGAGTTC-AAGCGGAAATTTTCGCGCAATCT 454

QY 461 CGTCTTCAGTTA-TAGACAGTAACCAAGATTCGTTGGGTTATAT 504
   |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
Db 455 CGTCTTCAGTTACGAATCTATAACCAAGATTCGTTGGGTTATAT 499

RESULT 5
US-08-765-332-112
; Sequence 112, Application US/08765332
; Patent No. 6025132
; GENERAL INFORMATION:
; APPLICANT: JANNES, GEERT
; APPLICANT: ROSSAU, RUDI
; APPLICANT: VAN HEUVERSWYN, HUGO
; TITLE OF INVENTION: SIMULTANEOUS DETECTION, IDENTIFICATION
; TITLE OF INVENTION: AND DIFFERENTIATION OF EUBACTERIAL TAXA USING A
; NUMBER OF SEQUENCES: 216
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: NIXON & VANDERHUYE P.C.
; STREET: 1100 NORTH GLEBE ROAD, 8TH FLOOR
; CITY: WASHINGTON
; STATE: D.C.
; COUNTRY: USA
; ZIP: 22201
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/765,332
; FILING DATE: 23-DEC-1996
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
```

```

ROSSAU, RUDI
VAN HEUVERSWEYN, HUGO
TITLE OF INVENTION: SIMULTANEOUS DETECTION, IDENTIFICATION
AND DIFFERENTIATION OF EUBACTERIAL TAXA USING A
HYBRIDIZATION ASSAY
NUMBER OF SEQUENCES: 216
CORRESPONDENCE ADDRESSES:
ADDRESSEE: NIXON & VANDERHYE P.C.
STREET: 1100 NORTH GLEBE ROAD, 8TH FLOOR
CITY: WASHINGTON
STATE: D.C.
COUNTRY: USA
ZIP: 22201
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/448,894
FILING DATE: 29-No. 6312903-1999
CLASSIFICATION: <Unknown>
07-APR-1995
24-JUN-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/765,332
FILING DATE: <Unknown>
APPLICATION NUMBER: EP 95870032.0
FILING DATE: 07-APR-1995
APPLICATION NUMBER: EP 94870106.5
FILING DATE: 24-JUN-1994
ATTORNEY/AGENT INFORMATION:
NAME: SADOFF, B.J.
REGISTRATION NUMBER: 36,663
REFERENCE/DOCKET NUMBER: 1487-14
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-816-4091
TELEFAX: 703-816-4100
INFORMATION FOR SEQ ID NO: 112:
SEQUENCE CHARACTERISTICS:
LENGTH: 520 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
SEQUENCE DESCRIPTION: SEQ ID NO: 112:
US-09-448-894-112

```

Query Match 44.8%; Score 225.8; DB 3; Length 471;  
Best Local Similarity 75.1%; Pred. No. 8.2e-70;  
Matches 396; Conservative 0; Mismatches 52; Indels 79; Gaps 6;

QY 1 ATCGAAGACACCGGCTTCGTCATAAGCTCCACACGAAATGCTTGATTCACCTTCGCGAAG 60  
Db 1 ATCGAAGATCCGGCTTCCTCATAGCTCCACACGAAATGCTTGATTCACCTTCGCTTAG-- 58  
QY 61 GCGATTGGGTTTACACCGAGAGTAAGATTGGGTCTGTAGCTCAGTTGGTTAGAGCGCA 120  
Db 59 -----ACGATTGGGTCTGTAGCTCAGTTGGTTAGAGCGCA 93  
QY 121 CCCTGTATAAGGTGAGGTGCGGAGTTCGAATCTGCCACACCAATCG----- 172  
Db 94 CCCTGTATAAGGTGAGGTGCGGAGTTCGAATCTGCCACACCAATCG----- 172  
QY 173 -----AAGGGCCATAGCTCAGCTGGGAGAGCGCTGCTTCGACGCGAGGA 218  
Db 154 CTGGGTGATCCGATACGGGCGCATAGCTCAGCTGGGAGAGCGCTGCTTCGACGCGAGGA 213  
QY 219 GGTGAGGTTTCGATCCGCTTGGCTCCACCAATTAATCTAGTCGCGGAAAGCTCAGAAA 278  
Db 214 GGTGAGGTTTCGATCCGCTTGGCTCCACCAATTAATCTAGTCGCGGAAAGCTCAGAAA 273  
QY 279 TGAGTGTTCACAGGATGAGGTTCGATTCGCTGGGTGGAACATGATTTCTGGACTTTGCG 338  
Db 274 TGAATGTT-----CGTGGATGAACATGATTTCTGGTCTTTGCA 312  
QY 339 CCAGAACTGTTCTTAAAAATTTGGGTATGTGATAGAGT--AGACCGATGTTGCTTTC 397  
Db 313 CCAGAACTGTTCTTAAAAATTTGGGTATGTGATAGAGTAAAGACTGAATGATCTCTTTC 372  
QY 398 ACTGGCAGCATGTCGCTCAAGGTAAATTTGCGTGTCTCTATGCAAAATTTTCGGCGAA 457  
Db 373 ACTGGTATCATTCAGTCAAGGTAAATTTGCGAGTTC--AAGCGCGAATTTTCGGCGAA 431  
QY 458 TGTCGCTTCACGTTATAGACAGTAACCAATTCGTTGGGGTTATAT 504  
Db 432 TGTCGCTTCACAGTA-----TAACCAAGATTGCTTGGGGTTATAT 471

Query Match 44.8%; Score 225.8; DB 4; Length 471;  
Best Local Similarity 75.1%; Pred. No. 8.2e-70;  
Matches 396; Conservative 0; Mismatches 52; Indels 79; Gaps 6;

QY 1 ATCGAAGACACCGGCTTCGTCATAAGCTCCACACGAAATGCTTGATTCACCTTCGCGAAG 60  
Db 1 ATCGAAGATCCGGCTTCCTCATAGCTCCACACGAAATGCTTGATTCACCTTCGCTTAG-- 58  
QY 61 GCGATTGGGTTTACACCGAGAGTAAGATTGGGTCTGTAGCTCAGTTGGTTAGAGCGCA 120  
Db 59 -----ACGATTGGGTCTGTAGCTCAGTTGGTTAGAGCGCA 93  
QY 121 CCCTGTATAAGGTGAGGTGCGGAGTTCGAATCTGCCACACCAATCG----- 172  
Db 94 CCCTGTATAAGGTGAGGTGCGGAGTTCGAATCTGCCACACCAATCG----- 172  
QY 173 -----AAGGGCCATAGCTCAGCTGGGAGAGCGCTGCTTCGACGCGAGGA 218  
Db 154 CTGGGTGATCCGATACGGGCGCATAGCTCAGCTGGGAGAGCGCTGCTTCGACGCGAGGA 213  
QY 219 GGTGAGGTTTCGATCCGCTTGGCTCCACCAATTAATCTAGTCGCGGAAAGCTCAGAAA 278  
Db 214 GGTGAGGTTTCGATCCGCTTGGCTCCACCAATTAATCTAGTCGCGGAAAGCTCAGAAA 273  
QY 279 TGAGTGTTCACAGGATGAGGTTCGATTCGCTGGGTGGAACATGATTTCTGGACTTTGCG 338  
Db 274 TGAATGTT-----CGTGGATGAACATGATTTCTGGTCTTTGCA 312  
QY 339 CCAGAACTGTTCTTAAAAATTTGGGTATGTGATAGAGT--AGACCGATGTTGCTTTC 397  
Db 313 CCAGAACTGTTCTTAAAAATTTGGGTATGTGATAGAGTAAAGACTGAATGATCTCTTTC 372  
QY 398 ACTGGCAGCATGTCGCTCAAGGTAAATTTGCGTGTCTCTATGCAAAATTTTCGGCGAA 457  
Db 373 ACTGGTATCATTCAGTCAAGGTAAATTTGCGAGTTC--AAGCGCGAATTTTCGGCGAA 431  
QY 458 TGTCGCTTCACGTTATAGACAGTAACCAATTCGTTGGGGTTATAT 504  
Db 432 TGTCGCTTCACAGTA-----TAACCAAGATTGCTTGGGGTTATAT 471

RESULT 9  
US-09-448-894-111  
; Sequence 111, Application US/09448894  
; Patent No. 6312903  
; GENERAL INFORMATION:  
; APPLICANT: JANNES, GEERT  
; ROSSAU, RUDI  
; VAN HEUVERSWYN, HUGO  
; TITLE OF INVENTION: SIMULTANEOUS DETECTION, IDENTIFICATION  
; AND DIFFERENTIATION OF BACTERIAL TAXA USING A  
; HYBRIDIZATION ASSAY  
; NUMBER OF SEQUENCES: 216  
; CORRESPONDENCE ADDRESS:  
; ADDRESS: NIXON & VANDERHIE P.C.  
; STREET: 1100 NORTH GLEBE ROAD, 8TH FLOOR  
; CITY: WASHINGTON  
; STATE: D.C.  
; COUNTRY: USA  
; ZIP: 22201  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/448,894  
; FILING DATE: 29-No. 6312903-1999  
; CLASSIFICATION: <Unknown>  
; 07-APR-1995  
; 24-JUN-1994  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/765,332



;; TITLE OF INVENTION: SIMULTANEOUS DETECTION, IDENTIFICATION  
;; TITLE OF INVENTION: AND DIFFERENTIATION OF EUBACTERIAL TAXA USING A  
;; TITLE OF INVENTION: HYBRIDIZATION ASSAY  
;; NUMBER OF SEQUENCES: 216  
;; CORRESPONDENCE ADDRESS:  
;; ADDRESSEE: NIXON & VANDERHYE P.C.  
;; CITY: WASHINGTON  
;; STATE: D.C.  
;; COUNTRY: USA  
;; ZIP: 22201  
;; COMPUTER READABLE FORM:  
;; MEDIUM TYPE: Floppy disk  
;; COMPUTER: IBM PC compatible  
;; OPERATING SYSTEM: PC-DOS/MS-DOS  
;; SOFTWARE: PatentIn Release #1.0, Version #1.30  
;; CURRENT APPLICATION DATA:  
;; APPLICATION NUMBER: US/08/765,332  
;; FILING DATE: 23-DEC-1996  
;; CLASSIFICATION: 435  
;; PRIOR APPLICATION DATA:  
;; APPLICATION NUMBER: WO PCT/EP95/02452  
;; FILING DATE: 23-JUN-1995  
;; PRIOR APPLICATION DATA:  
;; APPLICATION NUMBER: EP 95870032.0  
;; FILING DATE: 07-APR-1995  
;; PRIOR APPLICATION DATA:  
;; APPLICATION NUMBER: EP 94870106.5  
;; FILING DATE: 24-JUN-1994  
;; ATTORNEY/AGENT INFORMATION:  
;; NAME: SADOFF, B.J.  
;; REGISTRATION NUMBER: 36,663  
;; REFERENCE/DOCKET NUMBER: 1487-14  
;; TELECOMMUNICATION INFORMATION:  
;; TELEPHONE: 703-816-4091  
;; TELEFAX: 703-816-4100  
;; INFORMATION FOR SEQ ID NO: 115:  
;; SEQUENCE CHARACTERISTICS:  
;; LENGTH: 468 base pairs  
;; TYPE: nucleic acid  
;; STRANDEDNESS: single  
;; TOPOLOGY: linear  
;; MOLECULE TYPE: cDNA  
;; HYPOTHEICAL: NO  
;; ANTI-SENSE: NO  
US-08-765-332-115

Query Match 40.7%; Score 205.2; DB 3; Length 468;  
Best Local Similarity 74.7%; Pred. No. 1.5e-62;  
Matches 378; Conservative 0; Mismatches 88; Indels 40; Gaps 8;

Qy 1 ATCGAAGACACCGGCTTCGTCATAGCTCCACACGAAATGCTTGATTCACCTTCGCGAAG 60  
Db 1 ATCGACGACATCAGCTGTCTCATAGCTCCACACGAAATGCTTGATTCATCA-TTGAAGAAG 59

Qy 61 GCGATTGGTTAGACCGGAGTAAGATGGGTCTGTAGCTCAGTTGTTAGAGGCCA 120  
Db 60 ACGATTAGTTAGCAACCTT-----CGATTGGGTCTGTAGCTCAGTTGTTAGAGGCCA 113

Qy 121 CCCCTGATAAGGGTGAAGTCCGCGAGTTGCAATCTGCCAGACCCACCA-TCGAAGGGGC 179  
Db 114 CCCCTGATAAGGGTGAAGTCCGCGAGTTGCAATCTGCCAGACCCACCAATTTGCTGGGC 173

Qy 180 CATAGCTCAGTGGGAGAGCCCTGCTTTCACCCAGGAGTACCGGTCGATCCCGCT 239  
Db 174 CATAGCTCAGTGGGAGAGCCCTGCTTTCACCCAGGAGTACCGGTCGATCCCGCT 233

Qy 240 TGGCTCCACCATTAACCTAGTTCGCGGAAAGCTCAGAAATCAGTGTTCACGAGGATGAGG 299  
Db 234 TGGCTCCACCATTAACCTAGTTCGCGGAAAGCTCAGAAATCAGTGTTCACGAGGATGAGG 274

Qy 300 TTGATTGCTGGTTGAACATTTGATTTCTGGACTTTGCGCAGAACTGTTCTTTAAAAAT 359  
Db 300 TTGATTGCTGGTTGAACATTTGATTTCTGGACTTTGCGCAGAACTGTTCTTTAAAAAT 359

Db 275 ATGAATATCCGTCGCAATATTGATTCTGAACATTT--ATCAGAATCGTTCTTTAAAAAT 332  
Qy 360 TTGGGTATGTATGAGAGTAGA-CGATGTGTTCTTTCTACTGCGACAGATGTCGCGTCAA 418  
Db 333 TTGGGTATGTATGAGAGTAGAGACTGGACAGACACTTCTCACTGTGTGTTCAGGCTAA 392  
Qy 419 GGTAAATTTGCGTGTCTCTATGCAAAATTTTCGCGCAATGTCGTCTTCAGGTTATAGAC 478  
Db 393 GGTAAATTTGAGTAAT---TACAAGTTTTCGCGCAATGTTCTCTTCACAGTA----- 444  
Qy 479 AGTAACCAAGATTGCTTGGGTTATAT 504  
Db 445 --TAACCAAGATTGCTTGGGTTATAT 468

RESULT 10  
US-09-448-894-115  
; Sequence 115, Application US/09448894  
; Patent No. 6312903  
; GENERAL INFORMATION:  
; APPLICANT: JANNES, GEERT  
; VAN HEUVERSWYN, HUGO  
; ROSSAU, RUDI  
; TITLE OF INVENTION: SIMULTANEOUS DETECTION, IDENTIFICATION  
; AND DIFFERENTIATION OF EUBACTERIAL TAXA USING A  
; HYBRIDIZATION ASSAY  
; NUMBER OF SEQUENCES: 216  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: NIXON & VANDERHYE P.C.  
; STREET: 1100 NORTH GLEBE ROAD, 8TH FLOOR  
; CITY: WASHINGTON  
; STATE: D.C.  
; COUNTRY: USA  
; ZIP: 22201  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/448,894  
; FILING DATE: 29-NOV-6312903-1999  
; CLASSIFICATION: <Unknown>  
; 07-APR-1995  
; 24-JUN-1994  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/765,332  
; FILING DATE: <Unknown>  
; APPLICATION NUMBER: EP 95870032.0  
; FILING DATE: 07-APR-1995  
; APPLICATION NUMBER: EP 94870106.5  
; FILING DATE: 24-JUN-1994  
; ATTORNEY/AGENT INFORMATION:  
; NAME: SADOFF, B.J.  
; REGISTRATION NUMBER: 36,663  
; REFERENCE/DOCKET NUMBER: 1487-14  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 703-816-4091  
; TELEFAX: 703-816-4100  
; INFORMATION FOR SEQ ID NO: 115:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 468 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: cDNA  
; HYPOTHEICAL: NO  
; ANTI-SENSE: NO  
; SEQUENCE DESCRIPTION: SEQ ID NO: 115:  
US-09-448-894-115

Query Match 40.7%; Score 205.2; DB 4; Length 468;  
Best Local Similarity 74.7%; Pred. No. 1.5e-62;

Matches 378; Conservative 0; Mismatches 88; Indels 40; Gaps 8;

QY 1 ATCGAAGACACGGGCTTCCTATAGCTCCACACAGTTCCTGATTACCTTCGGAAG 60  
Db 1 ATCGAAGACACGGGCTTCCTATAGCTCCACACAGTTCCTGATTCA-TTGAAGAG 59

QY 61 GCGATTGGTTTAGACCGGAGAGTAACAGTGGGTCTAGCTAGTTGGTTAGACGCA 120  
Db 60 AGGATTAGTTAGCAACCTT-----CGATTGGGTCTAGCTAGTTGGTTAGACGCA 113

QY 121 CCCCTGATAAGGGTGGAGTTCGAGTTCGAATCTGCCAGACCCACCAA-TCGAAGGGC 179  
Db 114 CCCCTGATAAGGGTGGAGTTCGAGTTCGAATCTGCCAGACCCACCAA-TTGGGGC 173

QY 180 CATAGCTCAGCTGGAGAGCCCTGCTTTGACGAGGAGTTCAGCGTTCGATCCCGCT 239  
Db 174 CATAGCTCAGCTGGAGAGCCCTGCTTTGACGAGGAGTTCAGCGTTCGATCCCGCT 233

QY 240 TGGCTCCACCAATTAACCTAGTCCGCGAAGCTCAGAAATGAGTGTTCACAGGATGAGG 299  
Db 234 TGGCTCCAC-----ACCCGCTTGGCAGTTTGTCAAGGCTTAGAA 274

QY 300 TTGATGCTGGTGGTGAACATGATTTCTGGACTTTGGCCGAGAACTGTTCTTTAAAT 359  
Db 275 ATGAATATTCGCTCGAATATGATTTCTGAACCTT--ATCAGATCGTCTTTAAAT 332

QY 360 TTGGTATGATAGAGAGTAGA-CCGATGTTGCTTTCACTGGCAGAGTTCGCGTAA 418  
Db 333 TTGGTATGATAGAGAGTAGACTGGACAGCACTTTCACTGGTGTGTTCAGGCTAA 392

QY 419 GGTAAATTTGCGTGTCTCTATCAAAATTTTCGCGAATGCTGCTCTCAGTTATAGAC 478  
Db 393 GGTAAATTTGCGTGTCTCTATCAAAATTTTCGCGAATGCTGCTCTCAGTTATAGAC 478

QY 479 AGTAACAGATGCTTGGGGTTATAT 504  
Db 445 --TAACAGATGCTTGGGGTTATAT 468

RESULT 11  
US-08-412-614-89  
; Sequence 89, Application US/08412614  
; Patent No. 5536638  
; GENERAL INFORMATION:  
; APPLICANT: Rossau, Rudi  
; TITLE OF INVENTION: Hybridization Probes Derived from the  
; TITLE OF INVENTION: Spacer Region Between the 16S and 23S rRNA Genes for the  
; TITLE OF INVENTION: Detection of No. 5536638-Viral Microorganisms  
; NUMBER OF SEQUENCES: 104  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Merchant & Gould  
; STREET: 3100 No. 5536638west Center  
; CITY: Minneapolis  
; STATE: MN  
; COUNTRY: USA  
; ZIP: 55402-4131  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette 3.5 inch, 1.44 mb capacity  
; COMPUTER: IBM PC compatible (Compaq Deskpro 286e)  
; OPERATING SYSTEM: MS-DOS  
; SOFTWARE: Wordperfect Version #5.1  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/412,614  
; FILING DATE:  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 07/965,394  
; FILING DATE: 17-DEC-1992  
; APPLICATION NUMBER: PCT/EP91/00743  
; FILING DATE: 18-APR-1991  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: GB/90901054.3

FILING DATE: 18-APR-1990  
ATTORNEY/AGENT INFORMATION:  
NAME: Hillson, Randall A.  
REGISTRATION NUMBER: 31,838  
REFERENCE/DOCKET NUMBER: 8076.75-USWO  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 612-332-5300  
TELEFAX: 612-332-9081  
INFORMATION FOR SEQ ID NO: 89:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 664 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
ORIGINAL SOURCE:  
ORGANISM: Neisseria meningitidis  
STRAIN: NCTC 10025  
US-08-412-614-89

Query Match 23.3%; Score 117.2; DB 1; Length 664;  
Best Local Similarity 82.7%; Pred. No. 1.9e-31;  
Matches 134; Conservative 0; Mismatches 28; Indels 0; Gaps 0;

QY 92 GGGTCTGTAGCTCAGTTGGTTAGAGCGCACCCCTGATAGGTTGAGGTCGGCAGTTCCGA 151  
Db 100 GGGTCTGTAGCTCAGTTGGTTAGAGCGCACCCCTGATAGGTTGAGGTCGGCAGTTCAAG 159

QY 152 TCTGCCAGACCCACCAATCGAAGGGGCCATAGCTAGCTGGGAGAGCGCTGCTTTGCA 211  
Db 160 TCTGCCAGACCCACCAATCGAAGGGGCCATAGCTAGCTGGGAGAGCGCTGCTTTGCA 219

QY 212 CGCAGAGAGTTCAGCGTTCGATCCCGCTTGGCTCCACCAATA 253  
Db 220 AGCAGGGGTCATCGGTTCCGATCCCGCTTGGCTCCACCAATA 261

RESULT 12  
US-08-412-614-85  
; Sequence 85, Application US/08412614  
; Patent No. 5536638  
; GENERAL INFORMATION:  
; APPLICANT: Rossau, Rudi  
; TITLE OF INVENTION: Hybridization Probes Derived from the  
; TITLE OF INVENTION: Spacer Region Between the 16S and 23S rRNA Genes for the  
; TITLE OF INVENTION: Detection of No. 5536638-Viral Microorganisms  
; NUMBER OF SEQUENCES: 104  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Merchant & Gould  
; STREET: 3100 No. 5536638west Center  
; CITY: Minneapolis  
; STATE: MN  
; COUNTRY: USA  
; ZIP: 55402-4131  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette 3.5 inch, 1.44 mb capacity  
; COMPUTER: IBM PC compatible (Compaq Deskpro 286e)  
; OPERATING SYSTEM: MS-DOS  
; SOFTWARE: Wordperfect Version #5.1  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/412,614  
; FILING DATE:  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 07/965,394  
; FILING DATE: 17-DEC-1992  
; APPLICATION NUMBER: PCT/EP91/00743  
; FILING DATE: 18-APR-1991  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: GB/90901054.3

FILING DATE: 18-APR-1990  
ATTORNEY/AGENT INFORMATION:  
NAME: Hillson, Randall A.  
REGISTRATION NUMBER: 31,838  
REFERENCE/DOCKET NUMBER: 8076.75-USWO  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 612-332-5300  
TELEFAX: 612-332-9081  
INFORMATION FOR SEQ ID NO: 85:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 603 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
ORGANISM: Neisseria gonorrhoeae  
STRAIN: NCTC 8375  
US-08-412-614-85

Query Match 21.5%; Score 108.6; DB 1; Length 603;  
Best Local Similarity 84.3%; Pred. No. 2e-28;  
Matches 134; Conservative 0; Mismatches 24; Indels 1; Gaps 1;  
QY 92 GGGTCTGTAGCTCAGTTGGTTAGAGGGCCACCCCTGATAGGGTGGAGGTGGCGCAGTTTCGAA 151  
DB 99 GGGTTTGTAGCTCAGCTGGTTAGAGCACACCGCTTGATAGCGTGGAGTGGGAGGTTCAAG 158  
QY 152 TCTGCCACAGACACCAATCAAGGGCCATAGCTCAGCTGGAGAGCGCCTCTTTCGA 211  
DB 159 TCTCCACAGCCACCAAA-GAAGCGGGGCGATAGCTCAGTTGGTAGACACCTCTTTCGA 217  
QY 212 CGCAGGAGGTGAGGTTTCGATCCCGCTTGGCTCCACCA 250  
DB 218 AGCAGGGGTCATCGGTTTCGATCCCGCTTGGCTCCACCA 256

RESULT 13  
US-08-412-614-86  
Sequence 86, Application US/08412614  
Patent No. 5536638  
GENERAL INFORMATION:  
APPLICANT: Rossau, Rudi  
APPLICANT: Van Heuverswyn, Hugo  
TITLE OF INVENTION: Hybridization Probes Derived from the  
TITLE OF INVENTION: Spacer Region Between the 16S and 23S rRNA Genes for the  
TITLE OF INVENTION: Detection of No. 5536638-Viral Microorganisms  
NUMBER OF SEQUENCES: 104  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Merchant & Gould  
STREET: 3100 No. 5536638west Center  
CITY: Minneapolis  
STATE: MN  
COUNTRY: USA  
ZIP: 55402-4131  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette 3.5 inch, 1.44 mb capacity  
COMPUTER: IBM PC compatible (Compaq Deskpro 286e)  
OPERATING SYSTEM: MS-DOS  
SOFTWARE: Wordperfect Version 5.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/412,614  
FILING DATE:  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/965,394  
FILING DATE: 17-DEC-1992  
APPLICATION NUMBER: PCT/EP91/00743  
FILING DATE: 18-APR-1991  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: GB/90901054.3

FILING DATE: 18-APR-1990  
ATTORNEY/AGENT INFORMATION:  
NAME: Hillson, Randall A.  
REGISTRATION NUMBER: 31,838  
REFERENCE/DOCKET NUMBER: 8076.75-USWO  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 612-332-5300  
TELEFAX: 612-332-9081  
INFORMATION FOR SEQ ID NO: 86:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 603 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
ORGANISM: Neisseria gonorrhoeae  
STRAIN: ITM 4367  
US-08-412-614-86

Query Match 21.5%; Score 108.6; DB 1; Length 603;  
Best Local Similarity 84.3%; Pred. No. 2e-28;  
Matches 134; Conservative 0; Mismatches 24; Indels 1; Gaps 1;  
QY 92 GGGTCTGTAGCTCAGTTGGTTAGAGGGCCACCCCTGATAGGGTGGAGGTGGCGCAGTTTCGAA 151  
DB 99 GGGTTTGTAGCTCAGCTGGTTAGAGCACACCGCTTGATAGCGTGGAGTGGGAGGTTCAAG 158  
QY 152 TCTGCCACAGACACCAATCAAGGGCCATAGCTCAGCTGGAGAGCGCCTCTTTCGA 211  
DB 159 TCTCCACAGCCACCAAA-GAAGCGGGGCGATAGCTCAGTTGGTAGACACCTCTTTCGA 217  
QY 212 CGCAGGAGGTGAGGTTTCGATCCCGCTTGGCTCCACCA 250  
DB 218 AGCAGGGGTCATCGGTTTCGATCCCGCTTGGCTCCACCA 256

RESULT 14  
US-08-635-761-85  
Sequence 85, Application US/08635761  
Patent No. 5945282  
GENERAL INFORMATION:  
APPLICANT: Rossau, Rudi  
TITLE OF INVENTION: HYBRIDIZATION PROBES DERIVED FROM THE SPACER REGION BE  
NUMBER OF SEQUENCES: 104  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Merchant, Gould, Smith, Edell, Welter & Schmidt  
STREET: 3100 No. 5945282west Center, 90 S. 7th Street  
CITY: Minneapolis  
STATE: MN  
COUNTRY: U.S.A.  
ZIP: 55402  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: DOS  
SOFTWARE: PastSeq Version 1.5  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/635,761  
FILING DATE: 19-APR-1996  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/965,394  
FILING DATE: 17-DEC-1992  
APPLICATION NUMBER: 08/412,614  
FILING DATE: 29-MAR-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: Hillson, Randall A.  
REGISTRATION NUMBER: 31,838  
REFERENCE/DOCKET NUMBER: 8076.75USC1  
TELECOMMUNICATION INFORMATION:

TELEPHONE: 612/332-5300  
TELEFAX: 612/332/9081  
TELEX:  
INFORMATION FOR SEQ ID NO: 85:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 603 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: Genomic DNA  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
FRAGMENT TYPE:  
ORIGINAL SOURCE:  
US-08-635-761-85

Query Match 21.5%; Score 108.6; DB 2; Length 603;  
Best Local Similarity 84.3%; Pred. No. 2e-28;  
Matches 134; Conservative 0; Mismatches 24; Indels 1; Gaps 1;  
QY 92 GGGTCTGTAGCTCAGTGGTTAGAGCGCACCCCTGATAAGGTTGAGGTCGGCAGTTTCGAA 151  
|||||  
Db 99 GGGTTGTAGCTCAGCTGGTTAGAGCACACGCTTGATAAGCGTGAAGTTCGGAGGTTCAAG 158  
||  
QY 152 TCTGCCAGAGCCACCAATCGAAGGGGCCATAGCTCAGCTGGGAGAGGCGCTGCTTTGCA 211  
|||||  
Db 159 TCCTCCAGAGCCACCAAA-GAACGGGGGCATAGCTCAGTTGGTAGAGCACCTGCTTTGCA 217  
||  
QY 212 CGCAGGAGGTGAGGTTGATCCCGTTGGCTCCACCA 250  
|||||  
Db 218 AGCAGGGGTCATCGGTTTCGATCCCGTTGCTCCACCA 256

## RESULT 15

US-08-635-761-86  
Sequence 86, Application US/08635761  
Patent No. 5945282  
GENERAL INFORMATION:  
APPLICANT: Rossau, Rudi  
TITLE OF INVENTION: HYBRIDIZATION PROBES DERIVED FROM THE SPACER REGION BE  
NUMBER OF SEQUENCES: 104  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Merchant, Gould, Smith, Edell, Welter & Schmidt  
STREET: 3100 No. 5945282west Center, 90 S. 7th Street  
CITY: Minneapolis  
STATE: MN  
COUNTRY: U.S.A.  
ZIP: 55402  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: DOS  
SOFTWARE: FastSeq Version 1.5  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/635,761  
FILING DATE: 19-APR-1996  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/965,394  
FILING DATE: 17-DEC-1992  
APPLICATION NUMBER: 08/412,614  
FILING DATE: 29-MAR-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: Hillson, Randall A  
REGISTRATION NUMBER: 31,838  
REFERENCE/DOCKET NUMBER: 8076.75USC1  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 612/332-5300  
TELEFAX: 612/332/9081  
TELEX:  
INFORMATION FOR SEQ ID NO: 86:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 603 base pairs

TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: Genomic DNA  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
FRAGMENT TYPE:  
ORIGINAL SOURCE:  
US-08-635-761-86

Query Match 21.5%; Score 108.6; DB 2; Length 603;  
Best Local Similarity 84.3%; Pred. No. 2e-28;  
Matches 134; Conservative 0; Mismatches 24; Indels 1; Gaps 1;  
QY 92 GGGTCTGTAGCTCAGTGGTTAGAGCGCACCCCTGATAAGGTTGAGGTCGGCAGTTTCGAA 151  
|||||  
Db 99 GGGTTGTAGCTCAGCTGGTTAGAGCACACGCTTGATAAGCGTGAAGTTCGGAGGTTCAAG 158  
||  
QY 152 TCTGCCAGAGCCACCAATCGAAGGGGCCATAGCTCAGCTGGGAGAGGCGCTGCTTTGCA 211  
|||||  
Db 159 TCCTCCAGAGCCACCAAA-GAACGGGGGCATAGCTCAGTTGGTAGAGCACCTGCTTTGCA 217  
||  
QY 212 CGCAGGAGGTGAGGTTGATCCCGTTGGCTCCACCA 250  
|||||  
Db 218 AGCAGGGGTCATCGGTTTCGATCCCGTTGCTCCACCA 256

Search completed: February 1, 2003, 04:24:16  
Job time : 28.2031 secs

GenCore version 5.1.3  
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OM nucleic - nucleic search, using sw model

Run on: February 1, 2003, 03:05:22 ; Search time 28.0455 Seconds  
(without alignments)  
8073.649 Million cell updates/sec

Title: US-09-931-486-113

Perfect score: 504

Sequence: 1 ATCGAAGACACCGCTTCGT.....CAGATGCTGGGGTTATAT 504

Scoring table: IDENTITY\_NUC

Gapop 10.0 , Gapext 1.0

Searched: 396772 seqs, 224632407 residues

Total number of hits satisfying chosen parameters: 793544

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications\_NA:\*

- 1: /cgn2\_6/ptodata/1/pubpna/US07\_PUBCOMB.seq:\*
- 2: /cgn2\_6/ptodata/1/pubpna/PCT\_NEW\_PUB.seq:\*
- 3: /cgn2\_6/ptodata/1/pubpna/US06\_NEW\_PUB.seq:\*
- 4: /cgn2\_6/ptodata/1/pubpna/US06\_PUBCOMB.seq:\*
- 5: /cgn2\_6/ptodata/1/pubpna/US07\_NEW\_PUB.seq:\*
- 6: /cgn2\_6/ptodata/1/pubpna/PCTUS\_PUBCOMB.seq:\*
- 7: /cgn2\_6/ptodata/1/pubpna/US08\_NEW\_PUB.seq:\*
- 8: /cgn2\_6/ptodata/1/pubpna/US08\_PUBCOMB.seq:\*
- 9: /cgn2\_6/ptodata/1/pubpna/US09\_NEW\_PUB.seq:\*
- 10: /cgn2\_6/ptodata/1/pubpna/US09\_PUBCOMB.seq:\*
- 11: /cgn2\_6/ptodata/1/pubpna/US10\_NEW\_PUB.seq:\*
- 12: /cgn2\_6/ptodata/1/pubpna/US10\_PUBCOMB.seq:\*
- 13: /cgn2\_6/ptodata/1/pubpna/US60\_NEW\_PUB.seq:\*
- 14: /cgn2\_6/ptodata/1/pubpna/US60\_PUBCOMB.seq:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	108.6	21.5	603	10	US-09-863-086-85
2	108.6	21.5	603	10	US-09-863-086-86
3	108.6	21.5	640681	10	US-09-790-988-1
4	99.4	19.7	654	10	US-09-863-086-89
5	97.8	19.4	549	10	US-09-863-086-92
6	97.8	19.2	498	10	US-09-863-086-90
7	95	18.8	3309400	9	US-09-738-626-1
8	91.8	18.2	243	10	US-09-815-242-1358
9	91.2	18.1	255	10	US-09-815-242-1377
10	91.2	18.1	255	10	US-09-815-242-1402
11	91.2	18.1	255	10	US-09-815-242-1415
12	91.2	18.1	255	10	US-09-815-242-1423
13	91.2	18.1	255	10	US-09-815-242-1431
14	91.2	18.1	255	10	US-09-815-242-1434
15	91.2	18.1	255	10	US-09-815-242-1459
16	91.2	18.1	255	10	US-09-815-242-1473
17	91.2	18.1	255	10	US-09-815-242-1475
18	91.2	18.1	255	10	US-09-815-242-1544
19	91.2	18.1	255	10	US-09-815-242-1638

Sequence 87, Appl  
Sequence 88, Appl  
Sequence 550, Appl  
Sequence 4692, Ap  
Sequence 2687, Ap  
Sequence 4361, Ap  
Sequence 4403, Ap  
Sequence 4409, Ap  
Sequence 4418, Ap  
Sequence 8396, Ap  
Sequence 8438, Ap  
Sequence 8444, Ap  
Sequence 8453, Ap  
Sequence 869, App  
Sequence 4363, Ap  
Sequence 8398, Ap  
Sequence 95, Appl  
Sequence 96, Appl  
Sequence 102, Appl  
Sequence 5, Appl  
Sequence 1, Appl  
Sequence 2, Appl  
Sequence 3, Appl  
Sequence 4, Appl

Sequence 87, Appl  
Sequence 88, Appl  
Sequence 550, Appl  
Sequence 4692, Ap  
Sequence 2687, Ap  
Sequence 4361, Ap  
Sequence 4403, Ap  
Sequence 4409, Ap  
Sequence 4418, Ap  
Sequence 8396, Ap  
Sequence 8438, Ap  
Sequence 8444, Ap  
Sequence 8453, Ap  
Sequence 869, App  
Sequence 4363, Ap  
Sequence 8398, Ap  
Sequence 95, Appl  
Sequence 96, Appl  
Sequence 102, Appl  
Sequence 5, Appl  
Sequence 1, Appl  
Sequence 2, Appl  
Sequence 3, Appl  
Sequence 4, Appl

#### ALIGNMENTS

#### RESULT 1

US-09-863-086-85

; Sequence 85, Application US/09863086

; Patent No. US20020048762A1

; GENERAL INFORMATION:

; APPLICANT: Rossau, Rudi

; TITLE OF INVENTION: HYBRIDIZATION PROBES DERIVED FROM THE SPACER

; REGION BETWEEN THE 16S A

; NUMBER OF SEQUENCES: 104

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Merchant, Gould, Smith, Edell, Weiler & Schmidt

; STREET: 3100 No. US20020048762A1West Center, 90 S. 7th Street

; CITY: Minneapolis

; STATE: MN

; COUNTRY: U.S.A.

; ZIP: 55402

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Diskette

; COMPUTER: IBM Compatible

; OPERATING SYSTEM: DOS

; SOFTWARE: FastSeq Version 1.5

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/863,086

; FILING DATE: 22-May-2001

; CLASSIFICATION: <Unknown>

; PRIORITY INFORMATION:

; APPLICATION NUMBER: 09/312,520

; FILING DATE: <Unknown>

; APPLICATION NUMBER: 08/412,614

; FILING DATE: 29-MAR-1995

; ATTORNEY/AGENT INFORMATION:

; NAME: Hillson, Randall A

; REGISTRATION NUMBER: 31,838

; REFERENCE/DOCKET NUMBER: 8076.75USC1

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 612/332-5300

; TELEFAX: 612/332/9081

; TELEX: <Unknown>

; INFORMATION FOR SEQ ID NO: 85:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 603 base pairs

; TYPE: nucleic acid



;; TITLE OF INVENTION: HYBRIDIZATION PROBES DERIVED FROM THE SPACER  
;; REGION BETWEEN THE 16S A

;; NUMBER OF SEQUENCES: 104

;; CORRESPONDENCE ADDRESS:

;; ADDRESSEE: Merchant, Gould, Smith, Edell, Welter & Schmidt  
;; STREET: 3100 No. US20020048762Alwest Center, 90 S. 7th Street

;; CITY: Minneapolis

;; STATE: MN

;; COUNTRY: U.S.A.

;; ZIP: 55402

;; COMPUTER READABLE FORM:

;; MEDIUM TYPE: Diskette

;; COMPUTER: IBM Compatible

;; OPERATING SYSTEM: DOS

;; SOFTWARE: FastSeq Version 1.5

;; CURRENT APPLICATION DATA:

;; APPLICATION NUMBER: US/09/863,086

;; FILING DATE: 22-May-2001

;; CLASSIFICATION: <Unknown>

;; PRIOR APPLICATION DATA:

;; APPLICATION NUMBER: 09/312,520

;; FILING DATE: <Unknown>

;; APPLICATION NUMBER: 08/412,614

;; FILING DATE: 29-MAR-1995

;; ATTORNEY/AGENT INFORMATION:

;; NAME: Hillson, Randall A

;; REGISTRATION NUMBER: 31,838

;; REFERENCE/DOCKET NUMBER: 8076.75USC1

;; TELECOMMUNICATION INFORMATION:

;; TELEPHONE: 612/332-5300

;; TELEFAX: 612/332/9081

;; TELEX: <Unknown>

;; INFORMATION FOR SEQ ID NO: 89:

;; SEQUENCE CHARACTERISTICS:

;; LENGTH: 654 base pairs

;; TYPE: nucleic acid

;; STRANDEDNESS: single

;; TOPOLOGY: linear

;; MOLECULE TYPE: Genomic DNA

;; HYPOTHETICAL: NO

;; ANTI-SENSE: NO

;; FRAGMENT TYPE: <Unknown>

;; ORIGINAL SOURCE:

;; SEQUENCE DESCRIPTION: SEQ ID NO: 89:

US-09-863-086-89

Query Match 19.7%; Score 99.4; DB 10; Length 654;

Best Local Similarity 81.6%; Pred. No. 1.8e-23;

Matches 115; Conservative 0; Mismatches 26; Indels 0; Gaps 0;

Qy 113 AGACGGCACCCTGATAAGGCTGAGGTGCGGAGTTCGAATCTGCCAGACCCACCAATCG 172

||||| ||| ||||||| ||| ||||||| ||| ||| ||||||| |||||||

Db 111 AGACGACACGCTTGATAAGGCTGAGGTGCGGAGTTCGAATCTGCCAGACCCACCAAGAA 170

||||| ||| ||||||| ||| ||||||| ||| ||| ||||||| |||||||

Qy 173 AAGGGGCATAGCTACGCTGGGAGCGCTGCTTTTCACGAGGAGGTGAGCGGTTCGA 232

||||| ||| ||||||| ||| ||||||| ||| ||| ||||||| |||||||

Db 171 CGGGGGCATAGCTACGCTGGGAGGTGAGGACCTGCTTTGCAAGCAGGGGTCATCGGTTCGA 230

||||| ||| ||||||| ||| ||||||| ||| ||| ||||||| |||||||

Qy 233 TCCCGCTTGGCTCCACCATTA 253

||||| ||| ||||||| ||| ||||||| ||| ||| ||||||| |||||||

Db 231 TCCCGTTTGCCTCCACCAATA 251

RESULT 5

US-09-863-086-92

;; Sequence 92, Application US/09863086

;; Patent No. US20020048762A1

;; GENERAL INFORMATION:

;; APPLICANT: Rossau, Rudi

;; TITLE OF INVENTION: HYBRIDIZATION PROBES DERIVED FROM THE SPACER

;; REGION BETWEEN THE 16S A

;; NUMBER OF SEQUENCES: 104

;; CORRESPONDENCE ADDRESS:

;; ADDRESSEE: Merchant, Gould, Smith, Edell, Welter & Schmidt  
;; STREET: 3100 No. US20020048762Alwest Center, 90 S. 7th Street

;; CITY: Minneapolis

;; STATE: MN

;; COUNTRY: U.S.A.

;; ZIP: 55402

;; COMPUTER READABLE FORM:

;; MEDIUM TYPE: Diskette

;; COMPUTER: IBM Compatible

;; OPERATING SYSTEM: DOS

;; SOFTWARE: FastSeq Version 1.5

;; CURRENT APPLICATION DATA:

;; APPLICATION NUMBER: US/09/863,086

;; FILING DATE: 22-May-2001

;; CLASSIFICATION: <Unknown>

;; PRIOR APPLICATION DATA:

;; APPLICATION NUMBER: 09/312,520

;; FILING DATE: <Unknown>

;; APPLICATION NUMBER: 08/412,614

;; FILING DATE: 29-MAR-1995

;; ATTORNEY/AGENT INFORMATION:

;; NAME: Hillson, Randall A

;; REGISTRATION NUMBER: 31,838

;; REFERENCE/DOCKET NUMBER: 8076.75USC1

;; TELECOMMUNICATION INFORMATION:

;; TELEPHONE: 612/332-5300

;; TELEFAX: 612/332/9081

;; TELEX: <Unknown>

;; INFORMATION FOR SEQ ID NO: 92:

;; SEQUENCE CHARACTERISTICS:

;; LENGTH: 549 base pairs

;; TYPE: nucleic acid

;; STRANDEDNESS: single

;; TOPOLOGY: linear

;; MOLECULE TYPE: Genomic DNA

;; HYPOTHETICAL: NO

;; ANTI-SENSE: NO

;; FRAGMENT TYPE: <Unknown>

;; ORIGINAL SOURCE:

;; SEQUENCE DESCRIPTION: SEQ ID NO: 92:

US-09-863-086-92

Query Match

Best Local Similarity 19.4%; Score 97.8; DB 10; Length 549;

Matches 132; Conservative 0; Mismatches 37; Indels 2; Gaps 1;

Qy 89 ATTGGTCTGTAGCTAGCTGAGTGTGATAGAGCGCACCCCTGATAGAGGGTGGAGGTCGGCAGTTC 148

||||| ||| ||||||| ||| ||||||| ||| ||| ||||||| |||||||

Db 59 ATTGGTCTGTAGCTAGCTGAGTGTGATAGAGCGCACCCCTGATAGAGGGTGGAGGTCATAAGTTC 118

||||| ||| ||||||| ||| ||||||| ||| ||| ||||||| |||||||

Qy 149 GAATCTGCCAGACCCACCAATCGAAGGGCCATAGCTCAGCTGGGAGCGCCCTGCTTT 208

||||| ||| ||||||| ||| ||||||| ||| ||| ||||||| |||||||

Db 119 AAGTCTTATAGACCCACCAATT--TTGGGGTTATAGCTCAGTGTGGTAGAGCCCGCTT 176

||||| ||| ||||||| ||| ||||||| ||| ||| ||||||| |||||||

Qy 209 GCACGAGGAGGTGAGCGGTTCGATCCCTTGGTCCACCACTTAACCTTA 259

||||| ||| ||||||| ||| ||||||| ||| ||| ||||||| |||||||

Db 177 GCACGAGGAGGTGAGCGGTTCGACTCTCTTAACTCCACCACTTACAATA 227

||||| ||| ||||||| ||| ||||||| ||| ||| ||||||| |||||||

RESULT 6

US-09-863-086-90

;; Sequence 90, Application US/09863086

;; Patent No. US20020048762A1

;; GENERAL INFORMATION:

;; APPLICANT: Rossau, Rudi

;; TITLE OF INVENTION: HYBRIDIZATION PROBES DERIVED FROM THE SPACER

;; REGION BETWEEN THE 16S A

;; NUMBER OF SEQUENCES: 104

;; CORRESPONDENCE ADDRESS:

;; ADDRESSEE: Merchant, Gould, Smith, Edell, Welter & Schmidt

;; STREET: 3100 No. US20020048762Alwest Center, 90 S. 7th Street

;; CITY: Minneapolis

;; STATE: MN





RESULT# 11  
US-09-815-242-1415/c  
; Sequence 1415, Application US/09815242  
; Patent No. US20020061569A1  
; GENERAL INFORMATION:  
; APPLICANT: Haselbeck, Robert  
; APPLICANT: Ohlsen, Karl L.  
; APPLICANT: Ohlsen, Karl L.  
; APPLICANT: Zyskind, Judith W.

```
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; NUMBER OF SEQ ID NOS: 14110
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1423
; LENGTH: 255
; TYPE: DNA
; ORGANISM: Staphylococcus aureus
US-09-815-242-1423

Query Match      18.1%   Score 91.2
Best Local Similarity 78.4%   Pred. No. 0; Mismatch
Matches 127; Conservative

QY    85 AACGATTGGGTCTGTAGCTCAGTTCAGTTGGTTAGACGCG
Db    ||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY    145 GTTCGAATCTGCCACGACCACCA-----
Db    ||||| ||| ||||| ||||| ||||| ||||| ||||| |||||
QY    193 GGAGAGCCCTGCCTTGACGACGACGAGGTCAAGCG
Db    42 GGAGAGCCCTGCCTTGACGACGAGGTCAAGCG

RESULT 13
US-09-815-242-1431/c
; Sequence 1431, Application US/09815242
; Patent No. US20020061569A1
; GENERAL INFORMATION:
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Kari L.
; APPLICANT: Zyskind, Judith W.
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John D.
; APPLICANT: Carr, Grant J.
; APPLICANT: Yamamoto, Robert T.
; APPLICANT: Xu, H. Howard
; TITLE OF INVENTION: Identification of Esse
; TITLE OF INVENTION: Prokaryotes
; FILE REFERENCE: ELITRA.011A
; CURRENT APPLICATION NUMBER: US/09/815,242
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; NUMBER OF SEQ ID NOS: 14110
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1431
; LENGTH: 255
; TYPE: DNA
; ORGANISM: Staphylococcus aureus
US-09-815-242-1431
```

85 AACGATTGGGTCCTAGCTCAGTTGGTTAGACGCACCCCTCATTAAGGGTACGTCGGCA 144 QY  
162 AATTAATGGGGCTATAGCTCAGCTGGTTAGACGCACCCCTCATTAAGGGTACGTCGGTG 103 Db  
145 GTTCAATCTGCCAGACACCACA-----ATCGAAGGGGCCATAGCTCAGCTG 192 QY  
102 GTTCAGTCCAATTAGGCCACCAATTAATTTAATACCTATTTTGGGGCTTAGCTCAGCTG 43 Db  
193 GGAGAGCCCTGCTTTTCACGCAGAGGTCACGCGTTTCGATC 234 QY  
42 GGAGAGCCCTGCTTTTCACGCAGAGGTCACGCGTTTCGATC 1 Db

```

// APPLICANT: Haselbeck, Robert
// APPLICANT: Ohlsen, Karl L.
// APPLICANT: zyskind, Judith W.
// APPLICANT: Wall, Daniel
// APPLICANT: Trawick, John D.
// APPLICANT: Carr, Grant J.
// APPLICANT: Yamamoto, Robert T.
// APPLICANT: Xu, H. Howard
// TITLE OF INVENTION: Identification of Essential Genes in
// TITLE OF INVENTION: Prokaryotes
// FILE REFERENCE: ELITRA.011A
// CURRENT APPLICATION NUMBER: US/09/815,242
// CURRENT FILING DATE: 2001-03-21
// PRIOR APPLICATION NUMBER: 60/191,078
// PRIOR FILING DATE: 2000-03-21
// PRIOR APPLICATION NUMBER: 60/206,848
// PRIOR FILING DATE: 2000-05-23
// PRIOR APPLICATION NUMBER: 60/207,727
// PRIOR FILING DATE: 2000-05-26
// PRIOR APPLICATION NUMBER: 60/242,578
// PRIOR FILING DATE: 2000-10-23
// PRIOR APPLICATION NUMBER: 60/253,625
// PRIOR FILING DATE: 2000-11-27
// PRIOR APPLICATION NUMBER: 60/257,931
// PRIOR FILING DATE: 2000-12-22
// PRIOR APPLICATION NUMBER: 60/269,308
// PRIOR FILING DATE: 2001-02-16
// NUMBER OF SEQ ID NOS: 14110
// SOFTWARE: FastSeq for Windows Version 4.0
// SEQ ID NO 1454
// LENGTH: 255
// TYPE: DNA
// ORGANISM: Staphylococcus aureus
US-09-815-242-1454
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Query Match 18.1%; Score 91.2; DB 10; Length 255;  
Best Local Similarity 78.4%; Pred. No. 6.1e-21;  
Matches 127: Conservative 0; Mismatches 23; Indels 12; Gaps 1;

Query Match	Best Local Similarity	Mismatches	Score	DB 10;	Length
85	18.1%	0	91.2	DB 10;	Length
162	78.4%	23	6.1e-21	DB 10;	Length
145	Conservative	0	23	DB 10;	Length
102	Conservative	0	23	DB 10;	Length
193	Conservative	0	23	DB 10;	Length
42	Conservative	0	23	DB 10;	Length

Search completed: February 1, 2003, 07:03:32  
Job time : 766.045 secs



GenCore version 5.1.3  
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM nucleic - nucleic search, using sw model  
Run on: February 1, 2003, 01:09:56 ; Search time 940.445 Seconds  
(without alignments)  
8679.427 Million cell updates/sec

Title: US-09-931-486-113  
Perfect score: 504  
Sequence: 1 ATCGAGACACGGCTTCGT.....CAGATTGCTGGGGTTATAT 504

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 16154066 seqs, 8097743376 residues

Total number of hits satisfying chosen parameters: 32308132

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

EST.\*  
1: em\_estba.\*  
2: em\_esthm.\*  
3: em\_estin.\*  
4: em\_estnu.\*  
5: em\_estov.\*  
6: em\_estpl.\*  
7: em\_estro.\*  
8: em\_estc.\*  
9: gb\_estl.\*  
10: gb\_est2.\*  
11: gb\_hic.\*  
12: gb\_est3.\*  
13: gb\_est4.\*  
14: gb\_est5.\*  
15: em\_estfun.\*  
16: em\_estom.\*  
17: gb\_gss.\*  
18: em\_gss\_hum.\*  
19: em\_gss\_inv.\*  
20: em\_gss\_pln.\*  
21: em\_gss\_vrt.\*  
22: em\_gss\_fun.\*  
23: em\_gss\_mam.\*  
24: em\_gss\_mus.\*  
25: em\_gss\_other.\*  
26: em\_gss\_pro.\*  
27: em\_gss\_rod.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Query No.	Score	Match	Length	DB	ID	Description
C 1	251.8	50.0	507	17	BH200120	Sml-57J2.	BH200120 Sml-57J2.
C 2	248.6	49.3	629	17	BH201541	Sml-57P13	BH201541 Sml-57P13
C 3	204	40.5	639	17	AQ509640	nbxb0096P	AQ509640 nbxb0096P
4	102.6	20.4	319	10	BE092111	IL2-BT073	BE092111 IL2-BT073
5	87	17.3	497	13	BI544108	S071 Grac	BI544108 S071 Grac
6	87	17.3	548	13	BI544155	S129 Grac	BI544155 S129 Grac

7	85.4	16.9	539	13	BI544086	
8	79.8	15.8	593	17	BH400944	
9	79.8	15.8	760	17	BH393190	
10	69.8	13.8	649	17	BH771024	
11	66.2	13.1	577	17	BH819575	
12	64.8	12.9	191	17	AZ578476	
13	64.4	12.8	608	17	BH375641	
14	63	12.5	904	17	BH159957	
15	62.6	12.4	696	17	BH383241	
16	62.6	12.4	754	17	BH405252	
17	61	12.1	3268	17	BH770998	
18	60.2	11.9	712	17	BH397037	
19	57.8	11.5	287	17	BH614410	
20	56.6	11.2	579	17	BH375975	
21	56.2	11.2	541	17	BH387664	
22	56	11.1	713	13	BH096963	
23	54.8	10.9	619	9	AA680996	
24	54.8	10.9	774	12	BG354849	
25	54	10.7	2149	17	AQ012191	
26	52.8	10.5	617	9	AI526132	
27	51.8	10.3	551	10	BE092053	
28	51	10.1	679	13	BI263958	
29	49.2	9.8	690	17	C119B2	
30	48.2	9.6	963	17	AZ549906	
31	48	9.5	902	17	CNS06M5P	
32	47.6	9.4	615	17	CI6G5	
33	47.6	9.4	938	17	AZ683938	
34	47.4	9.4	330	14	BQ205940	
35	47	9.3	432	13	BI941477	
36	46.6	9.2	501	13	BJ313245	
37	46.6	9.2	973	17	AZ688146	
38	46.4	9.2	372	10	BE092243	
39	46.4	9.2	901	17	AZ531501	
40	46.4	9.2	923	17	AZ540828	
41	46.2	9.2	238	10	BE491959	
42	46	9.1	612	17	AQ989869	
43	46	9.1	653	13	BJ318992	
44	45.8	9.1	1258	17	BH770957	
45	45.6	9.0	905	17	AZ672622	

#### ALIGNMENTS

RESULT 1  
BH200120/c  
LOCUS Sml-57J2.TF Sml Schistosoma mansoni genomic clone Sml-57J2, DNA  
DEFINITION Sml-57J2.TF Sml Schistosoma mansoni genomic clone Sml-57J2, DNA  
ACCESSION BH200120  
VERSION BH200120.1 GI:16370164  
KEYWORDS GSS.  
SOURCE Schistosoma mansoni.  
ORGANISM Schistosoma mansoni  
REFERENCE 1 (bases 1 to 507)  
AUTHORS Shetty,J., Simpson,A., Malek,J., Koo,H., Loverde,P.T. and El-Sayed ,N.M.  
TITLE Use of end sequences from Schistosoma mansoni (Puerto Rico strain) Sml BAC library for gene discovery and map construction  
JOURNAL Unpublished (2001)  
COMMENT Other GSSs: Sml-57J2.TR  
Contact: Najib M. El-Sayed  
Department of Eukaryotic Genomics  
The Institute for Genomic Research  
712 Medical Center Dr., Rockville, MD 20850, USA  
Tel: 301 838 0200  
Fax: 301 838 0208  
Email: nelsayed@tigr.org  
lo.edu).  
Seq primer: M13 For  
Class: BAC ends.

BI544086 S042 Grac  
BH400944 AG-ND-158  
BH393190 AG-ND-168  
BH771024 LLMGtag74  
BH819575 BACPP13-E  
AZ578476 23h03 Sho  
BH375641 AG-ND-133  
BH159957 ENTSL13TF  
BH383241 AG-ND-137  
BH405252 AG-ND-127  
BH770998 LLMGtag72  
BH397037 AG-ND-137  
BH614410 IC22AG2 S  
BH375975 AG-ND-133  
BH387664 AG-ND-157  
BH096963 BJ096963  
AA680996 SW3D9CA51  
BG354849 MBT5MLA09  
AQ012191 430P1A043  
AI526132 pc3-2.B11  
BE092053 IL2-BT073  
BI263958 NF107H06P  
AJ226701 Clona int  
AZ549906 ENTDM46TR  
AL405059 T7 end of  
AJ227395 Clona int  
AZ683938 ENTJ28TR  
BQ205940 UI-R-EP0-  
BI941477 q07g11.Y  
BJ313245 BJ313245  
AZ688146 ENTLA19TR  
BE092243 IL2-BT073  
AZ531501 ENTCL155TF  
AZ540828 ENTDM42TF  
BE491959 EST18-2F  
AQ989869 RfG00532  
BJ318992 BJ318992  
BH770957 LLMGtag68  
AZ672622 ENTMR14TR

FEATURES  
source

## Location/Qualifiers

1..507  
/organism="Schistosoma mansoni"  
/strain="Puerto Rico"  
/db\_xref="taxon:6183"  
/clone="Sml-57J2"  
/clone\_lib="Sml"  
/note="Vector: pBelOBAC11; Site\_1: Hin dIII; Constructed in the laboratory of Dr. Denis Le Paslier at the Fondation Jean Dausset, CEPH, Paris, France. Briefly, Schistosoma mansoni agarose embedded DNA was partially digested with Hin dIII. High molecular weight fragments were ligated in pBelOBAC11 digested with Hin dIII. The average insert size is 100 kb. Total clone coverage: approx. 7.95 x the haploid genome. Further information can be found in Le Paslier et al. (2000) Construction and characterization of a Schistosoma mansoni bacterial artificial chromosome library. Genomics 65: 87-94."

BASE COUNT  
ORIGIN

136 a 129 c 117 g 125 t

Query Match 50.0%; Score 251.8; DB 17; Length 507;  
Best Local Similarity 78.1%; Pred. No. 2.9e-68;  
Matches 385; Conservative 0; Mismatches 62; Indels 46; Gaps 5;

QY 1 ATCAAGACACCGCTTCGTCATAGCTCCACACAGCAATTCCTGATTCACCTTCGGAAG 60  
DB 485 ATCAAGACCTCAGCTTCTTCATAGTTCCACACAGCAATTCCTGATTCACCTTCGGA 426  
QY 61 GCGATTGGTTTACACCCGAGAGTAAAGATTGGGTCTGTAGCTCAGTTGGTTAGAGCGCA 120  
DB 425 GCGATTGGTTTACACCCGAGAGTAAAGATTGGGTCTGTAGCTCAGTTGGTTAGAGCGCA 366  
QY 121 CCCGTGATAGGGTGGAGTTCGGCAGTTGGAATCTGCCAGACCCACCAATCG----- 172  
DB 365 CCCGTGATAGGGTGGAGTTCGGCAGTTGGAATCTGCCAGACCCACCAATCG----- 306  
QY 173 -----AAGGGCCATAGCTCAGCTGGGAGAGCGCTGCTTTCGACGAGGAGGT 221  
DB 305 GCCAGTGTCAATGGGGCCATAGCTCAGCTGGGAGAGCGCTGCTTTCGACGAGGAGGT 246  
QY 222 CAGCGGTTTCGATCCGCTTGGCTCCACCATTAAGCTCTAG-TCGCCGAAAGCTCAGAATG 280  
DB 245 CAGGAGTTCGATCCTCTTGGCTCCACCATCACTCAGATCGCTGAAAGCTCAGAATG 186  
QY 281 ASGTGTTTACCAGGATGAGTTGATTCGCTGGGTGGAATGATTTCTGGACCTTCGGCC 340  
DB 185 AACATT-----GGTAGTTCATGTTGATTTCTGCTTTCGCTTCGGCC 147  
QY 341 AGAAGTGTCTTTAAAAATTTGGTATGCTAGTAAGAGTACCGATGTTGCTTTCACCT 400  
DB 146 AGAAGTGTCTTTAAAAATTTGGTATGCTAGTAAGAGTACCGATGTTGCTTTCACCT 91  
QY 401 GGCAGCATGTCGGCTCAAGTAAATTTGGGTCTCTCTATGCAAAATTTTCGGCGAATG 460  
DB 90 CTGCAGCTTCTTAATCAAGGCAAAATTTGGGAGTTC-AAGCGGGAATTTTCGGCGAATG 32  
QY 461 CGTCTTCAGTTA 473  
DB 31 CGTCTTCAGTTA 19

## RESULT 2

BH201541/c

LOCUS Sml-57P13.TF Sml Schistosoma mansoni genomic clone Sml-57P13, DNA  
DEFINITION BH201541 629 bp DNA linear GSS 24-OCT-2001  
sequence.

VERSION BH201541

KEYWORDS BH201541.1 GI:16373041

SOURCE GSS:

ORGANISM Schistosoma mansoni.

Schistosoma mansoni

Eukaryota; Metazoa; Platyhelminthes; Trematoda; Digenea;

REFERENCE  
AUTHORS

Strigeidida; Schistosomatoidea; Schistosomatidae; Schistosoma.  
1 (bases 1 to 629)  
Shetty,J., Simpson,A., Malek,J., Koo,H., LoVerde,P.T. and El-Sayed,  
'N.M.

## TITLE

Use of end sequences from Schistosoma mansoni (Puerto Rico strain)  
Sml BAC library for gene discovery and map construction

JOURNAL  
COMMENT

Unpublished (2001)  
Other.GSSs: Sml-57P13.TF  
Contact: Najib M. El-Sayed  
Department of Eukaryotic Genomics  
The Institute for Genomic Research  
7912 Medical Center Dr., Rockville, MD 20850, USA  
Tel: 301 838 0200  
Fax: 301 838 0208  
Email: nelsayed@tigr.org  
lo.edu).

Seq primer: M13 For

Class: BAC ends.

FEATURES  
source

## Location/Qualifiers

1..629

/organism="Schistosoma mansoni"

/strain="Puerto Rico"

/db\_xref="taxon:6183"

/clone="Sml-57P13"

/clone\_lib="Sml"

/note="Vector: pBelOBAC11; Site\_1: Hin dIII; Constructed in the laboratory of Dr. Denis Le Paslier at the Fondation Jean Dausset, CEPH, Paris, France. Briefly, Schistosoma mansoni agarose embedded DNA was partially digested with Hin dIII. High molecular weight fragments were ligated in pBelOBAC11 digested with Hin dIII. The average insert size is 100 kb. Total clone coverage: approx. 7.95 x the haploid genome. Further information can be found in Le Paslier et al. (2000) Construction and characterization of a Schistosoma mansoni bacterial artificial chromosome library. Genomics 65: 87-94."

BASE COUNT 157 a 172 c 146 g 154 t

## ORIGIN

Query Match 49.3%; Score 248.6; DB 17; Length 629;

Best Local Similarity 77.7%; Pred. No. 3.4e-67;

Matches 385; Conservative 0; Mismatches 64; Indels 46; Gaps 5;

QY 1 ATCAAGACACCGCTTCGTCATAGCTCCACACAGCAATTCCTGATTCACCTTCGGAAG 60  
DB 485 ATCAAGACCTCAGCTTCTTCATAGTTCCACACAGCAATTCCTGATTCACCTTCGGA 426  
QY 61 GCGATTGGTTTACACCCGAGAGTAAAGATTGGGTCTGTAGCTCAGTTGGTTAGAGCGCA 120  
DB 425 GCGATTGGTTTACACCCGAGAGTAAAGATTGGGTCTGTAGCTCAGTTGGTTAGAGCGCA 366  
QY 121 CCCGTGATAGGGTGGAGTTCGGCAGTTGGAATCTGCCAGACCCACCAATCG----- 172  
DB 365 CCCGTGATAGGGTGGAGTTCGGCAGTTGGAATCTGCCAGACCCACCAATCG----- 306  
QY 173 -----AAGGGCCATAGCTCAGCTGGGAGAGCGCTGCTTTCGACGAGGAGGT 221  
DB 305 GCCAGTGTCAATGGGGCCATAGCTCAGCTGGGAGAGCGCTGCTTTCGACGAGGAGGT 246  
QY 222 CAGCGGTTTCGATCCGCTTGGCTCCACCATTAAGCTCTAG-TCGCCGAAAGCTCAGAATG 280  
DB 245 CAGGAGTTCGATCCTCTTGGCTCCACCATCACTCAGATCGCTGAAAGCTCAGAATG 186  
QY 281 ASGTGTTTACCAGGATGAGTTGATTCGCTGGGTGGAATGATTTCTGGACCTTCGGCC 340  
DB 185 AACATT-----GGTAGTTCATGTTGATTTCTGCTTTCGCTTCGGCC 147  
QY 341 AGAAGTGTCTTTAAAAATTTGGTATGCTAGTAAGAGTACCGATGTTGCTTTCACCT 400  
DB 146 AGAAGTGTCTTTAAAAATTTGGTATGCTAGTAAGAGTACCGATGTTGCTTTCACCT 91  
QY 401 GGCAGCATGTCGGCTCAAGTAAATTTGGGTCTCTCTATGCAAAATTTTCGGCGAATG 460

Db 90 CTGACGTTGTTAATCAAGGCAAAATTTGCGAGTTC-AAGCGGAATTTTGGCGGAATGT 32

QY 461 CGTCTTCACGTGA 473

Db 31 CGTCTTCACGTGA 19

RESULT 3

AQ509640/c 639 bp DNA linear GSS 04-MAY-1999

LOCUS nbx50096p15f CUGI Rice BAC Library Oryza sativa genomic clone

DEFINITION nbx50096p15f, DNA sequence.

ACCESSION AQ509640

VERSION AQ509640.1 GI:4733723

KEYWORDS GSS.

SOURCE Oryza sativa.

ORGANISM Oryza sativa.

REFERENCE Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzaceae; Oryza.

AUTHORS 1 (bases 1 to 639)

TITLE Wing, R.A. and Dean, R.A.

JOURNAL A BAC End Sequencing Framework to Sequence the Rice Genome

COMMENT Unpublished (1998)

Contact: Wing RA

Clemson University

Clemson University

100 Jordan Hall, Clemson, SC 29634, USA

Tel: 864 656 7288

Fax: 864 656 4293

Email: rwing@clemson.edu

Seq primer: TAATAGACTCACTATAGGG

Class: BAC ends

High quality sequence start: 86

High quality sequence stop: 304.

FEATURES

source

1..639

/organism="Oryza sativa"

/strain="Japonica"

/cultivar="Nipponbare"

/db\_xref="taxon:4530"

/clone="nbx50096p15f"

/clone.lib="CUGI Rice BAC Library"

/tissue\_type="Leaf"

/lab\_host="E. coli DH108"

/notes="Vector: pBeloBAC11; Site\_1: HindIII; Site\_2: HindIII; Rice is one of two most popular grains in the world. Half of the world population especially those inhabiting highly populated areas of the humid tropics and subtropics, rely on rice as their primary source of carbohydrate. Monocotyledonous rice is a diploid plant (2n=24) with a haploid genome equivalent of 431 Mbp (Arumuganathan and Earle, 1991). The relatively small genome of rice, three times larger than that of Arabidopsis, makes it suitable for genomic studies. In order to facilitate positional cloning, physical mapping and genome sequencing of rice, we have constructed a BAC library from Oryza sativa, Nipponbare variety. The library contains 36,864 clones with an average insert size of 128.5 Kb providing 10.9 haploid genome equivalents. The deep coverage allows the isolation a particular sequence with a probability of 99.9 %. Two high density filters, each containing 18,432 clones (doubly spotted), represent the whole library for colony screening."

BASE COUNT 158 a 175 c 148 g 156 t 2 others

ORIGIN

Query Match 40.5%; Score 204; DB 17; Length 639;

Best Local Similarity 73.9%; Pred. No. 4.1e-53;

Matches 328; Conservative 0; Mismatches 105; Indels 11; Gaps 5;

QY 33 CACGAATTCCTGATTCACCTGCGAAAGCGGATTCGGTTTGA-----CCGAGAGTAAC 87

|||||

Db 639 CACGAATTCCTGATTCAGTATAGAGCAATTTAGTTAGTAGACTCAAGGTAAGAC 580

QY 88 GATTGGGTCTGTAGCTCAGTTGGTTAGAGCGCACCCCTGATAGAGGTGAGGTGGCAGTT 147

Db 579 GATTGGGTCTGTAGCTCAGTTGGTTAGAGCGCACCCCTGATAGAGGTGAGGTGGCAGTT 520

QY 148 CGAATCTGCCAGAGGTTGCGATCGA-AGGGGCCATAGCTCAGCTGGGAGAGCGCCCTGCT 206

Db 519 CGAATCTGCCAGAGGTTGCGATCGA-AGGGGCCATAGCTCAGCTGGGAGAGCGCCCTGCT 460

QY 207 TTGCACGAGGAGGTTGCGATCGA-AGGGGCCATAGCTCAGCTGGGAGAGCGCCCTGCT 266

Db 459 TTGCACGAGGAGGTTGCGATCGA-AGGGGCCATAGCTCAGCTGGGAGAGCGCCCTGCT 400

QY 267 AAAGCTCAGAAATGAGTGTTCACAGGATGAGTTGATTCGCTGGGTTGAACATTTGATT 326

Db 399 ATAACAC---GATTGCTTTGAAAGAGCTCAGAAAGTGTTCGCTGGGAGATTCGACTT 343

QY 327 CTGGGACTTTGGCCCAAGAACTGTTCTTTAAAAATTTGGGTATGTGATAGAGAGTACCGAT 386

Db 342 CTGGGCTTTG-ATCAGAACTGTTCTTTAAAAATTTGGGAAAGTATAGAGTACACAT 284

QY 387 GTGTTGCTTTCACTGCGAGCATGTCGCTCAAGGTAAGTAAATTTGCGTCTCTATGCAA 446

Db 283 TGACTGTTTTCACCTGCGAGTCGATGTCGTCAGGTAAGTAAATTTGCGAACTCAAGCGCAAG 224

QY 447 TTTTCGGCG-AATGTCGCTTCAC 469

Db 223 TTTTCGGCGAAATGTCGCTTCAC 200

RESULT 4

BE092111 319 bp mRNA linear EST 12-JUN-2000

LOCUS IL2-BT0733-240400-073-G03 BT0733 Homo sapiens cDNA, mRNA sequence.

DEFINITION BE092111

ACCESSION BE092111

VERSION BE092111.1 GI:8482563

KEYWORDS EST.

SOURCE human.

ORGANISM Homo sapiens

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

AUTHORS 1 (bases 1 to 319)

Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R., Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F., Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H., Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare ,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and Simpson,A.J.

TITLE Shotgun sequencing of the human transcriptome with ORF expressed sequence tags

JOURNAL Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)

MEDLINE 20202663

COMMENT Contact: Simpson A.J.G.

Laboratory of Cancer Genetics

Ludwig Institute for Cancer Research

Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP, Brazil

Tel: +55-11-2704922

Fax: +55-11-2707001

Email: asimpson@ludwig.org.br

This sequence was derived from the FAPESP/LICR Human Cancer Genome project. This entry can be seen in the following URL (http://www.ludwig.org.br/scripts/gethtml2.pl?tl=62=IL2-BT0733-240400-073-G03&t3=2000-04-24&t4=1)

Seq primer: puc 18 forward

High quality sequence stop: 298.

FEATURES

source

1..319

/organism="Homo sapiens"

/db\_xref="taxon:9606"

/clone.lib="BT0733"

/dev\_stage="Adult"





	Query Match	17.3%	Score 87	DB 13	Length 548
	Best Local Similarity	74.5%	Pred. No. 3e-16		
	Matches 123	Conservative	0	Mismatches 40	Indels 2
				Gaps	1
QY	92	GGGTCTCTAGCTCAGTTGGTTAGAGCGCACCCCGATGAAGGTCGAGTTCGGCAGCTTCGAA	151		
Db	81	GGGCTATTAGCTCAGTTGGTTAGAGCGCACCCCGATGAAGGTCGAGTTCGGTTCGAA	140		
QY	152	TCGCCCCAGACCCACCA--ATCGAAGGGGCGATAGCTCAGCTGGGAGAGCGCTTCGCTTG	209		
Db	141	TCCAGGATAGCCCACTGATGAAGGGGTATAGCTCAGCTGGTAGAGCGCTGCTTTTG	200		
QY	210	CACGCAGGAGTCAAGCGTTTCGATCCGCGCTTGGCTCCACCAATTAA	254		
Db	201	CAAGGCAGATGTCAGCGTTTCAATTCGCTTATCTCCAAAGTTTAA	245		

RESULT 7	539 bp	mRNA	linear	EST 01-MAR-2002
BI544086				
LOCUS				
DEFINITION	S042 Gracilaria lemaneiformis gametophyte cDNA library Gracilaria lemaneiformis cDNA 5', mRNA sequence.			
ACCESSION	BI544086			
VERSION	BI544086.1	GI:19033768		
KEYWORDS	EST.			
SOURCE	Gracilaria lemaneiformis.			
ORGANISM	Gracilaria lemaneiformis Eukaryota; Rhodophyta; Florideophyceae; Gracilariales; Gracilariaceae; Gracilaria.			
REFERENCE	1 (bases 1 to 539) Sun, X., Yang, G.P., Mao, Y.X. and Zhang, X.C. Analysis of expressed sequence tags of a marine red alga, Gracilaria lemaneiformis Unpublished (2001)			
JOURNAL	Contact: Sun, X.; Zhang, X. C. College of Marine Life Sciences Ocean University of Qingdao Yushan Road 5, Qingdao, 266003, Shandong, China Tel: +86-0532-2032789 Fax: +86-0532-2032276 Email: xc Zhang@ouqd.edu.cn			
COMMENT	PCR Primers FORWARD: 5' -CGTGGTACCATGGTCTAGAGT-3' BACKWARD: 5' -CTGATCTAGACCTGCAGGCTC-3' Seq primer: 5' -CGTGGTACCATGGTCTAGAGT-3' POIVA=yes.			

FEATURES	Location/Qualifiers	source
	1. 539	
	/organism="Gracilaria lemaneiformis"	
	/db_xref="taxon:2778"	
	/clone_lib="Gracilaria lemaneiformis gametophyte cDNA library"	
	/tissue_type="gametophyte thalli"	
	/note="Vector: pMD 18-T; Site_1: EcoR V with a T hang-	
	wild type Gracilaria lemaneiformis were harvested from	
	Zhanshan Bay, Qingdao (China). After rinsed with boi	
	seawater, younger thalli was cut and washed every 3-	
	days until 1 month. Then thalli was cultivated in	
	provasoli medium. Total RNA was isolated from thalli	
	gametophyte algae, using UNIQ-10 Trizol Total RNA	
	preparation kit(Sangon Inc., Shanghai, China). The c	
	was synthesized, amplified and cloned using cDNA	
	Synthesis Kit, cDNA PCR Library Kit and pMD 18-T vect	
	(Takara Biotechnology Co., Ltd., Dalian, China),	
	respectively."	
BASE COUNT	179 a 89 c 109 g 162 t	
ORIGIN		

Query Match 16.9%; Score 85.4; DB 13; Length 539;  
Best Local Similarity 73.9%; Pred. No. 9.5e-16;  
Matches 122; Conservative 0; Mismatches 41; Indels 2; Gaps 1;  
ov 92 GGGCTCTAGCTTCACTTGTTAGACGCCACCCCTGATAGGGCTAGGCTGGCAGTTCCAA 151

Db	66	GGGCTATTAGCTCAGTTGGTTAGAGCCACCCCTGTAAGGTGAGTCCCTGGTCAAA	125
Qy	152	TCGCCCCAGAGCCACCA--ATCGAAGGGCCATAGCTCAGCTGGGAGAGCCCTGCTTTG	209
Db	126	TCCAGGATAGCCCAACCATGAATAAAGGGGTATAGCTCAGCTGGTAGAGTCTGCTTTTG	185
Qy	210	CACGCAGAGGTACGCGGTTGCATCCCGCTTGGCTCCACCATTTAA	254
Db	186	CAAGGCAGATGTCAGCGGTTCAAAATCGCGTTATCTCCAAGTTTAA	230

RESULT 8					
BH400944/c					
LOCUS	BH400944	593 bp	DNA	linear	GSS 11-DEC-2001
DEFINITION	AG-ND-158022.TF	ND-TAM Anopheles gambiae genomic clone AG-ND-158022			
					' DNA sequence.

ACCESSION	BH400944
VERSION	BH400944.1
KEYWORDS	GI:17347147
SOURCE	GSS.
ORGANISM	African malaria mosquito. Anopheles gambiae Eukaryota; Metazoa; Arthropoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea; Anopheles. 1 (bases 1 to 593) Shetty,J., Malek,J., Koo,H., Collins,F., Gardner,M. and Loftus,B.J. Direct Submission of BAC-end sequences from Anopheles gambiae Unpublished (2001) Other GSSs: AG-ND-158022.TF
REFERENCE	
AUTHORS	
TITLE	
JOURNAL	
COMMENT	

Contact: Brendan J Loftus  
Department of Eukaryotic Genomics  
The Institute for Genomic Research  
9712 Medical Center Dr., Rockville, MD 20850, USA  
Tel: 301 838 0208  
Fax: 301 838 3543  
Email: bjloftus@tigr.org

This clone is from an *A. gambiae* BAC library (ND-TAM) provided by F.H. Collins and sequenced by The Institute for Genomic Research (TIGR). The BAC library was generated from *A. gambiae* PEST strain DNA. All DNA was extracted from newly hatched larvae to minimize the inclusion of DNA from microorganisms that inhabit the gut. The DNA is derived from mixed sexes of larvae. The BAC library was constructed at Texas A&M University BAC Center, University, College Station, Texas 77843-2123, USA using a HindIII partial digest.

Seq primer: M13 For  
Class: BAC ends.

```

FEATURES
source
Location/Qualifiers
1. .593
/organism="Anopheles gambiae"
/strain="PEST"
/db_xref="taxon:7165"
/clone="AG-ND-158022"
/clone_lib="ND-TAM"
/note="vector: pECBAC1; Site_1: HindIII"
119 a 157 c 118 g 199 t
BASE COUNT
ORIGIN

```

Query Match	Score 79.8;	DB 17;	Length 593;
Best Local Similarity	15.8%;		
Matches 123	77.4%;		
Conservative		0;	
Mismatches		32;	
Indels		4;	
Gaps		2;	

QY 98 GTAGCTCAGTTGTTAGAGCGCACCCCTGTATAAAGGGTAGGTCGGAGTTCGAATCTGCC 157  
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||  
Db 574 GTAGCTCAGCTGTTAGAGCGCTACACTCATATGTAGAGTTCGGCAGTTCGAGGCTGCC 515  
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||  
QY 158 CAGACCACCAATCG --AAGGGGCATAGCTCAGCTGG -GAGAGCGCCTGCTTTGCAGC 213  
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||  
Db 514 CGAGACTACTTAATTGAAAAGGGGAATTAGCTCAGCTGGCTAGAGGCCCTGCCCTTGACAG 455  
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||  
QY 214 CAGGAGGTCAGCGGTTTCGATCCGCGTTGGCTCCACCAATT 252  
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||



	RESULT 13	BH375641/c LOCUS	BH375641	608 bp	DNA	linear	GSS 10-DEC-2001
	DEFINITION	AG-ND-133M11.TF ND-TAM Anopheles gambiae genomic clone AG-ND-133M11 , DNA sequence.					
	ACCESSION	BH375641					
	VERSION	BH375641.1	GI:17321783				
	KEYWORDS	GSS:	African malaria mosquito. Anopheles gambiae				
	SOURCE	Eukaryota; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea;	Anopheles.				
	REFERENCE	1 (bases 1 to 608)					
	AUTHORS	Shetty,J., Malek,J., Koo,H., Collins,F., Gardner,M. and Loftus,B.J.					
	TITLE	Direct Submission of BAC-end sequences from Anopheles gambiae					
	JOURNAL	Unpublished (2001)					
	COMMENT	Other GSSs: AG-ND-133M11.TR Contact: Brendan J Loftus Department of Eukaryotic Genomics The Institute for Genomic Research 9712 Medical Center Dr., Rockville, MD 20850, USA Tel: 301 838 0208 Fax: 301 838 3543 Email: bjloftus@tigr.org This clone is from an A. gambiae BAC library (ND-TAM) provided by F.H. Collins and sequenced by The Institute for Genomic Research (TIGR). The BAC library was generated from A. gambiae PEST strain DNA. All DNA was extracted from newly hatched first instar larvae to minimize the inclusion of DNA from microorganisms that inhabit the gut. The DNA is derived from mixed sexes of larvae. The BAC library was constructed at Texas A&M University BAC Center University, College Station, Texas 77843-2123, USA using a HindIII partial digest. Seq primer: M13 For Class: BAC ends.					
	FEATURES	source location/Qualifiers					
		1..608 /organism="Anopheles gambiae" /strain="PEST" /db_xref="taxon:7165" /clone_lib="AG-ND-133M11" /note="Vector: pECBACL1; Site_1: HindIII"					
	BASE COUNT	144 a 146 c 132 g 186 t					
	ORIGIN	Query Match 12.8%; Score 64.4; DB 17; Length 608; Best Local Similarity 78.6%; Pred.No. 4.4e-09; Matches 77; Conservative 0; Mismatches 21; Indels 0; Gaps 0;					
	Qy	175 GGCGCCATAGCTCAGCTGGGAGAGGCCGTTCCTTGCAAGCACGAGGTGCAGGTTCGATC 234					
	Db	561 GGGGGATTAGCTCAGCTGGGAGAGCACCTGTTTGAAGCAGCGGGTCTCGTTCGTTTCGATC 502					
	Qy	235 CCGETTGGCTCCACCATTACTTAGTCGCCGAAAGCT 272					
	Db	501 CCGCATCTCTCCACCAAATAATGTAAGCCGCGAAGGT 464					
	RESULT 14	BH159957/c	BH159957	904 bp	DNA	linear	GSS 24-SEP-2001
	LOCUS	ENTSI13TF Entamoeba histolytica Sheared DNA Entamoeba histolytica genomic, DNA sequence.					
	DEFINITION	BH159957					
	ACCESSION	BH159957					
	VERSION	BH159957.1	GI:15733395				
	KEYWORDS	GSS:	Entamoeba histolytica. Entamoeba histolytica				
	SOURCE	Eukaryota; Entamoebidae; Entamoeba.					
	ORGANISM	1 (bases 1 to 904) Loftus,B., Wang,Z., Van Aken,S. and Fraser,C.					
	REFERENCE	1 (bases 1 to 904)					
	AUTHORS	Loftus,B., Wang,Z., Van Aken,S. and Fraser,C.					
	TITLE	Genetic snapshots of the Rhizobium species NGR234 genome					
	JOURNAL	Genome Biol. 1 (6), RESEARCH0014 (2000)					
	MEDLINE	21114532					
	COMMENT	Contact: Virginie Viprey Laboratoire de Biologie Molculaire des Plantes Supérieures University of Geneva I Chemin de l'Imperatrice, Chambesey/Geneva 1292, Switzerland Tel: +44(0)1603450000 Fax: +44(0)1603450045 Email: virginie.viprey@bbsrc.ac.uk Class: shotgun.					
	FEATURES	Location/Qualifiers					
	source	1..191 /organism="Rhizobium sp. NGR234" /strain="ANU265" /db_xref="taxon:394" /clone_lib="Shot-gun genomic library of Rhizobium strain ANU265" /note="Vector: M13; derivative strain of NGR234 cured of pNGR234a"					
	BASE COUNT	47 a 62 c 44 g 37 t 1 others					
	ORIGIN	Query Match 12.9%; Score 64.8; DB 17; Length 191; Best Local Similarity 84.7%; Pred.No. 1.5e-09; Matches 72; Conservative 0; Mismatches 13; Indels 0; Gaps 0;					
	Qy	168 AATCGAAGGGCCCAGTACGTGGGAGAGGCCCTGCTTTCAGCAGGAGGTTCAGGG 227					
	Db	118 AACGGTTGGGCTGTAGCTCAGCTGGGAGAGCACNTGCTTTCAGAACGAGGGGTTCAGCGG 59					
	Qy	228 TTCGATCCCGCTTGGCTCCACATT 252					
	Db	58 TTGATCCCGCTCAGCTCCACCAAT 34					

## TITLE

Determination of clone end sequences from Entamoeba histolytica  
HMI:IMSS sheared DNA library (2001)  
Unpublished (2001)  
Contact: Brendan J Loftus  
Department of Eukaryotic Genomics  
The Institute for Genomic Research  
9712 Medical Center Dr., Rockville, MD 20850, USA  
Tel: 301 838 0208  
Fax: 301 838 3543  
Email: bjlloftus@tigr.org  
Clones are derived from the Entamoeba histolytica HMI:IMSS sheared  
DNA library  
Seq primer: M13-Forward  
Class: shotgun  
High quality sequence start: 34  
High quality sequence stop: 576.

## FEATURES

source

Location/Qualifiers

1. .904

/organism="Entamoeba histolytica"

/strain="HMI:IMSS"

/db\_xref="taxon:5759"

/clone\_lib="Entamoeba histolytica Sheared DNA"

/note="Vector: pHOS1; Site\_1: Bst I; Constructed at The  
Institute for Genomic Research (TIGR), Rockville, MD.  
Genomic DNA isolated from broth cultures of E. histolytica  
using a method described by Clark and Diamond (Clark,  
C.G., and Diamond, L.S. (1993) Entamoeba histolytica: a  
method for isolate identification. Exp. Parasitol.  
77:450.). The DNA was mechanically sheared to give a  
tight size distribution (~2 kb). The v + i method used for  
the library construction is described in detail in Smith,  
H.O. and Venter, J.C. (Making small insert libraries for  
whole genome shotgun sequencing projects. In Genome  
Sequencing: A Practical Approach, eds. M. Vaudin and B.  
Barell, Oxford University Press, 1999)."

## BASE COUNT

304 a

166 c

96 g

338 t

## Query Match

12.5%; Score 63; DB 17; Length 904;

Best Local Similarity 64.3%; Pred. No. 1.6e-08;

Matches 110; Conservative 0; Mismatches 60; Indels 1; Gaps 1;

## LOCUS

BH383241/c

DEFINITION

AG-ND-137F22.TF ND-TAM Anopheles gambiae genomic clone AG-ND-137F22

, DNA sequence.

ACCESSION

BH383241

VERSION

BH383241.1

KEYWORDS

GSS.

SOURCE

African malaria mosquito.

ORGANISM

Anopheles gambiae

Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;

Neoptera; Endopterygota; Diptera; Nematocera; Culicoidae;

Anopheles.

1 (bases 1 to 696)

Shetty, J., Malek, J., Koo, H., Collins, F., Gardner, M. and Loftus, B.J.

Direct Submission of BAC-end sequences from Anopheles gambiae

Unpublished (2001)

Other\_GSSs: AG-ND-137F22.TR

## CONTACT

Contact: Brendan J Loftus  
Department of Eukaryotic Genomics  
The Institute for Genomic Research  
9712 Medical Center Dr., Rockville, MD 20850, USA  
Tel: 301 838 0208  
Fax: 301 838 3543  
Email: bjlloftus@tigr.org  
This clone is from an A. gambiae BAC library (ND-TAM) provided by  
F.H. Collins and sequenced by the Institute for Genomic Research  
(TIGR). The BAC library was generated from A. gambiae PEST strain  
DNA. All DNA was extracted from newly hatched first instar larvae  
to minimize the inclusion of DNA from microorganisms that inhabit  
the gut. The DNA is derived from mixed sexes of larvae. The BAC  
library was constructed at Texas A&M University BAC Center  
University, College Station, Texas 77843-2123, USA using a HindIII  
partial digest.  
Seq primer: M13 For  
Class: BAC ends.

## FEATURES

source

Location/Qualifiers

1. .696

/organism="Anopheles gambiae"

/strain="PEST"

/db\_xref="taxon:7165"

/clone\_lib="AG-ND-137F22"

/clone\_lib="ND-TAM"

/note="Vector: pECBAC1; Site\_1: HindIII"

167 a

182 c

146 g

201 t

## Query Match

12.4%; Score 62.6; DB 17; Length 696;

Best Local Similarity 68.8%; Pred. No. 1.8e-08;

Matches 86; Conservative 0; Mismatches 39; Indels 0; Gaps 0;

## LOCUS

BH383241/c

## DEFINITION

AG-ND-137F22.TF ND-TAM Anopheles gambiae genomic clone AG-ND-137F22

, DNA sequence.

ACCESSION

BH383241

VERSION

BH383241.1

KEYWORDS

GSS.

SOURCE

African malaria mosquito.

ORGANISM

Anopheles gambiae

Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;

Neoptera; Endopterygota; Diptera; Nematocera; Culicoidae;

Anopheles.

1 (bases 1 to 696)

Shetty, J., Malek, J., Koo, H., Collins, F., Gardner, M. and Loftus, B.J.

Direct Submission of BAC-end sequences from Anopheles gambiae

Unpublished (2001)

Other\_GSSs: AG-ND-137F22.TR

Search completed: February 1, 2003, 04:22:00

Job time : 946.445 secs

GenCore version 5.1.3  
Copyright (c) 1993 - 2003 Compugen Ltd.

OM nucleic - nucleic search, using sw model  
Run on: February 1, 2003, 01:06:21 : Search time 1027.39 Seconds  
(without alignments)  
14135.156 Million cell updates/sec  
Title: US-09-931-486-114  
Perfect score: 499  
Sequence: 1 ATCGAAGACITCAGCTTCCTT.....CAGATTGCTTGGGCTTATAT 499

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 2054640 seqs, 14551402878 residues

Total number of hits satisfying chosen parameters: 4109280

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :

GenEmbl.\*

- 1: gb.ba.\*
- 2: gb.htg.\*
- 3: gb.in.\*
- 4: gb.om.\*
- 5: gb.ov.\*
- 6: gb.pat.\*
- 7: gb.ph.\*
- 8: gb.pl.\*
- 9: gb.pr.\*
- 10: gb.ro.\*
- 11: gb.sts.\*
- 12: gb.sy.\*
- 13: gb.un.\*
- 14: gb.vi.\*
- 15: em.ba.\*
- 16: em.fun.\*
- 17: em.hum.\*
- 18: em.in.\*
- 19: em.mu.\*
- 20: em.om.\*
- 21: em.or.\*
- 22: em.ov.\*
- 23: em.pat.\*
- 24: em.ph.\*
- 25: em.pl.\*
- 26: em.ro.\*
- 27: em.sts.\*
- 28: em.un.\*
- 29: em.vi.\*
- 30: em.htg\_hum.\*
- 31: em.htg\_inv.\*
- 32: em.htg\_other.\*
- 33: em.htg\_mus.\*
- 34: em.htg\_pln.\*
- 35: em.htg\_rod.\*
- 36: em.htg\_mam.\*
- 37: em.htg\_vrt.\*
- 38: em.sv.\*
- 39: em.htgo\_hum.\*
- 40: em.htgo\_mus.\*
- 41: em.htgo\_other.\*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB	ID	Description
1	499	100.0	499	6	A48047	A48047 Sequence 11
2	499	100.0	499	6	AR177092	AR177092 Sequence
3	499	100.0	499	6	AX191055	AX191055 Sequence
4	329.4	66.0	530	1	PST251907	AJ251907 Pseudomon
5	327.8	65.7	530	1	PST251906	AJ251906 Pseudomon
6	304.2	61.0	560	1	AF356514	AF356514 Pseudomon
7	302.8	60.7	529	1	PST251901	AJ251901 Pseudomon
8	302.8	60.7	529	1	PST251902	AJ251902 Pseudomon
9	300.6	60.2	529	1	PST390590	AJ390590 Pseudomon
10	300.4	60.2	528	1	PST251905	AJ251905 Pseudomon
11	298.8	59.9	528	1	PST390589	AJ390589 Pseudomon
12	294.6	59.0	529	1	PST251904	AJ251904 Pseudomon
13	294.6	59.0	529	1	PST390587	AJ390587 Pseudomon
14	292.8	58.7	528	1	PST251903	AJ251903 Pseudomon
15	280.2	56.2	5785	1	PSU65012	U65012 Pseudomonas
16	276.4	55.4	544	1	AF083211	AF083211 Azotobact
17	274.2	54.9	528	1	PAE439391	AJ439391 Pseudomon
18	274.2	54.9	11176	1	AE004949	AE004949 Pseudomon
19	274.2	54.9	12065	1	AE004883	AE004883 Pseudomon
20	273.8	54.9	521	1	PAE439389	AJ439389 Pseudomon
21	272.6	54.6	471	6	A48044	A48044 Sequence 11
22	272.6	54.6	471	6	AR177089	AR177089 Sequence
23	272.6	54.6	471	6	AX191052	AX191052 Sequence
24	270.6	54.2	498	1	PAE439392	AJ439392 Pseudomon
25	270	54.1	592	1	AF422498	AF422498 Unculture
26	268.6	53.8	505	1	PST251900	AJ251900 Pseudomon
27	267.8	53.7	531	1	PAE439388	AJ439388 Pseudomon
28	266	53.3	506	1	PST390588	AJ390588 Pseudomon
29	265.4	53.2	504	6	A48046	A48046 Sequence 11
30	265.4	53.2	504	6	AR177091	AR177091 Sequence
31	265.4	53.2	504	6	AX191054	AX191054 Sequence
32	265.4	53.2	505	1	PST251910	AJ251910 Pseudomon
33	265.4	53.2	505	1	PST390583	AJ390583 Pseudomon
34	265.4	53.2	505	1	PST390584	AJ390584 Pseudomon
35	265.2	53.1	523	1	PST390581	AJ390581 Pseudomon
36	265	53.1	505	1	PST390585	AJ390585 Pseudomon
37	264.8	53.1	538	1	AF083212	AF083212 Azotobact
38	263.4	52.8	505	1	PST390582	AJ390582 Pseudomon
39	261.6	52.4	660	1	PSEDFC	L28150 Pseudomonas
40	261.4	52.4	490	1	PAE439390	AJ439390 Pseudomon
41	261.2	52.3	506	1	PST251908	AJ251908 Pseudomon
42	261.2	52.3	659	1	PSBDA	L28148 Pseudomonas
43	260.4	52.2	533	1	AF079808	AF079808 Azotobact
44	258	51.7	659	1	PSDFB	L28149 Pseudomonas
45	252.4	50.6	477	1	PST251909	AJ251909 Pseudomon

ALIGNMENTS

RESULT 1  
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LOCUS A48047  
DEFINITION Sequence 114 from Patent WO9600298.  
ACCESSION A48047  
VERSION A48047.1 GI:2301909  
KEYWORDS  
SOURCE unidentified.  
ORGANISM unidentified.  
REFERENCE 1 (bases 1 to 499)  
AUTHORS James C. Resau, R. and Van H. H.  
TITLE SIMULTANEOUS DETECTION, IDENTIFICATION AND DIFFERENTIATION OF  
EUBACTERIAL TAXA USING A HYBRIDIZATION ASSAY  
JOURNAL Patent: WO 9600298-A 114 04-JAN-1996;

A48047 Sequence 114 from Patent WO9600298.  
499 bp DNA linear PAT 07-MAR-1997



QY 121 CCCTGATAGGCTGAGTGGCGAGTTCGATCTCCACACACCCACCAATTTGTCGGATG 180  
 Db 121 CCCTGATAGGCTGAGTGGCGAGTTCGATCTCCACACACCCACCAATTTGTCGGATG 180  
 QY 181 GCCAGTGTCAAAATGGGGCCATAGCTCAGCTGGGAGAGCGCTGCTTTGACAGCAGGAGGT 240  
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 QY 241 CAGGAGTTCGATCCTCTGCTGGCTCCACCATCAACTCAGCATCGCTGAAAGCTCAGAATG 300  
 Db 241 CAGGAGTTCGATCCTCTGCTGGCTCCACCATCAACTCAGCATCGCTGAAAGCTCAGAATG 300  
 QY 301 AACATTTGGTGTCAATGTTGATTTCTGGCTTTGCCAGAGACTGTTCTTTAAAAATTT 360  
 Db 301 AACATTTGGTGTCAATGTTGATTTCTGGCTTTGCCAGAGACTGTTCTTTAAAAATTT 360  
 QY 361 GGGTATGTAGTAGAAGTGAATAACAGCGTGTCTTCACTGCACGTTGTTAATCAAGGCAAAA 420  
 Db 361 GGGTATGTAGTAGAAGTGAATAACAGCGTGTCTTCACTGCACGTTGTTAATCAAGGCAAAA 420  
 QY 421 TTGCGAGTTCAAGCGGGAATTTTGGCGGAATGTCGCTTCACTGACGTTACGATCATTAACC 480  
 Db 421 TTGCGAGTTCAAGCGGGAATTTTGGCGGAATGTCGCTTCACTGACGTTACGATCATTAACC 480  
 QY 481 AGATTGCTTGGGGTTATAT 499  
 Db 481 AGATTGCTTGGGGTTATAT 499

RESULT 4  
 PST251907 530 bp DNA linear BCT 16-AUG-2000  
 LOCUS  
 DEFINITION Pseudomonas stutzeri internal transcribed spacer 1 (ITS1), rRNA-1le  
 and rRNA-Ala, strain ST27MN3.  
 ACCESSION AJ251907  
 VERSION  
 KEYWORDS Internal transcribed spacer 1; ITS1; transfer RNA-Ala; transfer RNA-1le; rRNA-Ala; rRNA-1le.

SOURCE Pseudomonas stutzeri.  
 ORGANISM Bacteria; Proteobacteria; gamma subdivision; Pseudomonadaceae; Pseudomonas.

REFERENCE 1 (bases 1 to 530)  
 AUTHORS Guasp,C., Moore,E.R., Lalucat,J. and Bannasar,A.  
 TITLE Utility of internally transcribed 16S-23S rDNA spacer regions for the definition of Pseudomonas stutzeri genomovars and other Pseudomonas species  
 JOURNAL Int. J. Syst. Evol. Microbiol. 50 Pt 4, 1629-1639 (2000)  
 MEDLINE 20393664  
 PUBMED 10939670

REFERENCE 2 (bases 1 to 530)  
 AUTHORS Bannasar,A.  
 TITLE Direct Submission  
 JOURNAL Submitted (14-DEC-1999) Bannasar A., Division of Microbiology, National Research Centre for Biotechnology, Mascheroder Weg 1, D-38124 Braunschweig, GERMANY  
 FEATURES Location/Qualifiers

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 trna 201..275  
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 Matches 443; Conservative 0; Mismatches 56; Indels 30; Gaps 5;

QY 1 ATCGAAGACTTCAGCTCTTTCATAGTTCCACACAGCAATTCCTGTTGATTCACCTTCGCAAAA 60  
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 QY 61 GCGATTGGGTGAGACCCGAGAGTGACGATTGGGTGCTGTAGCTCAGTTGGTTAGAGCCGA 120  
 Db 62 GCGATTGGGTGAGACCCGAGAGTGACGATTGGGTGCTGTAGCTCAGTTGGTTAGAGCCGA 121  
 QY 121 CCCGTGATAGGGTGAGGTGCGCAGTTGCAATCTGCCAGACCCACCAATTTGTC-----G 175  
 Db 122 CCCGTGATAGGGTGAGGTGCGCAGTTGCAATCTGCCAGACCCACCAATTTGTCATGGGA 181  
 QY 176 GGATGGCCAGTGTCAAATGGGGCCATAGCTCAGCTGGGAGAGCGCTCTTTGACGAG 235  
 Db 182 TGTGCCGATCTGTAGATGGGGCCATAGCTCAGCTGGGAGAGCGCTCTTTGACGAG 241  
 QY 236 GAGTCAAGAGTTCGATCCTCTTAAAAATTTGGGTATGTGATAGAGTAGATTTGAGTGCACCTT 294  
 Db 242 GAGTCAAGAGTTCGATCCTCTTAAAAATTTGGGTATGTGATAGAGTAGATTTGAGTGCACCTT 301  
 QY 295 GAAATGAACATTGGTGTAGTTCA-----ATGTTGATTTCTGGTCTTTG 335  
 Db 302 GAAATGAAGTGTCTTGGGCATCTGCCGATGTTGAGGTATTTGATTTCTGGTCTTTG 361  
 QY 336 CGCCAGAACTCTTCTTTAAAAATTTGGGTATGTGATAGAGTAGACTAACAGCG-----GTTT 392  
 Db 362 CGCCAGAACTCTTCTTTAAAAATTTGGGTATGTGATAGAGTAGATTTGAGTGCACCTT 421  
 QY 393 TCACATGCACGTTGTT--AATCAAGCAAAATTTGCGATTCAGCGCGCAATTTTCGGCGGA 450  
 Db 422 TCACATGCACGTTGTTTCAAGTCAAGTAAATTTGCGAGTAAATTTGCGGATTTTCGGCGGA 481  
 QY 451 ATGTCGCTTTCACGTTACGAAATCTATAACCAAGATTCGTTGGGGTTATAT 499  
 Db 482 ATGTCGCTTTCACGTTATAGACAGTACCAGATTCGTTGGGGTTATAT 530

RESULT 5  
 PST251906 530 bp DNA linear BCT 16-AUG-2000  
 LOCUS  
 DEFINITION Pseudomonas stutzeri internal transcribed spacer 1 (ITS1), rRNA-1le  
 and rRNA-Ala, strain 19SMN4.  
 ACCESSION AJ251906  
 VERSION  
 KEYWORDS Internal transcribed spacer 1; ITS1; transfer RNA-Ala; transfer RNA-1le; rRNA-Ala; rRNA-1le.

SOURCE Pseudomonas stutzeri.  
 ORGANISM Bacteria; Proteobacteria; gamma subdivision; Pseudomonadaceae; Pseudomonas.

REFERENCE 1 (bases 1 to 530)  
 AUTHORS Guasp,C., Moore,E.R., Lalucat,J. and Bannasar,A.  
 TITLE Utility of internally transcribed 16S-23S rDNA spacer regions for the definition of Pseudomonas stutzeri genomovars and other Pseudomonas species  
 JOURNAL Int. J. Syst. Evol. Microbiol. 50 Pt 4, 1629-1639 (2000)  
 MEDLINE 20393664  
 PUBMED 10939670

REFERENCE 2 (bases 1 to 530)  
 AUTHORS Bannasar,A.  
 TITLE Direct Submission  
 JOURNAL Submitted (14-DEC-1999) Bannasar A., Division of Microbiology, National Research Centre for Biotechnology, Mascheroder Weg 1, D-38124 Braunschweig, GERMANY  
 FEATURES Location/Qualifiers  
 source 1..530

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93..169
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/note="codon recognized: AUC"
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201..275
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127 a 107 c 145 g 151 t
BASE COUNT

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BASE COUNT      127 a      107 c      145 g      151 t
ORIGIN
Query Match      65.7%      Score 327.8;   DB 1;   Length 530;
Best Local Similarity 83.6%;   Pred. No. 9.5e-82;
Matches 442; Conservative 0; Mismatches 57; Indels 30; Gaps 5;

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QY	1	ATCGAAGACTTCAGCTTCCTTCATAGTCCACACGAATGCTGTGATTCACCTTGCAGAAA	60
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QY	61	GCATATGGGTGTGAGACCCGAGAGTGACGATTGGGTCTGTAGCTCAGTTCGGTTAGACGCGA	120
Db	62	GCATATGGGTTCGACCCGAGAGAGATGGGTCTGTAGCTCAGTTCGGTTAGACGCGA	121
QY	121	CCCTGANTAAGGTGAGGTGGCGAGTTCGAATCTGCCACAGCCCAATTCCTC-----G	175
Db	122	CCCTGATAGGTGAGGTGGCGAGTTCGAATCTGCCACAGCCCAATTCCTCATGGGA	181
QY	176	GGATGGCCAGTGTCAATGGGGCCATAGCTCAGCTGGGAGAGCGCTGCTTTCACGCGAG	235
Db	182	TGTGGCCGATCTGTAGATGGGCCATAGCTCAGCTGGGAGAGCGCTGCTTTCACGCGAG	241
QY	236	GAGGTGAGGAGTTCGATCTCTGTGGCTCCACCATCACTC-ACGATCGCTGAAAGCTCA	294
Db	242	GAGGTGAGGAGTTCGATCTCTGTGGCTCCACCATCACTCGATATATCGCTGAAAGCTCA	301
QY	295	GAATCAACATTTGGTAGTTCA-----ATGTTGATTCGTGCTTTG	335
Db	302	GAAATCAGTCTGCTTGGCATCTCTGCCGATCTTTCAGGGTATTGATTCCTGGTCTTTG	361
QY	336	CGCCAGAATGTTCTTTTAAAAATTTGGGTATGTGATAGAAGTGACTTAACAGCG---TGTT	392
Db	362	CGCCAGAATGTTCTTTTAAAAATTTGGGTATGTGATAGAAGTGAGATTTGAGTGATCACTT	421
QY	393	TCACTCCACGTTTGTT--AATCAAGGCAAAATTTGCGAGTTCGAAGCGCAATTTTCGGCGA	450
Db	422	TCACTGGTGGTTATTCAAGTCAAGGTAAATTTGCGAGTAAATTTCCGGATTTTCGGCGA	481
QY	451	ATGTCGTCTCTACGTTACGAATCTATAACGAGATTCCTTGGGGTTTATAT	499
Db	482	ATGTCGTCTCTACGTTATAGACAGTAAACGAGATTCCTTGGGGTTTATAT	530

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RESULT 6
AF356514
LOCUS
DEFINITION
AF356514 560 bp DNA linear BCT 12-DEC-2001
Pseudomonas stutzeri strain KC internal transcribed spacer 1,
complete sequence.

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ACCESSION AF356514  
VERSION AF356514.1 GI:14039667

**KEYWORDS**  
SOURCE  
ORGANISM  
REFERENCE  
AUTHORS

*Pseudomonas stutzeri*.  
*Pseudomonas stutzeri*.  
Bacteria; Proteobacteria; gamma subdivision; Pseudomonadaceae;  
*Pseudomonas*.  
1 (bases 1 to 560)  
Sepúlveda-Torres L.C., Zhou, J., Guasp, C., Lalucat, J., Knaebel,  
Plank, J.L. and Criddle, C.S.

TITLE	Pseudomonas sp. strain KC represents a new genomovar within Pseudomonas stutzeri
JOURNAL	Int. J. Syst. Evol. Microbiol. 51 (Pt 6), 2013-2019 (2001)
MEDLINE	21596749
PUBMED	11760942
REFERENCE	2 (bases 1 to 560)
AUTHORS	Sepulveda-Torres,L.C.
TITLE	Direct Submission
JOURNAL	Submitted (06-MAR-2001) Biology, University of Puerto Rico at Mayaguez, 221 Celis Building, PO Box 9012, Mayaguez, PR 00681, USA
FEATURES	Location/Qualifiers
source	1..560 /organism="Pseudomonas stutzeri" /strain="KC" /db_xref="taxon:316" 1..560 /product="internal transcribed spacer 1"
misc_RNA	132 a 113 c 152 g 163 t
BASE COUNT	
ORIGIN	

[illegible]

QY	236	GAGGTCAGGAGTTCGATCCCTCGCTCCACCATCAACTC-ACGATCGCTGAAAGCTCA	294
Db	251	GAGGTCAGGAGTTCGATCCCTCGCTCCACCATCAACTCGATAATCGCTGAAAGCTCA	310
QY	295	GAATGAACATTCGTAAGTTCA-----ATGTTGATTTCTGCTCTTTGC	336
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QY	337	GCACAGACTGTTCTTTAAATAATTTGGGTATGCTAGTAAGTACTGACT---AACACGGTGT	393
Db	371	GCACAGACTGTTCTTTAAATAATTTGGGTATGCTAGTAAGTACTGTTGGTAGTACTT	430
QY	394	CAGTCGACGTTGTT--AATCAAGCGCAAAATTCGCGATT-----CAAGCGCG	438
Db	431	CAGTGTAAATATCAAGTCAAGTAAAAATTCGCGATTGCTCTTTATGGCGCAAGATCG	490
QY	439	AATTTTCGGCGAATGTCGCTTCCACGTTACGAATCTATAACCAAGATTGCTTGGGGTTATA	498
Db	491	GATTTTCGGCGAATGTCGCTTCCACGTTATAGACAGTACCAAGATTGCTTGGGGTTATA	550
QY	499	T	499
Db	551	T	551

RESULT 7	
PST251901	
LOCUS	529 bp tRNA linear BCT 16-AUG-2000
DEFINITION	<i>Pseudomonas stutzeri</i> internal transcribed spacer 1 (ITS1) trna-Ile
ACCESSION	gene and trna-Ala gene, strain ATCC 17591.
VERSION	AJ251901
KEYWORDS	AJ251901.1 GI:9844589
	internal transcribed spacer 1; ITS1; transfer RNA-Ala; transfer







BASE COUNT 125 a 111 c 140 g 150 t 2 others

ORIGIN

Query Match 60.2%; Score 300.4; DB 1; Length 528;  
Best Local Similarity 82.8%; Pred. No. 5.3e-74;  
Matches 437; Conservative 0; Mismatches 61; Indels 30; Gaps 7;

1 ATCGAAGACTTCAGCTTCTTCATAGTCCACACAGAAATGCTTGATTCACCTTTGGGAAA 60  
Db 2 ATCGAAGACTTCAGCTTCTTCATAGTCCACACAGAAATGCTTGATTCACCTTTGGGAAA 61

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QY 121 CCCCTGATAGGTTGAGTGGCGAGTTCGAATCTGCCAGACCCACCAATTTGTC-----G 175  
Db 122 CCCCTGATAGGTTGAGTGGCGAGTTCGAATCTGCCAGACCCACCAATTTGTCATGGGA 181

QY 176 GGAATGCCAGTGTCAAAATGGGCGCATAGCTCAGCTGGGAGCGCTGCTTTGCACGCAG 235  
Db 182 TGTGGCGGATCTGTAGTGGGCGCATAGCTCAGCTGGGAGCGCTGCTTTGCACGCAG 241

QY 236 GAGGTGAGGAGTTCGATCTCTTGGCTCCACCATCACTC-ACGATCGCTGAAGCTCA 294  
Db 242 GAGGTGAGGAGTTCGATCTCTTGGCTCCACCATCACTC-ACGATCGCTGAAGCTCA 301

QY 295 GAAATGAACATTTGGTGTCA-----ATGTTGATTTCTGCTTTGGGTTATAT 337  
Db 302 GAAATGAACATTTGGTGTCA-----ATGTTGATTTCTGCTTTGGGTTATAT 361

QY 338 CCAGAACTGTTCTTTAAATTTGGGTATGTATAGAACTGCTAAACAGCG-----TGTTTC 394  
Db 362 CCAGAACTGTTCTTTAAATTTGGGTATGTATAGAACTGCTAAACAGCG-----TGTTTC 421

QY 395 ACTGCAGTTGTT--AATCAAGGCAAAATTTGGAGTTC-AAGCGGCAATTTTCGGCGAA 451  
Db 422 ACTGCAGTTGTT--AATCAAGGCAAAATTTGGAGTTC-AAGCGGCAATTTTCGGCGAA 481

QY 452 TGTGCTCTTCACGTTACGATCTATACAGATTGCTTGGGTTATAT 499  
Db 482 TGTGCTCTTCACGTTA-TAGACAGTAAACAGATTGCTTGGGTTATAT 528

RESULT 11  
PST390589  
LOCUS  
DEFINITION Pseudomonas stutzeri intergenic spacer, tRNA-Ile and tRNA-Ala  
genes, strain Pili.

ACCESSION AJ390589  
VERSION AJ390589.1 GI:9844770  
KEYWORDS IGS; intergenic spacer; transfer RNA Ile; transfer RNA-Ala;  
tRNA-Ala gene; tRNA-Ile gene.  
Pseudomonas stutzeri.  
Pseudomonas stutzeri.  
Bacteria; Proteobacteria; gamma subdivision; Pseudomonadaceae;  
Pseudomonas.

REFERENCE 1 (bases 1 to 528)  
AUTHORS Guasp,C., Moore,E.R., Lalucat,J. and Bennisar,A.  
TITLE Utility of internally transcribed 16S-23S rDNA spacer regions for  
the definition of Pseudomonas stutzeri genomovars and other  
Pseudomonas species

JOURNAL Int. J. Syst. Evol. Microbiol. 50 Pt 4, 1629-1639 (2000)  
MEDLINE 20393664  
PUBMED 10939670

REFERENCE 2 (bases 1 to 528)  
AUTHORS Bennisar,A.  
TITLE Direct Submission  
SUBMITTED (15-DEC-1999) Bennisar A., Division of Microbiology,  
National Research Centre for Biotechnology, Mascherod Weg 1,

D-38124 Braunschweig, GERMANY

FEATURES  
source Location/Qualifiers  
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201..275  
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/anticodon=(pos:228..230,aa:Ala)  
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ORIGIN

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Best Local Similarity 82.6%; Pred. No. 1.5e-73;  
Matches 436; Conservative 0; Mismatches 62; Indels 30; Gaps 7;

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Db 2 ATCGAAGACTTCAGCTTCTTCATAGTCCACACAGAAATGCTTGATTCACCTTTGGGAAA 61

QY 61 GCGATTGGGTTGAGACCCGAGAGTGACGATTGGGCTGTAGCTCAGTTGGTTAGAGCGCA 120  
Db 62 GCGATTGGGTTGAGACCCGAGAGAGCAGATTGGGCTGTAGCTCAGTTGGTTAGAGCGCA 121

QY 121 CCCCTGATAGGTTGAGTGGCGAGTTCGAATCTGCCAGACCCACCAATTTGTC-----G 175  
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QY 176 GGAATGCCAGTGTCAAAATGGGCGCATAGCTCAGCTGGGAGCGCTGCTTTGCACGCAG 235  
Db 182 TGTGGCGGATCTGTAGTGGGCGCATAGCTCAGCTGGGAGCGCTGCTTTGCACGCAG 241

QY 236 GAGGTGAGGAGTTCGATCTCTTGGCTCCACCATCACTC-ACGATCGCTGAAGCTCA 294  
Db 242 GAGGTGAGGAGTTCGATCTCTTGGCTCCACCATCACTC-ACGATCGCTGAAGCTCA 301

QY 295 GAAATGAACATTTGGTGTCA-----ATGTTGATTTCTGCTTTGGGTTATAT 337  
Db 302 GAAATGAACATTTGGTGTCA-----ATGTTGATTTCTGCTTTGGGTTATAT 361

QY 338 CCAGAACTGTTCTTTAAATTTGGGTATGTATAGAACTGCTAAACAGCG-----TGTTTC 394  
Db 362 CCAGAACTGTTCTTTAAATTTGGGTATGTATAGAACTGCTAAACAGCG-----TGTTTC 421

QY 395 ACTGCAGTTGTT--AATCAAGGCAAAATTTGGAGTTC-AAGCGGCAATTTTCGGCGAA 451  
Db 422 ACTGCAGTTGTT--AATCAAGGCAAAATTTGGAGTTC-AAGCGGCAATTTTCGGCGAA 481

QY 452 TGTGCTCTTCACGTTACGATCTATACAGATTGCTTGGGTTATAT 499  
Db 482 TGTGCTCTTCACGTTA-TAGACAGTAAACAGATTGCTTGGGTTATAT 528

RESULT 12  
PST251904  
LOCUS  
DEFINITION Pseudomonas stutzeri internal transcribed spacer 1 (ITS1), tRNA-Ile  
and tRNA-Ala, strain AN10.

ACCESSION AJ251904  
VERSION AJ251904.1 GI:9844592  
KEYWORDS Internal transcribed spacer 1; ITS1; transfer RNA-Ala; transfer  
RNA-Ile; tRNA-Ala; tRNA-Ile.  
Pseudomonas stutzeri.  
Pseudomonas stutzeri.  
Bacteria; Proteobacteria; gamma subdivision; Pseudomonadaceae;  
Pseudomonas.

REFERENCE 1 (bases 1 to 529)  
AUTHORS Guasp,C., Moore,E.R., Lalucat,J. and Bennasar,A.  
TITLE Utility of internally transcribed 16S-23S rDNA spacer regions for  
pseudomonas species  
JOURNAL Int. J. Syst. Evol. Microbiol. 50 Pt 4, 1629-1639 (2000)  
MEDLINE 20393664  
PUBMED 10939670  
REFERENCE 2 (bases 1 to 529)  
AUTHORS Bennasar,A.  
TITLE Direct Submission  
JOURNAL Submitted (14-DEC-1999) Bennasar A., Division of Microbiology,  
National Research Centre for Biotechnology, Mascheroder Weg 1,  
D-38124 Braunschweig, GERMANY  
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Query Match 59.0%; Score 294.6; DB 1; Length 529;  
Best Local Similarity 82.0%; Pred. No. 2.3e-72;  
Matches 434; Conservative 0; Mismatches 64; Indels 31; Gaps 7;  
QY 1 ATCGAAGACTTCAGCTTCTTCATAGTTCACACAGCAATTCCTTGATTTCACCTTCGCGAAA 60  
Db 2 ATCGAAGACTTCAGCTTCTTCATAGTTCACACAGCAATTCCTTGATTTCACCTTCGCGAAA 61  
QY 61 GCGATTGGTGTGAGCCGAGAGAGTTCGATGGGTCTGTAGCTCAGTTCAGTTCAGTTCAGCGCA 120  
Db 62 GCGATTGGTGTGAGCCGAGAGAGAGTTCGATGGGTCTGTAGCTCAGTTCAGTTCAGCGCA 121  
QY 121 CCCCTGATAAGGTTGAGTTCGCGAGTTCGATTCGATTCGCCAGACCCACCAATTCGTC-----G 175  
Db 122 CCCCTGATAAGGTTGAGTTCGCGAGTTCGATTCGATTCGCCAGACCCACCAATTCGTCGGGA 181  
QY 176 GGATGCCAGTGTCAATGGGGCCATAGCTCAGCTGGGAGAGCGCTTCGCTTCGACCGAG 235  
Db 182 TGTGGCGGATCTGTAGATGGGGCCATAGCTCAGCTGGGAGAGCGCTTCGCTTCGACCGAG 241  
QY 236 GAGTTCAGGATTCGATTCCTTCCTTCGCTTCGCTTCGCTTCGCTTCGCTTCGCTTCGCTTC 293  
Db 242 GAGTTCAGGATTCGATTCCTTCCTTCGCTTCGCTTCGCTTCGCTTCGCTTCGCTTCGCTTC 301  
QY 294 AGAATGAACATTTGGTAGTTCA-----ATGTTGATTCGCTTCGCTTCGCTTCGCTTCGCTTC 336  
Db 302 AGAATGAGTTCGCTTCGCTTCGCTTCGCTTCGCTTCGCTTCGCTTCGCTTCGCTTCGCTTC 361  
QY 337 GCCAGAACTGTTCTTTAAATTTGGGTATGTGATAGAGTTCGCTTCGCTTCGCTTCGCTTCGCTTC 393  
Db 362 GCCAGAACTGTTCTTTAAATTTGGGTATGTGATAGAGTTCGCTTCGCTTCGCTTCGCTTCGCTTC 421  
QY 394 CACTGCACGTTGTT--AATCAAGGAAAATTTCCGAGTTC--AAGCGCAATTTTCGCGCA 450  
Db 422 CACTGCATGATTTCAAGTCAAGTAAAATTTTCGCTTCGCTTCGCTTCGCTTCGCTTCGCTTCGCTTC 481  
QY 451 ATGCTGCTTCAGTTCAGCAATCTATAACAGATTCCTTGGGTTATAT 499  
Db 482 ATGCTGCTTCAGTTA--TAGACAGTAAACAGATTCCTTGGGTTATAT 529

RESULT 13  
PST390587  
LOCUS  
DEFINITION  
Pseudomonas stutzeri intergenic spacer, trna-ile and trna-ala  
genes, strain AER5.1.  
ACCESSION  
AJ390587  
VERSION  
GI:9844760  
KEYWORDS  
IGS; intergenic spacer; transfer RNA ile; transfer RNA-ala;  
trna-ala gene; trna-ile gene.  
SOURCE  
Pseudomonas stutzeri.  
ORGANISM  
Bacteria; Proteobacteria; gamma subdivision; Pseudomonadaceae;  
Pseudomonas.  
REFERENCE  
1 (bases 1 to 529)  
AUTHORS Guasp,C., Moore,E.R., Lalucat,J. and Bennasar,A.  
TITLE Utility of internally transcribed 16S-23S rDNA spacer regions for  
the definition of Pseudomonas stutzeri genomovars and other  
Pseudomonas species  
JOURNAL Int. J. Syst. Evol. Microbiol. 50 Pt 4, 1629-1639 (2000)  
MEDLINE 20393664  
PUBMED 10939670  
REFERENCE 2 (bases 1 to 529)  
AUTHORS Bennasar,A.  
TITLE Direct Submission  
JOURNAL Submitted (15-DEC-1999) Bennasar A., Division of Microbiology,  
National Research Centre for Biotechnology, Mascheroder Weg 1,  
D-38124 Braunschweig, GERMANY  
FEATURES  
source  
1. 529  
/organism="Pseudomonas stutzeri"  
/strain="AER5.1"  
/db\_xref="taxon:316"  
misc\_feature  
1. 529  
/note="intergenic spacer"  
93. 169  
/product="trna-ile"  
trna  
/note="codon recognized: AUC"  
/anticodon="(pos:127..129,aa:ile)"  
201..275  
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trna  
/note="codon recognized: GCA"  
/anticodon="(pos:228..230,aa:ala)"  
BASE COUNT 123 a 111 c 141 g 154 t  
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Query Match 59.0%; Score 294.6; DB 1; Length 529;  
Best Local Similarity 82.0%; Pred. No. 2.3e-72;  
Matches 434; Conservative 0; Mismatches 64; Indels 31; Gaps 7;  
QY 1 ATCGAAGACTTCAGCTTCTTCATAGTTCACACAGCAATTCCTTGATTTCACCTTCGCGAAA 60  
Db 2 ATCGAAGACTTCAGCTTCTTCATAGTTCACACAGCAATTCCTTGATTTCACCTTCGCGAAA 61  
QY 61 GCGATTGGTGTGAGCCGAGAGAGTTCGATGGGTCTGTAGCTCAGTTCAGTTCAGTTCAGCGCA 120  
Db 62 GCGATTGGTGTGAGCCGAGAGAGAGTTCGATGGGTCTGTAGCTCAGTTCAGTTCAGCGCA 121  
QY 121 CCCCTGATAAGGTTGAGTTCGCGAGTTCGATTCGATTCGCCAGACCCACCAATTCGTC-----G 175  
Db 122 CCCCTGATAAGGTTGAGTTCGCGAGTTCGATTCGATTCGCCAGACCCACCAATTCGTCGGGA 181  
QY 176 GGATGCCAGTGTCAATGGGGCCATAGCTCAGCTGGGAGAGCGCTTCGCTTCGACCGAG 235  
Db 182 TGTGGCGGATCTGTAGATGGGGCCATAGCTCAGCTGGGAGAGCGCTTCGCTTCGACCGAG 241  
QY 236 GAGTTCAGGATTCGATTCCTTCCTTCGCTTCGCTTCGCTTCGCTTCGCTTCGCTTCGCTTC 293  
Db 242 GAGTTCAGGATTCGATTCCTTCCTTCGCTTCGCTTCGCTTCGCTTCGCTTCGCTTCGCTTC 301  
QY 294 AGAATGAACATTTGGTAGTTCA-----ATGTTGATTCGCTTCGCTTCGCTTCGCTTCGCTTC 336  
Db 302 AGAATGAGTTCGCTTCGCTTCGCTTCGCTTCGCTTCGCTTCGCTTCGCTTCGCTTCGCTTC 361

QY	337	GCAGAACTGTTCTTAAATAATTTGGGTATGTGATAGAGTACATAACAGAG---TGTTT	393
Db	362	GCAGAACTGTTCTTAAATAATTTGGGTATGTGATAGAGTACATAACAGAGTTT	421
QY	394	CAGTCAGCAGTTGTT--AATCAAGGCAAAATTTGCGAGTTC-AAGCGGAAATTTTCGGGCA	450
Db	422	CAGTCAGCAGTTTAAATCAAGTCAAGGTAATAATTTGCGTGTCTCTATGCAAAATTTTCGGGCA	481
QY	451	ATGTCGCTCTACAGTTACAACTATATACACAGATTGCTTGGGGTTATAT	499
Db	482	ATGTCGCTCTACAGTTA-TAGACAGTAACAGATTGCTTGGGGTTATAT	529
RESULT	14		
PSU65012		528 bp DNA linear	BCT 16-AUG-2000
LOCUS			
DEFINITION		Pseudomonas stutzeri internal transcribed spacer 1 (ITS1), tRNA-Ile and tRNA-Ala, strain DSM 50227.	
ACCESSION		AJ251903	
VERSION		1	GI:9844591
KEYWORDS		internal transcribed spacer 1; ITS1; transfer RNA-Ala; transfer RNA-Ile; tRNA-Ala; tRNA-Ile.	
SOURCE		Pseudomonas stutzeri.	
ORGANISM		Pseudomonas stutzeri	
REFERENCE		1 (bases 1 to 528)	
AUTHORS		Quasp,C., Moore,E.R., Lalucat,J. and Bannasar,A.	
TITLE		Utility of internally transcribed 16S-23S rDNA spacer regions for the definition of Pseudomonas stutzeri genomovars and other Pseudomonas species	
JOURNAL		Int. J. Syst. Evol. Microbiol. 50 Pt 4, 1629-1639 (2000)	
MEDLINE		20393664	
PUBMED		10939670	
REFERENCE		2 (bases 1 to 528)	
AUTHORS		Bannasar,A.	
TITLE		Direct Submission	
JOURNAL		Submitted (14-DEC-1999), Bannasar A., Division of Microbiology, National Research Centre for Biotechnology, Mascheroder Weg 1, D-38124 Braunschweig, GERMANY	
FEATURES		Location/Qualifiers	
source		1..528	
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		/strain="DSM 50227"	
		/db_xref="taxon:316"	
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misc_feature		1..528	
		/note="internal transcribed spacer 1, ITS1"	
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		/anticodon=(pos:127..129,aa:ile)	
tRNA		201..275	
		/product="tRNA-Ala"	
		/note="codon recognized: GCA"	
		/anticodon=(pos:228..230,aa:ala)	
BASE COUNT		124 a 111 c 143 g 150 t	
ORIGIN			
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Best Local Similarity		80.7%; Pred. No. 7.4e-72;	
Matches 426; Conservative		0; Mismatches 72; Indels 30; Gaps 6;	
QY	1	ATCGAAGACTCAGCTTCTTCAATAGTCCACACGAATTCCTTACCTTCAGTTCGCAAAA	60
Db	2	ATCGAAGACTCAGCTTCTTCAATAGTCCACACGAATTCCTTACCTTCAGTTCGCAAAA	61
QY	61	GCATTCGGTTCAGACCCAGAGTGGGTCTGTAGTCTGATGCTGGTGGTTCAGTTCGCA	120
Db	62	GCATTCGGTTCAGACCCAGAGTGGGTCTGTAGTCTGATGCTGGTGGTTCAGTTCGCA	121
QY	121	CCCTGATAAGGGTGAAGTTCGGAGTTCGAATCTGCCACAGACCCACCAATTCGTC----	175
Db	122	CCCTGATAAGGGTGAAGTTCGGAGTTCGAATCTGCCACAGACCCACCAATTCGTCGGGA	181
QY	176	GGATGGCAGGTGTCAAATGGGGCCATAGCTAGCTAGTGGAGAGCGCTTCGCTTCACGCAG	235
Db	182	TGTGGCCGATCTGTAGATGGGGCCATAGCTAGCTAGTGGAGAGCGCTTCGCTTCACGCAG	241
QY	236	GAGTCAGAGTTCGATCCCTCTTGGCTCCACCATCAACTC-ACGATCGCTGAAAGCTCA	294
Db	242	GAGTCAGAGTTCGATCCCTCTTGGCTCCACCATCAACTC-ACGATCGCTGAAAGCTCA	301
QY	295	GAATATGAACATTTGGTAGTTCA-----ATGTTGATTTCTGGCTTTTGGCG	337
Db	302	GAATATGAATGCTGCTTGGCATCTCTGTGATGTGAGGGTATTGATTTCTGGCTTTGGCG	361
QY	338	CCAGAACTGTTCTTTAAATAATTTGGGTATGTGATAGAGTACATAACAGCGCTTTTCACT	397
Db	362	CCAGAACTGTTCTTTAAATAATTTGGGTATGTGATAGAGTACATAACAGCGCTTTTCACT	421
QY	398	GCACGCTGTTAATCAAGGCAA-----AATTTGCGAGTTC-AAGCGGAAATTTTCGGGAA	451
Db	422	ACTGTCGATTTTCAAGTCAAGTTCAGGTTAGATTTCGCGTGTCTCTATGCAAAATTTTCGGGAA	481
QY	452	TGTCGCTCTACAGTTACGAATCTATACACAGATTGCTTGGGGTTATAT	499
Db	482	TGTCGCTCTACAGTTA-TAGACAGTAACAGATTGCTTGGGGTTATAT	528
RESULT	15		
PSU65012		5785 bp DNA linear	BCT 11-DEC-1996
LOCUS			
DEFINITION		Pseudomonas stutzeri 16S rRNA, 23S rRNA, 5S rRNA, tRNA-Ile, and tRNA-Ala genes, complete sequences.	
ACCESSION		U65012	
VERSION		1	GI:1718243
KEYWORDS		Pseudomonas stutzeri.	
ORGANISM		Pseudomonas stutzeri	
REFERENCE		1 (bases 1 to 5785)	
AUTHORS		Kerkhof,L.	
TITLE		A ribosomal RNA operon from Pseudomonas stutzeri	
JOURNAL		Unpublished	
REFERENCE		2 (bases 1 to 5785)	
AUTHORS		Kerkhof,L.	
TITLE		Direct Submission	
JOURNAL		Submitted (24-JUL-1996) Inst. Mar. Coastal. Sci., Rutgers University, 15 Dudley Rd., New Brunswick, NJ 08903, USA	
COMMENT		On Dec 11, 1996 this sequence version replaced gi:1513132.	
FEATURES		Location/Qualifiers	
source		1..5785	
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		/db_xref="taxon:316"	
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-35_signal		102..108	
-10_signal		156..182	
misc_feature		/note="anti-terminator Box B"	
misc_feature		253..262	
		/note="anti-terminator Box A"	
misc_feature		281..289	
		/note="anti-terminator Box C"	
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tRNA		2071..2151	
		/product="tRNA-Ile"	
tRNA		2180..2255	
		/note="codon recognized: AUC"	
tRNA		2509..5277	
		/product="tRNA-Ala"	
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		/note="codon recognized: GCA"	
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rRNA 5540..5674
BASE COUNT 1513 a 1241 c 1732 g 1287 t 12 others
ORIGIN

Query Match 56.2%; Score 280.2; DB 1; Length 5785;
Best Local Similarity 80.0%; Pred. No. 3.2e-68;
Matches 421; Conservative 0; Mismatches 78; Indels 27; Gaps 7;

QY 1 ATCGAAGACTTCAGCTTCCTTCATAAGTTCCACACAGAAATGCTTGATTCACCTGCCGAAAA 60
Db 1984 ATCGAAGACTTCAGCTTCCTTCATAAGTTCCACACAGAAATGCTTGATTCACCTGCCGAAAA 2043
QY 61 GCGATTGGGTTGAGACCCGAGAGTAGAGATTGGGTCTGTAGCTCAGTTGTTAGAGCGCA 120
Db 2044 GCGATTGGGTTGAGACCCGAGAGTAGAGATTGGGTCTGTAGCTCAGTTGTTAGAGCGCA 2103
QY 121 CCCTGATAGGGTGAGGTGCGGAGTTCGAATCTGCCAGACCCCAACAATTGTCTGGGA 2163
Db 2104 CCCTGATAGGGTGAGGTGCGGAGTTCGAATCTGCCAGACCCCAACAATTGTCTGGGA 2163
QY 177 GATGGCCAGTGTCAAAATGGGGCCATAGCTCAGCTGGGAGAGCGCCTGCTTGACGCAGG 236
Db 2164 TGTGGCCGATCTGTAGATGGCCATAGCTCAGCTGGGAGAGCGCCTGCTTGACGCAGG 2223
QY 237 AGGTACAGGAGTTCGATCCTCTGGCTCCACCATCA--ACTCAGATCGCTGAAAG-CTC 293
Db 2224 AGGTACAGGAGTTCGATCCTCTGGCTCCACCATCA--ACTCAGATCGCTGAAAG-CTC 293
QY 294 AGAATGAACATGGTA-----GTTCAATGTTGATTTCTTGGTCTTTGGCCAGACTGT 347
Db 2284 AGAATGAACATGGTA-----GTTCAATGTTGATTTCTTGGTCTTTGGCCAGACTGT 2343
QY 348 TCCTTTAAATAATTTGGGTATGCTAGATAGAGTGACT---AACAGCGTGTCTTCACTGCACGTT 404
Db 2344 TCCTTTAAATAATTTGGGTATGCTAGATAGAGTGACT---AACAGCGTGTCTTCACTGCACGTT 2403
QY 405 GTTAA--TCAGGCAAAATTTGCGAGTTCAA-----GCGCGAATTTTCGGCGAATG 453
Db 2404 ATTCAGTCAAGGTAAATTTGCGAGTTGCTCGAGAGAGCGAATNGATTTNNNCGAATN 2463
QY 454 TCGTCTTCACGTTACGAATCTATAACAGATGCTTGGGGTTATAT 499
Db 2464 TCGTCTTCACGTTATAGACAGTAACACAGATTGCTTGGGGTTATAT 2509
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Search completed: February 1, 2003, 03:05:12  
Job time : 1032.39 secs

GenCore version 5.1.3  
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OM nucleic - nucleic search, using sw model

Run on: January 31, 2003, 19:23:36 : Search time 118.163 Seconds  
(without alignments)  
9510.154 Million cell updates/sec

Title: US-09-931-486-114

Perfect score: 499

Sequence: 1 ATCGAAGACTTCAGCTCTT.....CAGATTGCTTGGGGTTATAT 499

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 2185239 seqs, 1125999159 residues

Total number of hits satisfying chosen parameters: 4370478

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	499	100.0	499	17 AAT11845	P. alcaligenes LMG
2	272.6	54.6	471	17 AAT11842	P. aeruginosa UZG
3	265.4	53.2	504	17 AAT11844	P. stutzeri LMG 23
4	198.4	39.8	468	17 AAT11846	P. putida LMG 2232
5	193.2	38.7	520	17 AAT11843	P. psedocalligene
6	158.6	31.8	588	22 AAI69774	16S/23S rRNA spacer
7	108.8	21.8	470	17 AAT11898	Yersinia enterocol
c 8	106	21.2	2839	22 AAH54998	S. epidermidis gen
9	106	21.2	3444	22 AAH54992	S. epidermidis gen

10	106	21.2	4429	22 AAH54300	S. epidermidis gen
11	105.6	21.2	1396	22 AAH55089	S. epidermidis gen
12	102.4	20.5	400	18 AAV78022	Staphylococcus aur
c 13	102.4	20.5	400	18 AAV77902	Staphylococcus aur
14	102.4	20.5	1311	18 AAV77852	Staphylococcus aur
c 15	99.8	20.0	400	18 AAV77984	Staphylococcus aur
16	99	19.8	463	17 AAT11870	Listeria-like isol
17	99	19.8	475	17 AAT11869	Listeria-like isol
18	98.8	19.8	640681	24 ABA92787	Buchnera sp. genom
c 19	98.2	19.5	351	18 AAV78405	Staphylococcus aur
20	97.2	19.5	582	12 AAQ14104	B.pertussis ATCC 1
21	97.2	19.5	590	12 AAQ14105	B.bronchiseptica N
22	96.2	19.3	249	17 AAT11855	A. haemolyticus LM
23	96	19.2	5097	20 AAX24983	E. coli MG1655 rrr
c 24	96	19.2	5341	20 AAX24986	E. coli MG1655 rrr
25	95.2	19.1	808	17 AAT11889	Brucella melitensi
26	95.2	19.1	808	17 AAT11890	Brucella suis NIDO
27	95.2	19.1	809	17 AAT11891	Brucella abortus
28	92.8	18.6	5105	20 AAX24989	E. coli MG1655 rrr
c 29	92	18.4	243	23 AAS48781	Staphylococcus aur
c 30	91.4	18.3	255	23 AAS48800	Staphylococcus aur
c 31	91.4	18.3	255	23 AAS48825	Staphylococcus aur
c 32	91.4	18.3	255	23 AAS48838	Staphylococcus aur
c 33	91.4	18.3	255	23 AAS48846	Staphylococcus aur
c 34	91.4	18.3	255	23 AAS48854	Staphylococcus aur
c 35	91.4	18.3	255	23 AAS48877	Staphylococcus aur
c 36	91.4	18.3	255	23 AAS48882	Staphylococcus aur
c 37	91.4	18.3	255	23 AAS48896	Staphylococcus aur
c 38	91.4	18.3	255	23 AAS48898	Staphylococcus aur
c 39	91.4	18.3	255	23 AAS48967	Staphylococcus aur
c 40	91.4	18.3	255	23 AAS49061	Staphylococcus aur
c 41	89.4	17.9	2944528	24 ABA03041	Listeria monocytog
c 42	89.2	17.9	363	17 AAT11865	L. ivanovii CIP 78
43	88.4	17.7	343	18 AAV78492	Staphylococcus aur
44	88.2	17.7	591	21 AAAS9330	Z. raflinivorans
c 45	87.8	17.6	400	18 AAV77919	Staphylococcus aur

#### ALIGNMENTS

RESULT 1  
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ID AAT11845 standard; DNA; 499 BP.  
AC AAT11845;  
XX AAT11845;  
DT 03-SEP-1996 (first entry)  
XX  
XX P. alcaligenes LMG 1224 16S-23S rRNA spacer region.  
DE  
DE Probe: detection; identification; microorganism; amplify;  
KW 16S-23S rRNA spacer region; respiratory tract; universal;  
KW species-specific; ss.  
XX  
XX Pseudomonas alcaligenes.  
XX  
XX WO9600298-A1.  
XX  
PD 04-JAN-1996.  
XX  
XX 23-JUN-1995; 95WO-EP02452.  
XX  
PR 07-APR-1995; 95EP-0870032.  
PR 24-JUN-1994; 94EP-0870106.  
XX  
XX (INNO-) INNOGENETICS NV.  
PI Jannes G, Rossau R, Van Heuverswyn H;  
XX WPI; 1996-068882/07.  
XX  
XX Novel hybridisation assay for the detection of eubacteria - esp



PT Mycobacterium, comprises amplifying the 16S-23S rRNA spacer region  
PS Claim 2; Fig 39; 248pp; English.  
XX  
XX The sequences given in AAT11791-857 represent the 16S-23S rRNA spacer  
CC regions derived from various microorganisms. These sequences were  
CC used in the method of the invention for the detection and identification  
CC of at least one or more microorganisms. The method comprises amplifying  
CC the 16S-23S rRNA spacer region and hybridising one or more of the probes  
CC given in AAT34011-77 to the amplified sequence. These probes were  
CC specifically used to detect microorganisms in samples originating from  
CC the respiratory tract. This spacer region is derived from *Pseudomonas*  
CC *aeruginosa* LMG 1324.  
XX  
SQ Sequence 499 BP; 123 A; 109 C; 130 G; 137 T; 0 other;  
Query Match 100.0%; Score 499; DB 17; Length 499;  
Best Local Similarity 100.0%; Pred. No. 1.5e-158;  
Matches 499; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 ATCGAAGACTTCAGCTTCTTCATAAGTCCACACGAATTCGTTGATTCACCTTCGCAAAA 60  
Db 1 ATCGAAGACTTCAGCTTCTTCATAAGTCCACACGAATTCGTTGATTCACCTTCGCAAAA 60  
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QY 121 CCCTGATAAGGTTGAGTGGCGAGTTCGAATCTGCCACACCCACCAATTCGCGGATG 180  
Db 121 CCCTGATAAGGTTGAGTGGCGAGTTCGAATCTGCCACACCCACCAATTCGCGGATG 180  
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Db 181 GCCAGTGTCAAAATGGGSCCATAGCTCAGCTGGAGAGCGCTGTTTGCACGAGGAGT 240  
QY 241 CAGGAGTTCGATCCTCGTTGGTCCACCATCAACTCAGATCGCTGAAAGCTCAGAAATG 300  
Db 241 CAGGAGTTCGATCCTCGTTGGTCCACCATCAACTCAGATCGCTGAAAGCTCAGAAATG 300  
QY 301 AACATTGGTAGTCAATGTTGATTTCTGTTTGGCCAGAACTGTCTTTAAATAATTT 360  
Db 301 AACATTGGTAGTCAATGTTGATTTCTGTTTGGCCAGAACTGTCTTTAAATAATTT 360  
QY 361 GGATATGTATAGAGTACTAACACGCTGTTTCACTGCACTGTTGTTAATCAAGGCAAAA 420  
Db 361 GGATATGTATAGAGTACTAACACGCTGTTTCACTGCACTGTTGTTAATCAAGGCAAAA 420  
QY 421 TTTCGAGTTCAGCGGAAATTTTCGGCAATGTCGTTTCACTGCACTGTTTACGATCTATAAC 480  
Db 421 TTTCGAGTTCAGCGGAAATTTTCGGCAATGTCGTTTCACTGCACTGTTTACGATCTATAAC 480  
QY 481 AGATTGCTTGGGTTATAT 499  
Db 481 AGATTGCTTGGGTTATAT 499  
RESULT 2  
ID AAT11842  
XX AAT11842 standard; DNA; 471 BP.  
AC AAT11842;  
XX  
DT 03-SEP-1996 (first entry)  
XX  
DE *P. aeruginosa* UZG 5669 16S-23S rRNA spacer region.  
XX  
KW Probe; detection; identification; microorganism; amplify;  
KW 16S-23S rRNA spacer region; respiratory tract; universal;  
KW species-specific; ss.  
XX  
OS *Pseudomonas aeruginosa*.  
XX

PN W09600298-A1.  
XX  
PD 04-JAN-1996.  
XX  
PF 23-JUN-1995; 95WO-EP02452.  
XX  
PR 07-APR-1995; 95EP-0870032.  
PR 24-JUN-1994; 94EP-0870106.  
XX  
PA (INNO-) INNOGENETICS NV.  
XX  
PI Jannes G. Rossau R. Van Heuverswyn H;  
XX  
DR WPI; 1996-068882/07.  
XX  
PT Novel hybridisation assay for the detection of eubacteria - esp  
PT Mycobacterium, comprises amplifying the 16S-23S rRNA spacer region  
XX  
PS Claim 2; Fig 36; 248pp; English.  
XX  
XX The sequences given in AAT11791-857 represent the 16S-23S rRNA spacer  
CC regions derived from various microorganisms. These sequences were  
CC used in the method of the invention for the detection and identification  
CC of at least one or more microorganisms. The method comprises amplifying  
CC the 16S-23S rRNA spacer region and hybridising one or more of the probes  
CC given in AAT34011-77 to the amplified sequence. These probes were  
CC specifically used to detect microorganisms in samples originating from  
CC the respiratory tract. This spacer region is derived from *Pseudomonas*  
CC *aeruginosa* UZG 5669.  
XX  
SQ Sequence 471 BP; 116 A; 103 C; 120 G; 132 T; 0 other;  
Query Match 54.6%; Score 272.6; DB 17; Length 471;  
Best Local Similarity 80.7%; Pred. No. 7.5e-82;  
Matches 409; Conservative 0; Mismatches 54; Indels 44; Gaps 6;  
QY 1 ATCGAAGACTTCAGCTTCTTCATAAGTCCACACGAATTCGTTGATTCACCTTCGCAAAA 60  
Db 1 ATCGAAGACTTCAGCTTCTTCATAAGTCCACACGAATTCGTTGATTCACCTTCGTTA-- 57  
QY 61 GCATTTGGTTGAGACCCGAGAGTGGGCTGTAGTCAGTTGTTAGAGCGCA 120  
Db 58 -----GACGATGGGCTGTAGTCAGTTGTTAGAGCGCA 93  
QY 121 CCCTGATAAGGTTGAGTGGCGAGTTCGAATCTGCCACACCCACCAATTCGCGGATG 180  
Db 94 CCCTGATAAGGTTGAGTGGCGAGTTCGAATCTGCCACACCCACCAATTCGTTGTTG 153  
QY 181 GCAGTGTG---TCAAAATGGGSCCATAGCTCAGCTGGGAGAGCGCTGTTTGCAGCAGGA 237  
Db 154 CTGCGTATCCGATACGGGSCCATAGCTCAGCTGGGAGAGCGCTGTTTGCAGCAGGA 213  
QY 238 GGTCAAGGTTTCGATCCTCTTGGCTCCACCATCACTCAGATCGCTGAAGCTCAGAA 297  
Db 214 GGTCAAGGTTTCGATCCTCTTGGCTCCACCATCTA-AAACAATGTCGAAGCTCAGAA 272  
QY 298 ATGAACATTTGGTAGTCAATGTTGATTTCTGTTTGGCCAGAACTGTTCTTTAAAAA 357  
Db 273 ATGAATGTTGTTGATGAACATTTGATTTCTGTTTGGCCAGAACTGTTCTTTAAAAA 332  
QY 358 TTTGGGTATGTATAGAAATGA---CTAACAGCGTGTTCACCTGCAGCTGTTT--AATCA 412  
Db 333 TTTGGGTATGTATAGAAATGA---CTAACAGCGTGTTCACCTGCAGCTGTTTCAAGTCA 392  
QY 413 AGGCAAAATTTGGCAGTTCAGCGGAAATTTTCGGCAATGTCGTTTCACTGTTTACGAAT 472  
Db 393 AGGCAAAATTTGGCAGTTCAGCGGAAATTTTCGGCAATGTCGTTTCACTGTTTACGAAT 472  
QY 473 CTATAACAGATTCGTTGGGTTATAT 499  
Db 445 GTATAACAGATTCGTTGGGTTATAT 471



```

RESULT 3
AAT11844
ID AAT11844 standard; DNA; 504 BP.
XX
AC AAT11844;
XX
DT 03-SEP-1996 (first entry)
XX
DE P. stutzeri LMG 2333 16S-23S rRNA spacer region.
XX
KW Probe; detection; identification; microorganism; amplify;
KW 16S-23S rRNA spacer region; respiratory tract; universal;
KW species-specific; ss.
XX
OS Pseudomonas stutzeri.
XX
PN WO9600298-Al.
XX
PD 04-JAN-1996.
XX
PF 23-JUN-1995; 95WO-EP02452.
XX
PR 07-APR-1995; 95EP-0870032.
XX
PR 24-JUN-1994; 94EP-0870106.
XX
PA (INNO-) INNOGENETICS NV.
XX
PI Jannes G, Rossau R, Van Heuverswyn H;
XX
DR WPI; 1996-068882/07.
XX
PT Novel hybridisation assay for the detection of eubacteria - esp
PT Mycobacterium, comprises amplifying the 16S-23S rRNA spacer region
XX
PS Claim 2; Fig 38; 248pp; English.
XX
CC The sequences given in AAT11791-857 represent the 16S-23S rRNA spacer
CC regions derived from various microorganisms. These sequences were
CC used in the method of the invention for the detection and identification
CC of at least one or more microorganisms. The method comprises amplifying
CC the 16S-23S rRNA spacer region and hybridising one or more of the probes
CC given in AAT34011-77 to the amplified sequence. These probes were
CC specifically used to detect microorganisms in samples originating from
CC the respiratory tract. This spacer region is derived from Pseudomonas
CC stutzeri LMG 2333.
XX
SQ Sequence 504 BP; 119 A; 111 C; 137 G; 137 T; 0 other;

Query Match 53.2%; Score 265.4; DB 17; Length 504;
Best Local Similarity 78.5%; Pred. No. 2.2e-79;
Matches 412; Conservative 0; Mismatches 66; Indels 47; Gaps 6;

Qy 1 ATCGAAGACTTCAGCTTCTTCATAAGTTCACACGAATTCGTTGATTCACCTTGCAGAAA 60
Dy 1 ATCGAAGACACCGGCTTCGTCATAAGCTCCACACGAATTCGTTGATTCACCTTGCAGAA 60
Qy 61 GCGATTGGTGTAGACCCGAGAGTACGATGGTCTGTAGCTCAGTGTGTTAGAGCGCA 120
Dy 61 GCGATTGGTGTAGACCCGAGAGTACGATGGTCTGTAGCTCAGTGTGTTAGAGCGCA 120
Qy 121 CCCCTGATAGGGTGGGCGGAGTTCGAATCTGCCACAGCCACCAATTCGCGGATG 180
Dy 121 CCCCTGATAGGGTGGGCGGAGTTCGAATCTGCCACAGCCACCAATTCGCGGATG 180
Qy 181 GCCAGTGTCAAAATGGCCATAGCTCAGCTGGGAGAGCGCTGCTTGCACGAGGAGGT 240
Dy 173 -----AAGGGCCATAGCTCAGCTGGGAGAGCGCTGCTTGCACGAGGAGGT 221
Qy 241 CAGGAGTTCGATTCCTTGGCTCCACCACTCACTCAGATCGTGTAAAGCTCAGAAATG 300
Dy 222 CAGCGGTTTCGATCCCGCTTGGCTCCACCACTTAATCTAG-TCCGCCAAAGCTCAGAAATG 280
Qy 301 AACATT-----GGTAGTTCATGTTGATTTCTGCTCTTTGCGCC 339

Db 281 AGTGTTTACCAGGATGAGTTGATTCGCTGGTTGAACATGATTTCTGGACTTTGCGCC 340
Qy 340 AGAAGTGTCTTTAAAAATTTGGGTATGTGATAGAAGTGACTAACACGG-----TGTTC 395
Dy 341 AGAAGTGTCTTTAAAAATTTGGGTATGTGATAGAAGTGACTAACACGGTTGCTTTCAC 400
Qy 396 CTGCACGTTGTTAATCAAGCAAAATTTGCCAGTTC-AAGGCGCAATTTTCGGCGAATGT 454
Dy 401 GGCAGCATGTCGGTCAAGGTAATAATTTGCGTGTCTCTATGCAATTTTCGGCGAATGT 460
Qy 455 CGTCTTCACGTTAGCAATCTATAACCAAGATTCGTTGGGTTATAT 499
Dy 461 CGTCTTCAGTTA-TAGACAGTAACCAAGATTCGTTGGGTTATAT 504

RESULT 4
AAT11846
ID AAT11846 standard; DNA; 468 BP.
XX
AC AAT11846;
XX
DT 03-SEP-1996 (first entry)
XX
DE P. putida LMG 2232 16S-23S rRNA spacer region.
XX
KW Probe; detection; identification; microorganism; amplify;
KW 16S-23S rRNA spacer region; respiratory tract; universal;
KW species-specific; ss.
XX
OS Pseudomonas putida.
XX
PN WO9600298-Al.
XX
PD 04-JAN-1996.
XX
PF 23-JUN-1995; 95WO-EP02452.
XX
PR 07-APR-1995; 95EP-0870032.
XX
PR 24-JUN-1994; 94EP-0870106.
XX
PA (INNO-) INNOGENETICS NV.
XX
PI Jannes G, Rossau R, Van Heuverswyn H;
XX
DR WPI; 1996-068882/07.
XX
PT Novel hybridisation assay for the detection of eubacteria - esp
PT Mycobacterium, comprises amplifying the 16S-23S rRNA spacer region
XX
PS Claim 2; Fig 40; 248pp; English.
XX
CC The sequences given in AAT11791-857 represent the 16S-23S rRNA spacer
CC regions derived from various microorganisms. These sequences were
CC used in the method of the invention for the detection and identification
CC of at least one or more microorganisms. The method comprises amplifying
CC the 16S-23S rRNA spacer region and hybridising one or more of the probes
CC given in AAT34011-77 to the amplified sequence. These probes were
CC specifically used to detect microorganisms in samples originating from
CC the respiratory tract. This spacer region is derived from Pseudomonas
CC putida LMG 2232.
XX
SQ Sequence 468 BP; 117 A; 101 C; 117 G; 133 T; 0 other;

Query Match 39.8%; Score 198.4; DB 17; Length 468;
Best Local Similarity 72.8%; Pred. No. 1e-56;
Matches 367; Conservative 0; Mismatches 96; Indels 41; Gaps 7;

Qy 1 ATCGAAGACTTCAGCTTCTTCATAAGTTCACACGAATTCGTTGATTCACCTTGCAGAAA 60
Dy 1 ATCGAGCATCATCATCTGTCTCTAGCTCCACACGAATTCGTTGATTCATTTGAGAGAGA 60
Qy 61 GCGATTGGTGTAGACCCGAGAGTACGATGGTCTGTAGCTCAGTGTGTTAGAGCGCA 120

```

Db 61 CGATTAGTTAGCAACCTT-----CGATTGGTCTGTAGCTAGTTGGTTAGAGCGCA 113  
 QY 121 CCCCTGATAAGGGTGAGTGGCGAGTTCGAATCTGCCAGACCCACCAATTTGTCGGGATG 180  
 Db 114 CCCCTGATAAGGGTGAGTGGCGAGTTCGAATCTGCCAGACCCACCAATTTGC----- 167  
 QY 181 GCCAGTGTCAAAATGGGGCCATAGCTGGGAGAGCGCTGCTTTGCAGCGCAGGAGGT 240  
 Db 168 -----TGGGGCCATAGCTAGCTGGGAGAGCGCTGCTTTGCAGCGCAGGAGGT 215  
 QY 241 CAGGAGTTCGATCTCTTGGCTCCACCA--TCAACTCAGATCGCTGAAAGCTCAGAAA 298  
 Db 216 CAGCGGTTCGATCCGCTTGCTCCACCAACCCGCTTGCAGATTGTGCAAGCTTAGAAA 275  
 QY 299 TGAACATTGGTAGTCAATGTGATTCTGCTCTTGGCGCAGCACTGTTCTTTAAAAAT 358  
 Db 276 TGAATATTCG-CGTCGAATATTGATTTCTGACCTTT--ATCAGAACTCGTCTCTTTAAAAAT 332  
 QY 359 TTGGGTATGTGATAGA---AGTGACTAACAGCGGTGTTTCACTGCACCGTGTGTAATCAAGG 415  
 Db 333 TTGGGTATGTGATAGAAGATAGACTGGACGACACTTTCACCTGCTGTGTTTCAGGCTAA 392  
 QY 416 CAAAATTTGGCAGTTCAAGCGCGAATTTTCGGCGAATGCTCTTCACTGCTTACCAATCTA 475  
 Db 393 GGTAAATTTGTGAGTAATTTACAAAGTTTTCGGCGAATGTTGTCTTCAC-----AGTA 444  
 QY 476 TAACCAAGATTGCTTGGGGTTATAT 499  
 Db 445 TAACCAAGATTGCTTGGGGTTATAT 468

## RESULT 5

AA11843

ID AA11843 standard; DNA; 520 BP.

XX

AC

AA11843;

XX

03-SEP-1996 (first entry)

DE P. psedocaligenes IMG 1225 16S-23S rRNA spacer region.

XX Probe; detection; identification; microorganism; amplify;

KW 16S-23S rRNA spacer region; respiratory tract; universal;

KW species-specific; ss.

XX

OS Pseudomonas pseudoalcaligenes.

XX

WO9600298-A1.

XX

04-JAN-1996.

XX

23-JUN-1995; 95WO-EP02452.

XX

07-APR-1995; 95EP-0870032.

XX

24-JUN-1994; 94EP-0870106.

XX

(INNO-) INNOGENETICS NV.

XX

Jannes G, Rossau R, Van Heuverswyn H;

XX

WPI; 1996-068882/07.

XX

Novel hybridisation assay for the detection of eubacteria - esp

PT Mycobacterium, comprises amplifying the 16S-23S rRNA spacer region

XX

Claim 2; Fig 37; 248pp; English.

XX

The sequences given in AAT11791-857 represent the 16S-23S rRNA spacer

CC regions derived from various microorganisms. These sequences were

CC used in the method of the invention for the detection and identification

CC of at least one or more microorganisms. The method comprises amplifying

CC the 16S-23S rRNA spacer region and hybridising one or more of the probes

CC

CC given in AAT34011-77 to the amplified sequence. These probes were  
 CC specifically used to detect microorganisms in samples originating from  
 CC the respiratory tract. This spacer region is derived from Pseudomonas  
 CC pseudoalcaligenes IMG 1225.

XX  
 SQ Sequence 520 BP; 126 A; 109 C; 134 G; 151 T; 0 other;

Query Match 38.7%; Score 193.2; DB 17; Length 520;  
 Best Local Similarity 72.8%; Pred. No. 6.4e-55;  
 Matches 386; Conservative 0; Mismatches 103; Indels 41; Gaps 9;

QY 1 ATCGAAGACTTTACAGCTTCTTCATAAGTTCCACACAGAAATGCTTGATTCACCTTGGCAAAA 60  
 Db 1 ATCGAAGACATCAGCTTCTTCATAAGTATCCACAGCAATGCTTGATTCATAGTCAAGC 60

QY 61 GCGATTGGTTGACACCGCAGAGTGCAGATTGGGTCTCTAGCTCAGTTGGTTAGAGCGCA 120  
 Db 61 AATGCTGTAAAGCGCGACCGCTGTATA-----GGTCTGTAGCTCAGTTGGTTAGAGCGCA 114

QY 121 CCCCTGATAAGGGTGAGGTGCGCAGTTCGAATCTGCCAGACCCACCAATTTGCGGGATG 180  
 Db 115 CCCCTGATAAGGGTGAGGTGCGCAGTTCGAATCTGCCAGACCCACCAATTTGCTTGG 171

QY 181 GCCAGTGTCAAAATGGGCCATAGCTCAGCTGGGAGAGCGCTGCTTTGCACGAGGAGGT 240  
 Db 172 TCGAGAAGAAATACGGGGCCATAGCTCAGCTGGGAGAGCGCTGCTTTGCACGAGGAGGT 231

QY 241 CAGGAGTTCGATCTCTTGGCTCCACCATCACTCAG-----ATCGCTGAAAGC 291  
 Db 232 CAGCGTTTCGATCCCGCTTGGCTCCACCATCTCTCTGTTGCGGTGAGTGTAAAGAGT 291

QY 292 TCAGAAATGA-----ACATTGGTAGTTCAATGTTGATTTCTGCTTT----- 334  
 Db 292 TCAGAAATGATGCGGCTTCAGGTTTCTCTGCTGCTGCTGCTGCTGCTTTGACCG 351

QY 335 GCGCCAGAACTGTTCTTTAAAAATTTGGGTATGTGATAGTAGAGTCAACAGCGCTG-TTT 393  
 Db 352 GTACGAAATCGTCTTTAAAAATTTGGATATGTGATAGTAGAGTCACTGATTAATGCTTT 411

QY 394 CACTGCACTGTG--TTAATCAAGGCAAAATTTG--CGAGTTCAGCGCGAATTTTCGCG 449  
 Db 412 CACTGCAATGTATGCTGCTCAAGTAAATTTGTAGTTCACAGACCGCAATTTTCGCG 471

QY 450 AATGTCGTCTTCAGTTACGAATCTATACCAAGATTCCTTTGGGTTATAT 499  
 Db 472 AATGTCGTCTTCAGAT-TGAGACAGTAACCAAGATTCCTTTGGGTTATAT 520

## RESULT 6

AA169774

ID AA169774 standard; DNA; 588 BP.

XX

AC

AA169774;

XX

13-DEC-2001 (first entry)

XX

16S/23S rRNA spacer region.

XX

Bacterium detection; 16S/23S rRNA spacer region; ds.

XX

Pseudomonas putida.

XX

JP2001190279-A.

XX

17-JUL-2001.

XX

13-JAN-2000; 2000JP-0004160.

XX

13-JAN-2000; 2000JP-0004160.

XX

(MITO) MITSUBISHI JUKOGYO KK.

XX

WPI; 2001-605311/69.

XX

XX PT Detection method of Pseudomonas bacteria -  
 XX PS Claim 6; Page 7; 11pp; Japanese.  
 XX CC The present invention relates to a method for the detection of the  
 CC present DNA sequence: the 16S/23S rRNA spacer region of Pseudomonas  
 CC putida. The method can be used to detect Pseudomonas bacteria.  
 XX SQ Sequence 588 BP; 147 A; 134 C; 153 G; 149 T; 5 other;  
 Query Match 31.8%; Score 158.6; DB 22; Length 588;  
 Best Local Similarity 71.5%; Pred. No. 3.6e-43;  
 Matches 369; Conservative 0; Mismatches 84; Indels 63; Gaps 10;  
 QY 1 ATCGAAGACTTCAGCTTCCTTCATAGTCCACAGCAATGCTGATTACACTTGGCAAAA 60  
 DB 63 ATCGAGCATCAGCTGCTGATGAGTCCACAGCAATGCTGATTACACTTGGCAAGA 122  
 QY 61 GCGATTGGTTGAGACCCGAGAGTGACGATTGGTCTGAGCTCAGTTGGTTAGAGCGCA 120  
 DB 123 C-----GATCAAGACCCCTATA-----TAGGCTGTAGCTCAGTTGGTTAGAGCGCA 168  
 QY 121 CCCTGATAGGTGAGTGGCGAGTTCGAATCTGCCAGACCCACCAATGTCGGGATG 180  
 DB 169 CCCTGATAGGTGAGTGGCGAGTTCGAATCTGCCAGACCTACCAAT----- 218  
 QY 181 GCCAGTGTCAAAATGGGGCCATAGCTCAGCTGGGAGAGCCCTGCTTTGCACGAGGAGT 240  
 DB 219 -----ATGCGGGGCCATAGCTCAGCTGGGAGAGCCCTGCTTTGCACGAGGAGT 269  
 QY 241 CAGGAGTTCGATCTCTTGGCTCCACCATCACTCAGCTCAGCTGCTCAAGAGCTCAGAAATG 300  
 DB 270 CAGCGGATCATCCGCTTGGCTTCCACCACTTGTCTGCTACCTGATGATCAAA-CTCANAATG 328  
 QY 301 AACATTGGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 360  
 DB 329 AGCAAT-CCGCTATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 384  
 QY 361 GGGTATGTATAGA-AGTGAATCAACAGCGTGTGTTTCACTGACGCTTGTAA--TCAAGGCA 417  
 DB 385 GGATATGTATAGATATAGACTGAACACCAAGTTTCACTGCTGTTGGATCAGGCTAANGTA 444  
 QY 418 AATTTCCGAGTTC-----RAGCGCAATTTTCGGCAATGTCGCTTTCAC 463  
 DB 445 AATTTGNGAGTTCTGCTCGAAGAGCACTTTCGGAATTTTCGGCAATGTCGCTTTCAC 504  
 QY 464 GTTACGAATCTATAACCAAGATGCTTGGGTTATAT 499  
 DB 505 -----AGTATAACCAAGATGCTTGGGTTATAT 532  
 RESULT 7  
 AAT11898  
 ID AAT11898 standard; DNA; 470 BP.  
 XX AC AAT11898;  
 XX DT 03-SEP-1996 (first entry)  
 XX DE Yersinia enterocolitica strain p95 16S-23S rRNA spacer region (#1).  
 XX KW Probe; detection; identification; microorganism; amplify;  
 XX KW 16S-23S rRNA spacer region; food; universal;  
 XX KW species-specific; ss.  
 XX OS Yersinia enterocolitica.  
 XX PN WO9600298-A1.  
 XX PD 04-JAN-1996.  
 XX PF 23-JUN-1995; 95WO-EP02452.

XX PR 07-APR-1995; 95EP-0870032.  
 XX PR 24-JUN-1994; 94EP-0870106.  
 XX PA (INNO-) INNOGENETICS NV.  
 XX PI Jannes G, Rossau R, Van Heuverswyn H;  
 XX DR WPI; 1996-068882/07.  
 XX PT Novel hybridisation assay for the detection of eubacteria - esp  
 XX PT Mycobacterium, comprises amplifying the 16S-23S rRNA spacer region  
 XX PS Claim 5; Fig 98; 248pp; English.  
 XX CC The sequences given in AAT11889-905 represent the 16S-23S rRNA spacer  
 CC regions derived from various microorganisms. These sequences were  
 CC used in the method of the invention for the detection and identification  
 CC of at least one or more microorganisms. The method comprises amplifying  
 CC the 16S-23S rRNA spacer region and hybridising one or more probes to  
 CC the amplified sequence. These probes were specifically used to detect  
 CC microorganisms in samples originating from food. This spacer region is  
 CC derived from Yersinia enterocolitica strain P95.  
 XX SQ Sequence 470 BP; 129 A; 101 C; 120 G; 120 T; 0 other;  
 Query Match 21.8%; Score 108.8; DB 17; Length 470;  
 Best Local Similarity 72.9%; Pred. No. 2.4e-26;  
 Matches 159; Conservative 0; Mismatches 47; Indels 12; Gaps 1;  
 QY 91 TGGGTCTCTAGCTCAGTTGGTTAGAGCGCACCCCTCTGATTAAGGGTGAAGTTCGAGTTGCA 150  
 DB 75 TAGGCTTGTAGCTCAGTTGGTTAGAGCGCACCCCTCTGATTAAGGGTGAAGTTCGAGTTGCA 134  
 QY 151 AFTCTCCACAGACCCACCAATGTCGGGATGCGGCTGT-----CAAAATGGGCG 198  
 DB 135 GTTCCACTCAGGCTTACCACCTTCTCGAAGTGGAAAAGGTAAGTGCAGTGCAGTGCAGTGCAGT 194  
 QY 199 CATACCTCAGCTGGGAGAGCGCTCTTTGACGAGGAGGTCAGGAGTTCGATCCTCT 258  
 DB 195 TATACCTCAGCTGGGAGAGCGCTCTGCTTGCACGAGGAGTTCAGGATCCCGCT 254  
 QY 259 TGGTCCACCACTCAACTCAGATCAGTCTGAAAGCTCAGA 296  
 DB 255 TAGTCCACCAATATAGTCTGCTGATTTCAATACTTCAGA 292  
 RESULT 8  
 AAH54998/c  
 ID AAH54998 standard; DNA; 2839 BP.  
 XX AC AAH54998;  
 XX DT 03-SEP-2001 (first entry)  
 XX DE S. epidermidis genomic polynucleotide sequence SEQ ID NO:4362.  
 XX KW Staphylococcus epidermidis SR1 strain; infection; diagnosis;  
 XX KW vaccination; endocarditis; ds.  
 XX OS Staphylococcus epidermidis.  
 XX PN WO200134809-A2.  
 XX PD 17-MAY-2001.  
 XX PF 09-NOV-2000; 2000WO-US30782.  
 XX PR 09-NOV-1999; 99US-0164258.  
 XX PA (GLAXO) GLAXO GROUP LTD.  
 XX PI Kimmerly WJ;





DT 16-MAR-1999 (first entry)  
 DE Staphylococcus aureus contig SEQ ID #3711.  
 XX  
 KW Computer readable medium; vaccine; S.aureus infection; immunodetection;  
 KW cellulitis; eyelid infection; food poisoning; osteomyelitis; therapy;  
 KW skin infection; surgical wound infection; scalded skin syndrome;  
 KW toxic shock syndrome; ds.  
 XX  
 OS Staphylococcus aureus.  
 XX  
 XX EP786519-A2.  
 PN 30-JUL-1997.  
 PD  
 XX 07-JAN-1997; 97EP-0100117.  
 XX  
 XX 05-JAN-1996; 96US-0009861.  
 XX (HUMA-) HUMAN GENOME SCI INC.  
 PA  
 PI Barash SC, Choi GH, Dillon PJ, Fannon MR, Kunsch CA;  
 PI Rosen CA;  
 XX WPI; 1997-374922/35.  
 DR  
 XX Polynucleotide(s) and proteins derived from Staphylococcus aureus -  
 PT stored on computer readable medium and used in the production of  
 PT anti-S.aureus vaccines  
 XX  
 XX Claim 1; Page 2654; 3271pp; English.  
 XX  
 CC This sequence represents one of 5191 Staphylococcus aureus DNA sequences  
 CC of the invention. The DNA sequences are recorded on a computer readable  
 CC medium, preferably selected from a floppy or hard disk, random access  
 CC memory (RAM), read-only memory (ROM) or CD-ROM. Homology searches using  
 CC the S.aureus DNA sequences allows putative functions to be assigned so  
 CC that protein-encoding or regulatory regions of commercial, therapeutic or  
 CC industrial importance can be obtained. Specifically, sequences which are  
 CC likely to encode antigens have been identified and these polypeptides can  
 CC be used in a vaccine composition against S.aureus infection. The  
 CC polypeptides can also be used in a kit for the immunodetection of  
 CC S.aureus in a sample. S.aureus is implicated in numerous human diseases,  
 CC including cellulitis, eyelid infections, food poisoning, osteomyelitis,  
 CC skin and surgical wound infections, scalded skin syndrome, toxic shock  
 CC syndrome, etc. Organisms transformed with the DNA sequences can be used  
 CC for recombinant production of the polypeptides. The new DNA sequences  
 CC (and their fragments) are useful as primers or probes for isolating  
 CC homologues of any of the S.aureus DNA sequences contained on the  
 CC computer readable medium.  
 XX  
 SQ Sequence 400 BP; 104 A; 79 C; 104 G; 113 T; 0 other;  
 Query Match 20.5%; Score 102.4; DB 18; Length 400;  
 Best Local Similarity 76.6%; Pred. No. 3.2e-24;  
 Matches 141; Conservative 0; Mismatches 36; Indels 7; Gaps 1;  
 QY 89 ATTGGGCTCTAGCTAGTGGTGTAGAGCCACCCCTGATAGAGGTGAGTGGCAGTTC 148  
 Db 187 AATGGCCCTATAGCTAGCTAGTGGTGTAGAGCCACCCCTGATAGAGGTGAGTGGTTC 246  
 QY 149 GAATCTGCCAGACCCACCAATGTGCGGATGCGCAGTGTCAATGGGCCATAGTTCAG 208  
 Db 247 GAGTCCACTTAGGCCACCCACCATTTTATATACCTATTTGGGGCTTAGTCTCAG 299  
 QY 209 CTGGGAGAGGCGCTGTTTGCAGCAGGAGGTGAGTTCGATCCTCTGGCTCCACC 268  
 Db 300 CTGGGAGAGCGCGCTGTTTGCAGCAGGAGGTGAGTTCGATCCTCTGGCTCCACC 359  
 QY 269 ATCA 272  
 Db 360 ATTA 363

RESULT 13  
 AAV77902/c  
 ID AAV77902 standard; DNA; 400 BP.  
 XX  
 AC AAV77902;  
 XX  
 DT 16-MAR-1999 (first entry)  
 XX  
 DE Staphylococcus aureus contig SEQ ID #3591.  
 XX  
 KW Computer readable medium; vaccine; S.aureus infection; immunodetection;  
 KW cellulitis; eyelid infection; food poisoning; osteomyelitis; therapy;  
 KW skin infection; surgical wound infection; scalded skin syndrome;  
 KW toxic shock syndrome; ds.  
 XX  
 OS Staphylococcus aureus.  
 XX  
 XX EP786519-A2.  
 PN 30-JUL-1997.  
 PD  
 XX 07-JAN-1997; 97EP-0100117.  
 XX  
 XX 05-JAN-1996; 96US-0009861.  
 XX (HUMA-) HUMAN GENOME SCI INC.  
 PA  
 PI Barash SC, Choi GH, Dillon PJ, Fannon MR, Kunsch CA;  
 PI Rosen CA;  
 XX WPI; 1997-374922/35.  
 DR  
 XX Polynucleotide(s) and proteins derived from Staphylococcus aureus -  
 PT stored on computer readable medium and used in the production of  
 PT anti-S.aureus vaccines  
 XX  
 XX Claim 1; Page 2600; 3271pp; English.  
 XX  
 CC This sequence represents one of 5191 Staphylococcus aureus DNA sequences  
 CC of the invention. The DNA sequences are recorded on a computer readable  
 CC medium, preferably selected from a floppy or hard disk, random access  
 CC memory (RAM), read-only memory (ROM) or CD-ROM. Homology searches using  
 CC the S.aureus DNA sequences allows putative functions to be assigned so  
 CC that protein-encoding or regulatory regions of commercial, therapeutic or  
 CC industrial importance can be obtained. Specifically, sequences which are  
 CC likely to encode antigens have been identified and these polypeptides can  
 CC be used in a vaccine composition against S.aureus infection. The  
 CC polypeptides can also be used in a kit for the immunodetection of  
 CC S.aureus in a sample. S.aureus is implicated in numerous human diseases,  
 CC including cellulitis, eyelid infections, food poisoning, osteomyelitis,  
 CC skin and surgical wound infections, scalded skin syndrome, toxic shock  
 CC syndrome, etc. Organisms transformed with the DNA sequences can be used  
 CC for recombinant production of the polypeptides. The new DNA sequences  
 CC (and their fragments) are useful as primers or probes for isolating  
 CC homologues of any of the S.aureus DNA sequences contained on the  
 CC computer readable medium.  
 XX  
 SQ Sequence 400 BP; 105 A; 82 C; 66 G; 107 T; 40 other;  
 Query Match 20.5%; Score 102.4; DB 18; Length 400;  
 Best Local Similarity 76.6%; Pred. No. 3.2e-24;  
 Matches 141; Conservative 0; Mismatches 36; Indels 7; Gaps 1;

QY 89 ATTGGGCTCTAGCTAGTGGTGTAGAGCCACCCCTGATAGAGGTGAGTGGCAGTTC 148



CC skin and surgical wound infections, scalded skin syndrome, toxic shock  
CC syndrome, etc. Organisms transformed with the DNA sequences can be used  
CC for recombinant production of the polypeptides. The new DNA sequences  
CC (and their fragments) are useful as primers or probes for isolating  
CC homologues of any of the *S. aureus* DNA sequences contained on the  
CC computer readable medium.

Sequence 400 BP; 115 A; 95 C; 78 G; 109 T; 3 other;

Query Match 20.0%; Score 99.8; DB 18; Length 400;  
Best Local Similarity 75.5%; Pred. No. 2.5e-23;  
Matches 139; Conservative 0; Mismatches 38; Indels 7; Gaps 1;

Qy 89 ATTGGGTCTGTAGCTCAGTTGGTTAGAGCGCACCCCTCATTAAGGTGAGGTGCGCAGTTC 148

Db 272 AATGGGCCTATAGCTCAGCTGGTTAGAGCGCAGCCCTGATACGCTGAGGTGGTGGTTC 213

Qy 149 GAATCTGCCAGACCCACCAATTGTCGGGATGGCCAGTGTCAAATGGGGCCATAGCTCAG 208

Db 212 GAGTCCACTTAGGCCCCCATT-----AATTTAATACCTNTTTGGGGGCTTAGCTCAG 160

QY 209 CTGGGAGAGCGCTGCTTTGCACGCAGGAGGTCAGAGTTTCGATCCTCCTTGGCTCCACC 268

Db 159 CTGGGAGAGCGCCTGCTTTGCA CGCAGGAGGTACAGCGGTTCCGATCCCGTAGTCTCCACC 100

QY 269 ATCA 272

99 ATT A 96

Search completed: February 1, 2003, 01:37:30  
Job time : 127.163 secs

•



GenCore version 5.1.3  
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: February 1, 2003, 01:17:06 : Search time 25.9431 Seconds  
(without alignments)  
5898.736 Million cell updates/sec

Title: US-09-931-486-114

Perfect score: 499

Sequence: 1 ATCGAAGACTTCAGCTTCTT.....CAGATTGCTTGGGGTATAT 499

Scoring table: IDENTITY\_NUC

Gapop 10.0 , Gapext 1.0

Searched: 441362 seqs, 15338381 residues

Total number of hits satisfying chosen parameters: 882724

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

- 1: /cgn2\_6/ptodata/1/ina/5A\_COMB.seq.\*
- 2: /cgn2\_6/ptodata/1/ina/5B\_COMB.seq.\*
- 3: /cgn2\_6/ptodata/1/ina/6A\_COMB.seq.\*
- 4: /cgn2\_6/ptodata/1/ina/6B\_COMB.seq.\*
- 5: /cgn2\_6/ptodata/1/ina/PTUS\_COMB.seq.\*
- 6: /cgn2\_6/ptodata/1/ina/backfiles1.seq.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	499	100.0	499	3	US-08-765-332-114
2	499	100.0	499	4	US-09-448-894-114
3	272.6	54.6	471	3	US-08-765-332-111
4	272.6	54.6	471	4	US-09-448-894-111
5	265.4	53.2	504	3	US-08-765-332-113
6	265.4	53.2	504	4	US-09-448-894-113
7	198.4	39.8	468	3	US-08-765-332-115
8	198.4	39.8	468	4	US-09-448-894-115
9	193.2	38.7	520	3	US-08-765-332-112
10	193.2	38.7	520	4	US-09-448-894-112
11	108.8	21.8	470	3	US-08-765-332-195
12	108.8	21.8	470	4	US-09-448-894-195
13	99	19.8	463	3	US-08-765-332-215
14	99	19.8	463	4	US-09-448-894-215
15	99	19.8	475	3	US-08-765-332-214
16	99	19.8	475	4	US-09-448-894-214
17	97.2	19.5	582	1	US-08-412-614-87
18	97.2	19.5	582	2	US-08-635-761-87
19	97.2	19.5	582	4	US-09-312-520-87
20	97.2	19.5	590	1	US-08-412-614-88
21	97.2	19.5	590	2	US-08-635-761-88
22	97.2	19.5	590	4	US-09-312-520-88
23	96.2	19.3	249	3	US-08-765-332-128
24	96.2	19.3	249	4	US-09-448-894-128
25	95.2	19.1	808	3	US-08-765-332-131
26	95.2	19.1	808	4	US-09-448-894-131
27	95.2	19.1	808	4	US-09-448-894-131

28	95.2	19.1	808	4	US-09-448-894-132
29	95.2	19.1	809	3	US-08-765-332-134
30	95.2	19.1	809	4	US-09-448-894-134
31	89.2	17.9	363	3	US-08-765-332-119
32	89.2	17.9	363	4	US-09-448-894-119
33	89.2	17.9	618	4	US-09-703-807-15
34	87.6	17.6	619	4	US-09-703-807-13
35	87	17.4	549	1	US-08-412-614-92
36	87	17.4	549	2	US-08-635-761-92
37	87	17.4	549	4	US-09-312-520-92
38	87	17.4	603	1	US-08-412-614-85
39	87	17.4	603	2	US-08-635-761-85
40	87	17.4	603	2	US-08-635-761-86
41	87	17.4	603	2	US-08-635-761-86
42	87	17.4	603	4	US-09-312-520-85
43	87	17.4	603	4	US-09-312-520-86
44	84.6	17.0	496	3	US-08-765-332-120
45	84.6	17.0	496	4	US-09-448-894-120

## ALIGNMENTS

RESULT 1  
US-08-765-332-114  
; Sequence 114, Application US/08765332  
; Patent No. 6025132  
; GENERAL INFORMATION:  
; APPLICANT: JANNES, GEERT  
; APPLICANT: ROSSAU, RUDI  
; APPLICANT: VAN HEUVERSWIN, HUGO  
; TITLE OF INVENTION: SIMULTANEOUS DETECTION, IDENTIFICATION  
; TITLE OF INVENTION: AND DIFFERENTIATION OF EUBACTERIAL TAXA USING A  
; NUMBER OF SEQUENCES: 216  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: NIXON & VANDERHYE P.C.  
; STREET: 1100 NORTH GLEBE ROAD, 8TH FLOOR  
; CITY: WASHINGTON  
; STATE: D.C.  
; COUNTRY: USA  
; ZIP: 22201  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICANT NUMBER: US/08765,332  
FILING DATE: 23-DEC-1996  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: WO PCT/EP95/02452  
FILING DATE: 23-JUN-1995  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: EP 95870032.0  
FILING DATE: 07-APR-1995  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: EP 94870106.5  
FILING DATE: 24-JUN-1994  
ATTORNEY/AGENT INFORMATION:  
NAME: SADOFF, B.J.  
REGISTRATION NUMBER: 36,663  
REFERENCE/DOCKET NUMBER: 1487-14  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 703-816-4091  
TELEFAX: 703-816-4100  
INFORMATION FOR SEQ ID NO: 114:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 499 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear

CLASSIFICATION: <Unknown>  
07-APR-1995  
24-JUN-1994

PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/765,332  
FILING DATE: <Unknown>  
APPLICATION NUMBER: EP 95870032.0  
FILING DATE: 07-APR-1995  
APPLICATION NUMBER: EP 94870106.5  
FILING DATE: 24-JUN-1994

ATTORNEY/AGENT INFORMATION:  
NAME: SADOFF, B.J.  
REGISTRATION NUMBER: 36,663  
REFERENCE/DOCKET NUMBER: 1487-14  
TELEPHONE: 703-816-4091  
TELEFAX: 703-816-4100

INFORMATION FOR SEQ ID NO: 114:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 499 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
SEQUENCE DESCRIPTION: SEQ ID NO: 114:  
US-09-448-894-114

Query Match 100.0%; Score 499; DB 4; Length 499;  
Best Local Similarity 100.0%; Pred. No. 2e-165;  
Matches 499; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATCGAAGACTTCAGCTTCTTCATAAGTTCACACAGCAATTCGTTGATTCACCTTCGAAAA 60  
DB 1 ATCGAAGACTTCAGCTTCTTCATAAGTTCACACAGCAATTCGTTGATTCACCTTCGAAAA 60

QY 61 CGGATTGGTGTAGAGCCGAGAGTCAGATTCGGTCTGTAGCTCAGTTGGTGTAGAGCGCA 120  
DB 61 CGGATTGGTGTAGAGCCGAGAGTCAGATTCGGTCTGTAGCTCAGTTGGTGTAGAGCGCA 120

QY 121 CCCCTGATAAAGGTGAGTTCGGAGTTCGAATCTGCCAGACCCACCAATTCGCGGATG 180  
DB 121 CCCCTGATAAAGGTGAGTTCGGAGTTCGAATCTGCCAGACCCACCAATTCGCGGATG 180

QY 181 GCCAGTGTCAATGGGCCATAGCTCAGCTGGGAGAGCGCTGCTTGCACGAGGAGT 240  
DB 181 GCCAGTGTCAATGGGCCATAGCTCAGCTGGGAGAGCGCTGCTTGCACGAGGAGT 240

QY 241 CAGGAGTTCGATCCTCTTGGCTCCACCATCACTCAGATCGCTGAAAGCTCAGAAATG 300  
DB 241 CAGGAGTTCGATCCTCTTGGCTCCACCATCACTCAGATCGCTGAAAGCTCAGAAATG 300

QY 301 AACATTGGTGTCAATGTGATTCGTTGCTTGGCCAGAACTGTTCTTTAAAAATTT 360  
DB 301 AACATTGGTGTCAATGTGATTCGTTGCTTGGCCAGAACTGTTCTTTAAAAATTT 360

QY 361 GGTATGTGATAGAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGT 420  
DB 361 GGTATGTGATAGAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGT 420

QY 421 TTTCGAGTTCAAGCGGAAATTTTCGCGCAATTCGCTCTTCAGTTCAGTTCAGTTCAGTTCAGT 480  
DB 421 TTTCGAGTTCAAGCGGAAATTTTCGCGCAATTCGCTCTTCAGTTCAGTTCAGTTCAGTTCAGT 480

QY 481 AGATTGCTTGGGGTTATAT 499  
DB 481 AGATTGCTTGGGGTTATAT 499

RESULT 3  
US-08-765-332-111  
; Sequence 111, Application US/08765332

MOLECULE TYPE: cDNA  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
US-08-765-332-114

Query Match 100.0%; Score 499; DB 3; Length 499;  
Best Local Similarity 100.0%; Pred. No. 2e-165;  
Matches 499; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATCGAAGACTTCAGCTTCTTCATAAGTTCACACAGCAATTCGTTGATTCACCTTCGAAAA 60  
DB 1 ATCGAAGACTTCAGCTTCTTCATAAGTTCACACAGCAATTCGTTGATTCACCTTCGAAAA 60

QY 61 GCATTTGGTGTAGACCCGAGAGTTCGATTCGGTCTGTAGCTCAGTTGGTGTAGAGCGCA 120  
DB 61 GCATTTGGTGTAGACCCGAGAGTTCGATTCGGTCTGTAGCTCAGTTGGTGTAGAGCGCA 120

QY 121 CCCCTGATAAAGGTGAGTTCGGAGTTCGAATCTGCCAGACCCACCAATTCGCGGATG 180  
DB 121 CCCCTGATAAAGGTGAGTTCGGAGTTCGAATCTGCCAGACCCACCAATTCGCGGATG 180

QY 181 GCCAGTGTCAATGGGCCATAGCTCAGCTGGGAGAGCGCTGCTTGCACGAGGAGT 240  
DB 181 GCCAGTGTCAATGGGCCATAGCTCAGCTGGGAGAGCGCTGCTTGCACGAGGAGT 240

QY 241 CAGGAGTTCGATCCTCTTGGCTCCACCATCACTCAGATCGCTGAAAGCTCAGAAATG 300  
DB 241 CAGGAGTTCGATCCTCTTGGCTCCACCATCACTCAGATCGCTGAAAGCTCAGAAATG 300

QY 301 AACATTGGTGTCAATGTGATTCGTTGCTTGGCCAGAACTGTTCTTTAAAAATTT 360  
DB 301 AACATTGGTGTCAATGTGATTCGTTGCTTGGCCAGAACTGTTCTTTAAAAATTT 360

QY 361 GGTATGTGATAGAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGT 420  
DB 361 GGTATGTGATAGAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGT 420

QY 421 TTTCGAGTTCAAGCGGAAATTTTCGCGCAATTCGCTCTTCAGTTCAGTTCAGTTCAGTTCAGT 480  
DB 421 TTTCGAGTTCAAGCGGAAATTTTCGCGCAATTCGCTCTTCAGTTCAGTTCAGTTCAGTTCAGT 480

QY 481 AGATTGCTTGGGGTTATAT 499  
DB 481 AGATTGCTTGGGGTTATAT 499

RESULT 2  
US-09-448-894-114  
; Sequence 114, Application US/09448894  
; Patent No. 6312903  
; GENERAL INFORMATION:  
; APPLICANT: JANNES, GEERT  
; ROSSAU, RUDI  
; VAN HEUVERSWYN, HUGO  
; TITLE OF INVENTION: SIMULTANEOUS DETECTION, IDENTIFICATION  
; AND DIFFERENTIATION OF EUBACTERIAL TAXA USING A  
; HYBRIDIZATION ASSAY  
; NUMBER OF SEQUENCES: 216  
; CORRESPONDENCE ADDRESS:  
; ADDRESS: NIXON & VANDERHIE P.C.  
; STREET: 1100 NORTH GLEBE ROAD, 8TH FLOOR  
; CITY: WASHINGTON  
; STATE: D.C.  
; COUNTRY: USA  
; ZIP: 22201  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/448,894  
; FILING DATE: 29-No. 6312903-1999

Patent No. 6025132  
GENERAL INFORMATION:  
APPLICANT: JANNES, GEERT  
APPLICANT: ROSSAU, RUDI  
APPLICANT: VAN HEUVERSWYN, HUGO  
TITLE OF INVENTION: SIMULTANEOUS DETECTION, IDENTIFICATION  
AND DIFFERENTIATION OF EUBACTERIAL TAXA USING A  
NUMBER OF SEQUENCES: 216  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: NIXON & VANDERHYE P.C.  
STREET: 1100 NORTH GLEBE ROAD, 8TH FLOOR  
CITY: WASHINGTON  
STATE: D.C.  
COUNTRY: USA  
ZIP: 22201  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/765,332  
FILING DATE: 23-DEC-1996  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: WO PCT/EP95/02452  
FILING DATE: 23-JUN-1995  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: EP 95870032.0  
FILING DATE: 07-APR-1995  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: EP 94870106.5  
FILING DATE: 24-JUN-1994  
ATTORNEY/AGENT INFORMATION:  
NAME: SADOFF, B.J.  
REGISTRATION NUMBER: 36,663  
REFERENCE/DOCKET NUMBER: 1487-14  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 703-816-4091  
INFORMATION FOR SEQ ID NO: 111:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 471 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: CDNA  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
US-08-765-332-111

Query Match 54.68; Score 272.6; DB 3; Length 471;  
Best Local Similarity 80.7%; Pred. No. 6.1e-86;  
Matches 409; Conservative 0; Mismatches 54; Indels 44; Gaps 6;  
QY 1 ATCGAAGACCTTCAGCTTCTTCATAGTTCCACAGCAATGCTGATTCACCTTGGGAAA 60  
Db 1 ATCGAAGATCCGGCTTCTTCATAGTCCACAGCAATGCTGATTCACCTGGTTA--- 57  
QY 61 CGGATTTGGTTGAGACCGGAGAGTGACAGATTGGGTCTGTAGCTCAGTTGGTTAGACGCA 120  
Db 58 -----GACGATTGGGTCTGTAGCTCAGTTGGTTAGACGCA 93  
QY 121 CCCTGATAGGGTGGGCTCGGATCGAATCTGCCAGACCCACCAATTTGTCGGGATG 180  
Db 94 CCCTGATAGGGTGGGCTCGGATCGAATCTGCCAGACCCACCAATTTGTCGGGATG 153  
QY 181 GCCAGTG---TCAATGGGGCCATAGCTCAGCTGGGAGAGCGCTGCTTTTCACGCGAGA 237  
Db 154 CTGGGTGATCGGATACGGGCCATAGCTCAGCTGGGAGAGCGCTGCTTTTCACGCGAGA 213  
QY 238 GGTCAAGGATTCGATCTCTCTTGGCTCCACCATCACTCAGGATCGTGAAGAGCTCAGAA 297

Db 214 GGTCAAGGATTCGATCTCTCTTGGCTCCACCATCTA-AAACAATCGTGAAGCTCAGAA 272  
QY 298 ATGAACATTTGGTAGTTCAATTTGATTTCTGGTCTTTGCGCCAGAACTGTTCTTTAAAAA 357  
Db 273 ATGAATTTCTGGTGGATGAACATTTGATTTCTGGTCTTTGCGCCAGAACTGTTCTTTAAAAA 332  
QY 358 TTTGGGTATGTGATAGAAGTGA---CTACAGAGGTTGTTTTCACGTCGAGTTGTT---AATCA 412  
Db 333 TTCGGGTATGTGATAGAAGTGAAGTGAATGATCTCTTTTTCACGTCGATCATTCAGTCA 392  
QY 413 AGCAAAATTTGGAGTTCAAGCGCAATTTTTCGGGCAATGCTGCTTTCACGTTACGAAT 472  
Db 393 AGTAAATTTGGAGTTCAAGCGCAATTTTTCGGGCAATGCTGCTTTCACGTTACGAAT 472  
QY 473 CTATAACCAAGATTTGGGTTTATAT 499  
Db 445 GTATAACCAAGATTTGGGTTTATAT 471

## RESULT 4

US-09-448-894-111  
Sequence 111, Application US/09448894  
Patent No. 6312903  
GENERAL INFORMATION:  
APPLICANT: JANNES, GEERT  
ROSSAU, RUDI  
VAN HEUVERSWYN, HUGO  
TITLE OF INVENTION: SIMULTANEOUS DETECTION, IDENTIFICATION  
AND DIFFERENTIATION OF EUBACTERIAL TAXA USING A  
HYBRIDIZATION ASSAY  
NUMBER OF SEQUENCES: 216  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: NIXON & VANDERHYE P.C.  
STREET: 1100 NORTH GLEBE ROAD, 8TH FLOOR  
CITY: WASHINGTON  
STATE: D.C.  
COUNTRY: USA  
ZIP: 22201  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/448,894  
FILING DATE: 29-NOV-1999  
CLASSIFICATION: <Unknown>  
07-APR-1995  
24-JUN-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/765,332  
FILING DATE: <Unknown>  
APPLICATION NUMBER: EP 95870032.0  
FILING DATE: 07-APR-1995  
APPLICATION NUMBER: EP 94870106.5  
FILING DATE: 24-JUN-1994  
ATTORNEY/AGENT INFORMATION:  
NAME: SADOFF, B.J.  
REGISTRATION NUMBER: 36,663  
REFERENCE/DOCKET NUMBER: 1487-14  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 703-816-4091  
TELEFAX: 703-816-4100  
INFORMATION FOR SEQ ID NO: 111:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 471 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: CDNA  
HYPOTHETICAL: NO  
ANTI-SENSE: NO

```
;
SEQUENCE DESCRIPTION: SEQ ID NO: 111;
US-09-448-894-111

Query Match          54.6%; Score 272.6; DB 4; Length 471;
Best Local Similarity 80.7%; Pred. No. 6.1e-86;
Matches 409; Conservative 0; Mismatches 54; Indels 44; Gaps 6;

QY 1 ATCGAGACTTCAGCTCTTCATAGTTCCACACAGCAATGCTGATTCACCTTCGCAAAA 60
   |||||||  |||||||  |||||||  |||||||  |||||||  |||||||  |||||||  |||||||
Db 1 ATCGAGATCCCGCTCTTCATAGCTCCACACAGCAATGCTGATTCACCTTCGCAAAA 57
   |||||||  |||||||  |||||||  |||||||  |||||||  |||||||  |||||||  |||||||

QY 61 GCGATTGGGTGAGACCCGAGAGTGGGTCTGTAGCTCAGTTCAGTGGTTAGAGCGCA 120
   |||||||  |||||||  |||||||  |||||||  |||||||  |||||||  |||||||  |||||||
Db 58 -----GACGATTGGGTCTGTAGCTCAGTTCAGTGGTTAGAGCGCA 93
   |||||||  |||||||  |||||||  |||||||  |||||||  |||||||  |||||||  |||||||

QY 121 CCCCTGATAGAGGTGAGGTGCGGAGTTCGAATCTGCCACACACCAATGTCGGGATG 180
   |||||||  |||||||  |||||||  |||||||  |||||||  |||||||  |||||||  |||||||
Db 94 CCCCTGATAGAGGTGAGGTGCGGAGTTCGAATCTGCCACACACCAATGTCGGGTG 153
   |||||||  |||||||  |||||||  |||||||  |||||||  |||||||  |||||||  |||||||

QY 181 GCCAGTG---TCAATGGGGCCATAGCTCAGCTGGGAGAGCGCTGCTTTGCAGCGAGA 237
   |||||||  |||||||  |||||||  |||||||  |||||||  |||||||  |||||||  |||||||
Db 154 CTGGTGATCCGATACGCGGCCATAGCTCAGCTGGGAGAGCGCTGCTTTGCAGCGAGA 213
   |||||||  |||||||  |||||||  |||||||  |||||||  |||||||  |||||||  |||||||

QY 238 GGTGAGAGTTCGATCCTCTTGGCTCCACACATCACTCAGGATCGCTGAAAGCTCAGAA 297
   |||||||  |||||||  |||||||  |||||||  |||||||  |||||||  |||||||  |||||||
Db 214 GGTGAGAGTTCGATCCTCTTGGCTCCACACATCTA-AAACAATFCGCGAAAGCTCAGAA 272
   |||||||  |||||||  |||||||  |||||||  |||||||  |||||||  |||||||  |||||||

QY 298 ATGAACATTTGGTACGTTCAATGTTGATTTCTTGGCTTTCGCGCAGAACTGTTCTTTAAAAA 357
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Db 273 ATGAATGTTGGTGAACAACTGATTTCTTGGCTTTCGCGCAGAACTGTTCTTTAAAAA 332
   |||||||  |||||||  |||||||  |||||||  |||||||  |||||||  |||||||  |||||||

QY 358 TTTGGGTATGATAGAGTGA---CTAACAGCGCTGTTTCACTGCAGCTGTTGTT--AATCA 412
   |||||||  |||||||  |||||||  |||||||  |||||||  |||||||  |||||||  |||||||
Db 333 TTTGGGTATGATAGAGTGA---CTAACAGCGCTGTTTCACTGCAGCTGTTGTT--AATCA 392
   |||||||  |||||||  |||||||  |||||||  |||||||  |||||||  |||||||  |||||||

QY 413 AGGCAAAATTCGAGTTCAGCGCGAATTTTCGCGCAATGCTGCTCTTCAGGTTACGAAT 472
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Db 393 AGGCAAAATTCGAGTTCAGCGCGAATTTTCGCGCAATGCTGCTCTTCAGGTTACGAAT 444
   |||||||  |||||||  |||||||  |||||||  |||||||  |||||||  |||||||  |||||||

QY 473 CTATAACACAGATTGCTTTGGGGTTATAT 499
   |||||||  |||||||  |||||||  |||||||  |||||||  |||||||  |||||||  |||||||
Db 445 GTATAACACAGATTGCTTTGGGGTTATAT 471
   |||||||  |||||||  |||||||  |||||||  |||||||  |||||||  |||||||  |||||||

RESULT 5
US-09-765-332-113
; Sequence 113, Application US/08765332
; Patent No. 6025132
; GENERAL INFORMATION:
; APPLICANT: JANNES, GEERT
; APPLICANT: ROSSAU, RUDI
; APPLICANT: VAN HEUVERSWYN, HUGO
; TITLE OF INVENTION: SIMULTANEOUS DETECTION, IDENTIFICATION
; TITLE OF INVENTION: AND DIFFERENTIATION OF EUBACTERIAL TAXA USING A
; TITLE OF INVENTION: HYBRIDIZATION ASSAY
; NUMBER OF SEQUENCES: 216
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: NIXON & VANDERHYE P.C.
; STREET: 1100 NORTH GLEBE ROAD, 8TH FLOOR
; CITY: WASHINGTON
; STATE: D.C.
; COUNTRY: USA
; ZIP: 22201
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08765,332
; FILING DATE: 23-DEC-1996
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
```

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; APPLICATION NUMBER: WO PCT/EP95/02452
; FILING DATE: 23-JUN-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: EP 95870032.0
; FILING DATE: 07-APR-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: EP 94870106.5
; FILING DATE: 24-JUN-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: SADOFF, B. J.
; REGISTRATION NUMBER: 36,663
; REFERENCE/DOCKET NUMBER: 1487-14
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 703-816-4091
; TELEFAX: 703-816-4100
; INFORMATION FOR SEQ ID NO: 113:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 504 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; US-08-765-332-113

Query Match          53.2%; Score 265.4; DB 3; Length 504;
Best Local Similarity 78.5%; Pred. No. 2.1e-83;
Matches 412; Conservative 0; Mismatches 66; Indels 47; Gaps 6;

QY 1 ATCGAAGACTTCAGCTCTTCATAGTTCCACACAGCAATGCTGATTCACCTTCGCAAAA 60
   |||||||  |||||||  |||||||  |||||||  |||||||  |||||||  |||||||  |||||||
Db 1 ATCGAAGACACCGGCTTCGTCATAGTCCACACAGCAATGCTGATTCACCTTCGCAAAA 60
   |||||||  |||||||  |||||||  |||||||  |||||||  |||||||  |||||||  |||||||

QY 61 GCGATTGGGTGAGACCCGAGAGTGGGTCTGTAGCTCAGTTCAGTGGTTAGAGCGCA 120
   |||||||  |||||||  |||||||  |||||||  |||||||  |||||||  |||||||  |||||||
Db 61 GCGATTGGGTGAGACCCGAGAGTGGGTCTGTAGCTCAGTTCAGTGGTTAGAGCGCA 120
   |||||||  |||||||  |||||||  |||||||  |||||||  |||||||  |||||||  |||||||

QY 121 CCCCTGATAGAGGTGAGGTGCGGAGTTCGAATCTGCCACACACCAATGTCGGGATG 180
   |||||||  |||||||  |||||||  |||||||  |||||||  |||||||  |||||||  |||||||
Db 121 CCCCTGATAGAGGTGAGGTGCGGAGTTCGAATCTGCCACACACCAATGTCGGGATG 172
   |||||||  |||||||  |||||||  |||||||  |||||||  |||||||  |||||||  |||||||

QY 181 GCCAGTGCAAAATGGGGCCATAGCTCAGCTGGGAGAGCGCTGCTTTGCAGCGAGAGGT 240
   |||||||  |||||||  |||||||  |||||||  |||||||  |||||||  |||||||  |||||||
Db 173 -----AAGGGCCATAGCTCAGCTGGGAGAGCGCTGCTTTGCAGCGAGAGGT 221
   |||||||  |||||||  |||||||  |||||||  |||||||  |||||||  |||||||  |||||||

QY 241 CAGGAGTTCGATCCTCTTGGCTCCACCATCACTCAGATCGCTGGAAGCTCAGAAATG 300
   |||||||  |||||||  |||||||  |||||||  |||||||  |||||||  |||||||  |||||||
Db 222 CAGCGGTTGATCCCGCTTGGCTCCACCATTAACCTCTAG-TCCGCCGAAAGCTCAGAAATG 280
   |||||||  |||||||  |||||||  |||||||  |||||||  |||||||  |||||||  |||||||

QY 301 AACATT-----CGTAGTTCAATGTTGATTTCTGCTTTGCGGCC 339
   |||||||  |||||||  |||||||  |||||||  |||||||  |||||||  |||||||  |||||||
Db 281 AGTGTTTACCAGGATGAGGTTGATTCGCTGGGTGGAACATTGATTTCTGGACTTTGCGGCC 340
   |||||||  |||||||  |||||||  |||||||  |||||||  |||||||  |||||||  |||||||

QY 340 AGAAGTGTCTTTAAAAATTTGGGTATGATAGAAAGTGACTTAACAGCG---TCTTTCA 395
   |||||||  |||||||  |||||||  |||||||  |||||||  |||||||  |||||||  |||||||
Db 341 AGAAGTGTCTTTAAAAATTTGGGTATGATAGAAAGTGACTTAACAGCG---TCTTTCA 400
   |||||||  |||||||  |||||||  |||||||  |||||||  |||||||  |||||||  |||||||

QY 396 CTGCAGCTGTTGTAATCAAGGCAAAATTTGCGAGTTC-AAGCGCGAAATTTTCGCGCAATG 454
   |||||||  |||||||  |||||||  |||||||  |||||||  |||||||  |||||||  |||||||
Db 401 GCGAGCATGTCGCGTCAAGGTAATAATTTGCGGTGTTCTCTCTATGCAAAATTTTCGCGCAATG 460
   |||||||  |||||||  |||||||  |||||||  |||||||  |||||||  |||||||  |||||||

QY 455 CGTCTTCAGTTACGAATCTATAACACAGATTGCTTTGGGGTTATAT 499
   |||||||  |||||||  |||||||  |||||||  |||||||  |||||||  |||||||  |||||||
Db 461 CGTCTTCAGTTA-TAGACAGTAACACAGATTGCTTTGGGGTTATAT 504
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RESULT 6
US-09-448-894-113
; Sequence 113, Application US/09448894
; Patent No. 6312903
; GENERAL INFORMATION:
; APPLICANT: JANNES, GEERT
```



```
Query Match      39.8%; Score 198.4; DB 3; Length 468;
Best Local Similarity 72.8%; Pred. No. 6.9e-60;
Matches 367; Conservative 0; Mismatches 96; Indels 41; Gaps 7;

QY 1 ATCGAAGACTTCAGCTCTTCATAGTCCACACGAAATGCTTGATTCAGTTCGCGAAA 60
Db 1 ATCGAAGACTTCAGCTCTTCATAGTCCACACGAAATGCTTGATTCAGTTCGCGAAA 60
QY 61 GCGATTGGTGTGACCCGAGAGTGGCTGTGTAGCTCAGTTCAGTTCGCGAAA 120
Db 61 GCGATTGGTGTGACCCGAGAGTGGCTGTGTAGCTCAGTTCAGTTCGCGAAA 120
QY 121 CCCCTGATAAGGTTGAGGTCGGCATCTGCAATCTGCCACGACCAATGTCGCGATG 180
Db 121 CCCCTGATAAGGTTGAGGTCGGCATCTGCAATCTGCCACGACCAATGTCGCGATG 180
QY 114 CCCCTGATAAGGTTGAGGTCGGCATCTGCAATCTGCCACGACCAATGTCGCGATG 167
Db 114 CCCCTGATAAGGTTGAGGTCGGCATCTGCAATCTGCCACGACCAATGTCGCGATG 167
QY 181 GCCAGTGTCAAAATGGGCGCCATAGCTCAGCTGGGAGAGCGCTGCTTTCACGAGGAGGT 240
Db 181 GCCAGTGTCAAAATGGGCGCCATAGCTCAGCTGGGAGAGCGCTGCTTTCACGAGGAGGT 240
QY 241 CAGGAGTTCGATCCTCTGGCTCCACCA--TCAACTCAGATCGCTGAAAGCTCAGAAA 298
Db 241 CAGGAGTTCGATCCTCTGGCTCCACCA--TCAACTCAGATCGCTGAAAGCTCAGAAA 298
QY 216 CAGCGGTTGATCCCGCTTGGCTCCACCCAGCTTGCAGTTTGTCAAAGCTTAGAAA 275
Db 216 CAGCGGTTGATCCCGCTTGGCTCCACCCAGCTTGCAGTTTGTCAAAGCTTAGAAA 275
QY 299 TGAACATTTGAGTTCATGTTGATTTCTGTTTTCGCGAGAGCGCTGCTTTCACGAGGAGGT 358
Db 299 TGAACATTTGAGTTCATGTTGATTTCTGTTTTCGCGAGAGCGCTGCTTTCACGAGGAGGT 358
QY 276 TGAATATTCG-CGTGCAATATTTGATTTCTGAACCTT--ATCAGAATCGTTCTTAAAT 332
Db 276 TGAATATTCG-CGTGCAATATTTGATTTCTGAACCTT--ATCAGAATCGTTCTTAAAT 332
QY 359 TTGGGTATGTGATAGA---AGTGACTAACAGCGTGTTCACGACGCTTGTTCATCAAGT 415
Db 359 TTGGGTATGTGATAGA---AGTGACTAACAGCGTGTTCACGACGCTTGTTCATCAAGT 415
QY 333 TTGGGTATGTGATAGAAGATAGACTGGACAGCAGCTTTCAGTGGTGTGCTCAGGCTAA 392
Db 333 TTGGGTATGTGATAGAAGATAGACTGGACAGCAGCTTTCAGTGGTGTGCTCAGGCTAA 392
QY 416 CAAAATTTGCGAGTTTCAAGCGCGAAATTTTCGCGGAATGTCGCTTTCAGTTACGAATCTA 475
Db 416 CAAAATTTGCGAGTTTCAAGCGCGAAATTTTCGCGGAATGTCGCTTTCAGTTACGAATCTA 475
QY 393 GGTAAAATTTGTCAGTAATTTACAAGTTTTCGCGGAATGTTGTCTTCAC-----AGTA 444
Db 393 GGTAAAATTTGTCAGTAATTTACAAGTTTTCGCGGAATGTTGTCTTCAC-----AGTA 444
QY 476 TAACAGATTCGTTGGGGTTATAT 499
Db 476 TAACAGATTCGTTGGGGTTATAT 499
QY 445 TAACAGATTCGTTGGGGTTATAT 468
Db 445 TAACAGATTCGTTGGGGTTATAT 468

RESULT 8
US-09-448-894-115
; Sequence 115, Application US/09448894
; Patent No. 6312903
; GENERAL INFORMATION:
; APPLICANT: JANNES, GEERT
; APPLICANT: ROSSAU, RUDI
; APPLICANT: VAN HEUVERSWYN, HUGO
; TITLE OF INVENTION: SIMULTANEOUS DETECTION, IDENTIFICATION
; AND DIFFERENTIATION OF EUBACTERIAL TAXA USING A
; HYBRIDIZATION ASSAY
; NUMBER OF SEQUENCES: 216
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: NIXON & VANDERHUYE P.C.
; STREET: 1100 NORTH GLEBE ROAD, 8TH FLOOR
; CITY: WASHINGTON
; STATE: D.C.
; COUNTRY: USA
; ZIP: 22201
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/448.894
; FILING DATE: 29-JUN-1999
; CLASSIFICATION: <Unknown>
; 07-APR-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/765,332
```

```
; FILING DATE: <Unknown>
; APPLICATION NUMBER: EP 95870032.0
; FILING DATE: 07-APR-1995
; APPLICATION NUMBER: EP 94870106.5
; FILING DATE: 24-JUN-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: SADOFF, B.J.
; REGISTRATION NUMBER: 36,663
; REFERENCE/DOCKET NUMBER: 1487-14
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 703-816-4091
; TELEFAX: 703-816-4100
; INFORMATION FOR SEQ ID NO: 115:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 468 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: CDNA
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; SEQUENCE DESCRIPTION: SEQ ID NO: 115:
US-09-448-894-115
```

```
Query Match      39.8%; Score 198.4; DB 4; Length 468;
Best Local Similarity 72.8%; Pred. No. 6.9e-60;
Matches 367; Conservative 0; Mismatches 96; Indels 41; Gaps 7;

QY 1 ATCGAAGACTTCAGCTCTTCATAGTCCACACGAAATGCTTGATTCAGTTCGCGAAA 60
Db 1 ATCGAAGACTTCAGCTCTTCATAGTCCACACGAAATGCTTGATTCAGTTCGCGAAA 60
QY 61 GCGATTGGTGTGACCCGAGAGTGGCTGTGTAGCTCAGTTCAGTTCGCGAAA 120
Db 61 GCGATTGGTGTGACCCGAGAGTGGCTGTGTAGCTCAGTTCAGTTCGCGAAA 120
QY 121 CCCCTGATAAGGTTGAGGTCGGCATCTGCAATCTGCCACGACCAATGTCGCGATG 180
Db 121 CCCCTGATAAGGTTGAGGTCGGCATCTGCAATCTGCCACGACCAATGTCGCGATG 180
QY 114 CCCCTGATAAGGTTGAGGTCGGCATCTGCAATCTGCCACGACCAATGTCGCGATG 167
Db 114 CCCCTGATAAGGTTGAGGTCGGCATCTGCAATCTGCCACGACCAATGTCGCGATG 167
QY 181 GCCAGTGTCAAAATGGGCGCCATAGCTCAGCTGGGAGAGCGCTGCTTTCACGAGGAGGT 240
Db 181 GCCAGTGTCAAAATGGGCGCCATAGCTCAGCTGGGAGAGCGCTGCTTTCACGAGGAGGT 240
QY 241 CAGGAGTTCGATCCTCTGGCTCCACCA--TCAACTCAGATCGCTGAAAGCTCAGAAA 298
Db 241 CAGGAGTTCGATCCTCTGGCTCCACCA--TCAACTCAGATCGCTGAAAGCTCAGAAA 298
QY 216 CAGCGGTTGATCCCGCTTGGCTCCACCCAGCTTGCAGTTTGTCAAAGCTTAGAAA 275
Db 216 CAGCGGTTGATCCCGCTTGGCTCCACCCAGCTTGCAGTTTGTCAAAGCTTAGAAA 275
QY 299 TGAACATTTGAGTTCATGTTGATTTCTGTTTTCGCGAGAGCGCTGCTTTCACGAGGAGGT 358
Db 299 TGAACATTTGAGTTCATGTTGATTTCTGTTTTCGCGAGAGCGCTGCTTTCACGAGGAGGT 358
QY 276 TGAATATTCG-CGTGCAATATTTGATTTCTGAACCTT--ATCAGAATCGTTCTTAAAT 332
Db 276 TGAATATTCG-CGTGCAATATTTGATTTCTGAACCTT--ATCAGAATCGTTCTTAAAT 332
QY 359 TTGGGTATGTGATAGA---AGTGACTAACAGCGTGTTCACGACGCTTGTTCATCAAGT 415
Db 359 TTGGGTATGTGATAGA---AGTGACTAACAGCGTGTTCACGACGCTTGTTCATCAAGT 415
QY 333 TTGGGTATGTGATAGAAGATAGACTGGACAGCAGCTTTCAGTGGTGTGCTCAGGCTAA 392
Db 333 TTGGGTATGTGATAGAAGATAGACTGGACAGCAGCTTTCAGTGGTGTGCTCAGGCTAA 392
QY 416 CAAAATTTGCGAGTTTCAAGCGCGAAATTTTCGCGGAATGTCGCTTTCAGTTACGAATCTA 475
Db 416 CAAAATTTGCGAGTTTCAAGCGCGAAATTTTCGCGGAATGTCGCTTTCAGTTACGAATCTA 475
QY 393 GGTAAAATTTGTCAGTAATTTACAAGTTTTCGCGGAATGTTGTCTTCAC-----AGTA 444
Db 393 GGTAAAATTTGTCAGTAATTTACAAGTTTTCGCGGAATGTTGTCTTCAC-----AGTA 444
QY 476 TAACAGATTCGTTGGGGTTATAT 499
Db 476 TAACAGATTCGTTGGGGTTATAT 499
QY 445 TAACAGATTCGTTGGGGTTATAT 468
Db 445 TAACAGATTCGTTGGGGTTATAT 468
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RESULT 9
US-08-765-332-112
; Sequence 112, Application US/08765332
; Patent No. 6025132
; GENERAL INFORMATION:
; APPLICANT: JANNES, GEERT
; APPLICANT: ROSSAU, RUDI
; APPLICANT: VAN HEUVERSWYN, HUGO
```

;; TITLE OF INVENTION: SIMULTANEOUS DETECTION, IDENTIFICATION  
;; TITLE OF INVENTION: AND DIFFERENTIATION OF EUBACTERIAL TAXA USING A  
;; TITLE OF INVENTION: HYBRIDIZATION ASSAY  
;; NUMBER OF SEQUENCES: 216  
;; CORRESPONDENCE ADDRESS:  
;; ADDRESSEE: NIXON & VANDERHYE P.C.  
;; STREET: 1100 NORTH GLEBE ROAD, 8TH FLOOR  
;; CITY: WASHINGTON  
;; STATE: D.C.  
;; COUNTRY: USA  
;; ZIP: 22201  
;; COMPUTER READABLE FORM:  
;; MEDIUM TYPE: Floppy disk  
;; COMPUTER: IBM PC compatible  
;; OPERATING SYSTEM: PC-DOS/MS-DOS  
;; SOFTWARE: PatentIn Release #1.0, Version #1.30  
;; CURRENT APPLICATION DATA:  
;; APPLICATION NUMBER: WO PCT/EP95/02452  
;; FILING DATE: 23-JUN-1995  
;; PRIOR APPLICATION DATA:  
;; APPLICATION NUMBER: EP 95870032.0  
;; FILING DATE: 07-APR-1995  
;; PRIOR APPLICATION DATA:  
;; APPLICATION NUMBER: EP 94870106.5  
;; FILING DATE: 24-JUN-1994  
;; ATTORNEY/AGENT INFORMATION:  
;; NAME: SADOFF, B.J.  
;; REGISTRATION NUMBER: 36,663  
;; REFERENCE/DOCKET NUMBER: 1487-14  
;; TELECOMMUNICATION INFORMATION:  
;; TELEPHONE: 703-816-4091  
;; TELEFAX: 703-816-4100  
;; INFORMATION FOR SEQ ID NO: 112:  
;; SEQUENCE CHARACTERISTICS:  
;; LENGTH: 520 base pairs  
;; TYPE: nucleic acid  
;; STRANDEDNESS: single  
;; MOLECULE TYPE: CDNA  
;; HYPOTHETICAL: NO  
;; ANTI-SENSE: NO  
;; US-08-765-332-112

Query Match 38.7%; Score 193.2; DB 3; Length 520;  
Best Local Similarity 72.8%; Pred. No. 4.9e-58;  
Matches 386; Conservative 0; Mismatches 103; Indels 41; Gaps 9;

QY 1 ATCGAAGACTTCAGCTTCTTCAATAGTCCACACGAATTCGTTGATTCACATGCGGAAA 60  
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DB 1 ATCGAAGACATCAGCTTCTTCAATAGTATCCACACGAATTCGTTGATTCACATGCGAAG 60  
||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||  
QY 61 GCATTTGGTTGAGACCCGAGAGTGACGATGGTGTGTAGCTCAGTTGTTGAGCGCA 120  
||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||  
DB 61 ATGCTGTAAACGGACCGCGTTTATA-----GGTCTGTAGCTCAGTTGTTGAGCGCA 114  
||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||  
QY 121 CCCTGATAGGTTGAGTGGCGAGTTCGAATCTGCCACGACCCACCAATTCGCGGATG 180  
||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||  
DB 115 CCCTGATAGGTTGAGTGGCGAGTTCGAATCTGCCACGACCCACCAATTCGCGGATG 171  
||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||  
QY 181 GCAGTGTCAATGGGCGCATAGCTCAGCTGGGAGAGCGCTGCTTTCGACGAGGAGGT 240  
||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||  
DB 172 TCAGAAGAATACGGGCGCATAGCTCAGCTGGGAGAGCGCTGCTTTCGACGAGGAGGT 231  
||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||  
QY 241 CAGGAGTTCGATCTCTTGGCTCCACCATCACTCAG-----ATCGCTGAAGC 291  
||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||  
DB 232 CAGCGGTTGATCCCGCTGGCTGGCTCCACCATCTCTCTGTTGGGTCGAGTGAAGAGT 291  
||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||  
QY 292 TCAGAATGA-----ACATGGTAGTTCAATGTTGATTTCTGCTCTTT----- 334  
||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||

DB 292 TCAGAATGATGCCCTTCAGGTTTGTCTCTGTGAGTCTGCTGATTTCTGCTCTTTGACCG 351  
QY 335 GCGCCAGAACCTGTTCTTTAAAAAATTTGGGTATGTGATAGAGTGAACAGCGTG-TTT 393  
||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||  
DB 352 GTACGAAAATCGTTCTTTAAAAAATTTGGGTATGTGATAGAGTGAACAGCGTG-TTT 411  
||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||  
QY 394 CACTGCACGTTG--TTAATCAAGGCAAAATTTG--CGAGTTCAAGCGGCAATTTTCGGCG 449  
||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||  
DB 412 CACTGGCAATTCATCTGCTCAAGGTAAATTTGTAGTTCTCAAGACGCAAAATTTTCGGCG 471  
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QY 450 AATGTCGCTTTCACGTTACGAATCTATAACAGAGATTGCTTGGGTTATAT 499  
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DB 472 AATGTCGCTTTCAGGAT-TGACAGAGTACACAGATTGCTTGGGTTATAT 520  
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RESULT 10  
US-09-448-894-112  
; Sequence 112, Application US/09448894  
; Patent No. 6312503  
; GENERAL INFORMATION:  
; APPLICANT: JANNES, GEERT  
; VAN HEUVERSWYN, HUGO  
; ROSSAU, RUDI  
; TITLE OF INVENTION: SIMULTANEOUS DETECTION, IDENTIFICATION  
; AND DIFFERENTIATION OF EUBACTERIAL TAXA USING A  
; HYBRIDIZATION ASSAY  
; NUMBER OF SEQUENCES: 216  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: NIXON & VANDERHYE P.C.  
; STREET: 1100 NORTH GLEBE ROAD, 8TH FLOOR  
; CITY: WASHINGTON  
; STATE: D.C.  
; COUNTRY: USA  
; ZIP: 22201  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/448,894  
; FILING DATE: 29-No. 6312503-1999  
; CLASSIFICATION: <Unknown>  
; 07-APR-1995  
; 24-JUN-1994  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/765,332  
; FILING DATE: <Unknown>  
; APPLICATION NUMBER: EP 95870032.0  
; FILING DATE: 07-APR-1995  
; APPLICATION NUMBER: EP 94870106.5  
; FILING DATE: 24-JUN-1994  
; ATTORNEY/AGENT INFORMATION:  
; NAME: SADOFF, B.J.  
; REGISTRATION NUMBER: 36,663  
; REFERENCE/DOCKET NUMBER: 1487-14  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 703-816-4091  
; TELEFAX: 703-816-4100  
; INFORMATION FOR SEQ ID NO: 112:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 520 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; MOLECULE TYPE: CDNA  
; HYPOTHETICAL: NO  
; ANTI-SENSE: NO  
; SEQUENCE DESCRIPTION: SEQ ID NO: 112:  
US-09-448-894-112

Query Match 38.7%; Score 193.2; DB 4; Length 520;  
Best Local Similarity 72.8%; Pred. No. 4.9e-58;

Matches 386; Conservative 0; Mismatches 103; Indels 41; Gaps 9;

```
QY 1 ATCGAGACTTCAGCTTCTTCAATAGCTCCACACGAATTCCTGATTCACATTCGGAAGA 60
||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
Db 1 ATCGAAGACATCAGCTTCTTCAATAGCTCCACACGAATTCCTGATTCACATTCGGAAGA 60
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QY 61 GCGATTGGTTCAGACCCGAGAGTACGAGTTCGGTCTGTAGTTCAGTTCGTTAGAGCGCA 120
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Db 61 AATGCTGTAAACCGACCGCTGTATATATATATATATATATATATATATATATATATAT 114
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QY 121 CCCGTGATAGAGGTGAGTTCGAGTTCGAATCTGCCACAGACCCCAATTCGCGGATG 180
||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
Db 115 CCCGTGATAGAGGTGAGTTCGAGTTCGAATCTGCCACAGACCCCAATTCGCGGATG 171
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QY 181 GCCAGTGTCAATGGGGCCATAGCTCAGCTGGGAGAGCGCTGCTTGCACGAGGAGT 240
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Db 172 TCGAAGAAATACGGGGCCATAGCTCAGCTGGGAGAGCGCTGCTTGCACGAGGAGT 231
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QY 241 CAGGAGTTCGATCTCTTGGTTCACCATCAACTCAGC-----ATCGCTGAAAGC 291
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Db 232 CAGCGTTCGATCCCGCTTGGCTCCACCACTCTCTCGTGTGGGTGAGTGTAAAGAGT 291
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QY 292 TCAGAAATGA-----ACATTTGAGTTCAATGTTGATTTCTGCTCTT----- 334
||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
Db 292 TCAGAAATGATGCGCTTTCAGGTTTCTCTGCTTGTAGTGTGATTTCTGCTCTTTGACCG 351
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QY 335 GCGCCAGAACTGTTCTTAAATTTGGTATCTGATAGTGAAGTGAACAGCGTG-TTT 393
||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
Db 352 GTACGAAATCGTCTTAAATTTGGATATGTAGTGAAGTGAAGTGAATTAATTCCTT 411
||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
QY 394 CACTGCACCTGT--TTAATCAAGGCAAAATTTG--CGAGTTCAAGCGCAATTTTCGGGG 449
||||| ||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
Db 412 CACTGCCAATGTATCTGGTCAAGTAAATTTGTAGTCTCAAGACGCAAAATTTTCGGGG 471
||||| ||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
QY 450 AATGTCGTCTTCAGTTAGCAATCTATAACAGATTCGTTGGGGTTATAT 499
||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
Db 472 AATGTCGTCTTCAGAT-TCAGACAGTAACAGATTCGTTGGGGTTATAT 520
||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
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RESULT 11
US-08-765-332-195
; Sequence 195, Application US/08765332
; Patent No. 6025132
; GENERAL INFORMATION:
; APPLICANT: JANNES, GEERT
; APPLICANT: ROSSAU, RUDI
; APPLICANT: VAN HEUVERSWYN, HUGO
; TITLE OF INVENTION: SIMULTANEOUS DETECTION, IDENTIFICATION
; AND DIFFERENTIATION OF EUBACTERIAL TAXA USING A
; HYBRIDIZATION ASSAY
; NUMBER OF SEQUENCES: 216
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: NIXON & VANDERHVE P.C.
; STREET: 1100 NORTH GLEBE ROAD, 8TH FLOOR
; CITY: WASHINGTON
; STATE: D.C.
; COUNTRY: USA
; ZIP: 22201
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/765,332
; FILING DATE: 23-DEC-1996
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: WO PCT/EP95/02452
; FILING DATE: 23-JUN-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: EP 95870032.0
; FILING DATE: 07-APR-1995
```

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; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: EP 94870106.5
; FILING DATE: 24-JUN-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: SADOFF, B.J.
; REGISTRATION NUMBER: 36,663
; REFERENCE/DOCKET NUMBER: 1487-14
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 703-816-4091
; TELEFAX: 703-816-4100
; INFORMATION FOR SEQ ID NO: 195:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 470 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: CDNA
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; US-08-765-332-195
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Query Match 21.8%; Score 108.8; DB 3; Length 470;
Best Local Similarity 72.9%; Pred. No. 2e-28;
Matches 159; Conservative 0; Mismatches 47; Indels 12; Gaps 1;

QY 91 TGGTCTGTAGCTCAGTTGGTTAGAGCGACCCCTGATAGAGGTGAGGTGCGAGTTTCA 150
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Db 75 TAGGCTGTAGCTCAGTTGGTTAGAGCGACCCCTGATAGAGGTGAGGTGCGAGTTTCA 134
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QY 151 ATCTGCCAGACCCACCAATTTGCGGATGGCCAGTGT-----CAATGGGCG 198
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Db 135 GTCCACTCAGCTGCGGAGCGCTGCTTTCGAAAGTGGAAAGTACTGCACGTGATGGGGC 194
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QY 199 CATAGCTCAGCTGGGAGCGCTGCTTTCGACGAGGAGTGCAGAGTTTCGATCCCT 258
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Db 195 TATAGCTCAGCTGGGAGCGCTGCTTTCGACGAGGAGTGCAGCGTTTCGATCCCGCT 254
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QY 259 TGCTCCACCATCAACTCAGCTGCTGTTGAAAGTCTAGA 296
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Db 255 TAGCTCCACCATATAGTCTCTGTTTCAATCACTTCTAGA 292
||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
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RESULT 12
US-09-448-894-195
; Sequence 195, Application US/09448894
; Patent No. 6312903
; GENERAL INFORMATION:
; APPLICANT: JANNES, GEERT
; APPLICANT: ROSSAU, RUDI
; APPLICANT: VAN HEUVERSWYN, HUGO
; TITLE OF INVENTION: SIMULTANEOUS DETECTION, IDENTIFICATION
; AND DIFFERENTIATION OF EUBACTERIAL TAXA USING A
; HYBRIDIZATION ASSAY
; NUMBER OF SEQUENCES: 216
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: NIXON & VANDERHVE P.C.
; STREET: 1100 NORTH GLEBE ROAD, 8TH FLOOR
; CITY: WASHINGTON
; STATE: D.C.
; COUNTRY: USA
; ZIP: 22201
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/448,894
; FILING DATE: 29-NOV-1999
; CLASSIFICATION: <Unknown>
; 07-APR-1995
; 24-JUN-1994
; PRIOR APPLICATION DATA:
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APPLICATION NUMBER: 08/765,332  
FILING DATE: <Unknown>  
APPLICATION NUMBER: EP 95870032.0  
FILING DATE: 07-APR-1995  
APPLICATION NUMBER: EP 94870106.5  
FILING DATE: 24-JUN-1994  
ATTORNEY/AGENT INFORMATION:  
NAME: SADOFF, B.J.  
REGISTRATION NUMBER: 36,663  
REFERENCE/DOCKET NUMBER: 1487-14  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 703-816-4091  
TELEFAX: 703-816-4100  
INFORMATION FOR SEQ ID NO: 195:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 470 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
SEQUENCE DESCRIPTION: SEQ ID NO: 195:  
US-09-448-894-195

Query Match 21.8%; Score 108.8; DB 4; Length 470;  
Best Local Similarity 72.9%; Pred. No. 2e-28;  
Matches 159; Conservative 0; Mismatches 47; Indels 12; Gaps 1;  
QY 91 TGGGTCTGTAGCTAGCTGTGGTGTAGAGCGCACCCCTGTATAGAGGTGAGGTGGCGAGTTCGA 150  
DB 75 TAGCCTTGTAGCTAGCTAGCTGTGGTGTAGAGCGCACCCCTGTATAGAGGTGAGGTGGTGGTCAA 134  
QY 151 ATGTGCCAGACCCACCAATGTCGGGATGCCAGTGT-----CAATGCGGC 198  
DB 135 GTCACTCAGCGCTACCACTTCGAAAGTGGAAAGGTACTGCACGTGACTGTATGCGGC 194  
QY 199 CATAGCTCAGCTGGGAGCGCCTGCTTTGCAGCGAGGAGTTCAGGAGTTCGATCCCT 258  
DB 195 TATAGCTCAGCTGGGAGCGCCTGCCTTCACGAGGAGTTCAGCGGTTTCGATCCCGCT 254  
QY 259 TGGCTCACCATCACTCAGCTCAGCTGCGTGAAGTTCAGA 296  
DB 255 TAGCTCACCATCACTCAGCTCAGCTGATTTCAATACCTTCAGA 292

RESULT 13  
US-08-765-332-215  
Sequence 215, Application US/08765332  
Patent No. 6025132  
GENERAL INFORMATION:  
APPLICANT: JANNES, GEERT  
APPLICANT: ROSSAU, RUDI  
APPLICANT: VAN HEUVERSWYN, HUGO  
TITLE OF INVENTION: SIMULTANEOUS DETECTION, IDENTIFICATION  
AND DIFFERENTIATION OF EUBACTERIAL TAXA USING A  
TITLE OF INVENTION: HYBRIDIZATION ASSAY  
NUMBER OF SEQUENCES: 216  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: NIXON & VANDERHVE P.C.  
STREET: 1100 NORTH GLEBE ROAD, 8TH FLOOR  
CITY: WASHINGTON  
STATE: D.C.  
COUNTRY: USA  
ZIP: 22201  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/765,332  
FILING DATE: 23-DEC-1996

CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: WO PCT/EP95/02452  
FILING DATE: 23-JUN-1995  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: EP 95870032.0  
FILING DATE: 07-APR-1995  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: EP 94870106.5  
FILING DATE: 24-JUN-1994  
ATTORNEY/AGENT INFORMATION:  
NAME: SADOFF, B.J.  
REGISTRATION NUMBER: 36,663  
REFERENCE/DOCKET NUMBER: 1487-14  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 703-816-4091  
TELEFAX: 703-816-4100  
INFORMATION FOR SEQ ID NO: 215:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 463 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
US-08-765-332-215  
Query Match 19.8%; Score 99; DB 3; Length 463;  
Best Local Similarity 66.8%; Pred. No. 5.5e-25;  
Matches 161; Conservative 0; Mismatches 70; Indels 10; Gaps 1;  
QY 92 GGGTCTGTAGCTCAGTGTGGTGTAGAGCGCACCCCTGTATAGAGGTGAGGTGGCGAGTTCGAA 151  
DB 115 GGGCTTATAGCTAGCTAGCTGTGGTGTAGAGCGCACCCCTGTATAGAGGTGAGGTGGTTCGAG 174  
QY 152 TCTCCCCAGACCCACCAATGTCGGGA-----TGGCCAGTGTCAAAATGGGCGCAT 201  
DB 175 TCCACTTAGGCCCACTTTTGAATAAACCTTCTTTTATATGTTAATAAGGGGCTT 234  
QY 202 AGCTCAGCTGGGAGAGCGCCTGCTTTGCACGAGGAGTTCAGAGTTCGATCCTCCTTGG 261  
DB 235 AGCTCAGCTGGGAGAGCGCCTGCTTTGCACGAGGAGTTCAGAGTTCGATCCTCCTAGG 294  
QY 262 CTCCACCATCACTCAGATCGCTGAAAGCTCAAAATGAACATTTGGTAGTTCAATGTTG 321  
DB 295 CTCACCAAGAGATAGTTGTTCTTTGAAACTAGATAAGAAAAGTTAGTGTAAAAAGACG 354  
QY 322 A 322  
DB 355 A 355

RESULT 14  
US-09-448-894-215  
Sequence 215, Application US/09448894  
Patent No. 6312903  
GENERAL INFORMATION:  
APPLICANT: JANNES, GEERT  
APPLICANT: ROSSAU, RUDI  
APPLICANT: VAN HEUVERSWYN, HUGO  
TITLE OF INVENTION: SIMULTANEOUS DETECTION, IDENTIFICATION  
AND DIFFERENTIATION OF EUBACTERIAL TAXA USING A  
HYBRIDIZATION ASSAY  
NUMBER OF SEQUENCES: 216  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: NIXON & VANDERHVE P.C.  
STREET: 1100 NORTH GLEBE ROAD, 8TH FLOOR  
CITY: WASHINGTON  
STATE: D.C.  
COUNTRY: USA  
ZIP: 22201  
COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/448,894  
FILING DATE: 29-NOV-1999  
CLASSIFICATION: <Unknown>  
07-APR-1995  
24-JUN-1994

PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/765,332  
FILING DATE: <Unknown>  
APPLICATION NUMBER: EP 95870032.0  
FILING DATE: 07-APR-1995  
APPLICATION NUMBER: EP 94870106.5  
FILING DATE: 24-JUN-1994

ATTORNEY/AGENT INFORMATION:  
NAME: SADOFF, B.J.  
REGISTRATION NUMBER: 36,663  
REFERENCE/DOCKET NUMBER: 1487-14  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 703-816-4091  
TELEFAX: 703-816-4100

INFORMATION FOR SEQ ID NO: 215:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 463 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
SEQUENCE DESCRIPTION: SEQ ID NO: 215:

US-09-448-894-215

Query Match 19.8%; Score 99; DB 4; Length 463;  
Best Local Similarity 66.8%; Pred. No. 5.5e-25;  
Matches 161; Conservative 0; Mismatches 70; Indels 10; Gaps 1;

QY 92 GGGTCTGTAGCTCAGTGGTTAGAGCGCACCCCTGTATAGGGTGAGGTGCGGCAGTTCGAA 151  
DB 115 GGGCCCTATAGCTCAGCTGGTTAGAGCGCACCCCTGTATAGGGTGAGGTGCGGTTCGAG 174  
QY 152 TCTGCCAGACCCACCAATTTGTCGGA-----TGGCCAGTGTCAAAATGGGCCAT 201  
DB 175 TCCACTTAGGCCACCTTTTGTGATAAACCTTTCTTTTATATGTTAATAAGGGCCCT 234  
QY 202 AGCTACGTGGGAGAGCGCTGTTTGCACGAGAGGTGAGGTTCGATCCCTCCTGG 261  
DB 235 AGCTACGTGGGAGAGCGCTGTTTGCACGAGAGGTGAGGTTCGATCCCGCTAGG 294  
QY 262 CTCACCATCACTCAGATCGCTGAAAGCTCAGAAATCAAGATGCTGTTCAATGTTG 321  
DB 295 CTCACCAAGATAGTTGTTCTTTGAAAACTAGATAAGAAAGTAGTGTAAAAAGACG 354  
QY 322 A 322  
DB 355 A 355

RESULT 15  
US-08-765-332-214  
; Sequence 214, Application US/08765332  
; Patent No. 6025132  
; GENERAL INFORMATION:  
; APPLICANT: JANNES, GEERT  
; APPLICANT: ROSSAU, RUDI  
; APPLICANT: VAN HEUVERSWYN, HUGO  
; TITLE OF INVENTION: SIMULTANEOUS DETECTION, IDENTIFICATION  
; TITLE OF INVENTION: AND DIFFERENTIATION OF EUBACTERIAL TAXA USING A  
; TITLE OF INVENTION: HYBRIDIZATION ASSAY  
; NUMBER OF SEQUENCES: 216

CORRESPONDENCE ADDRESS:  
ADDRESSEE: NIXON & VANDERHVE P.C.  
STREET: 1100 NORTH GLEBE ROAD, 8TH FLOOR  
CITY: WASHINGTON  
STATE: D.C.  
COUNTRY: USA  
ZIP: 22201  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/765,332  
FILING DATE: 23-DEC-1996  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: WO PCT/EP95/02452  
FILING DATE: 23-JUN-1995  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: EP 95870032.0  
FILING DATE: 07-APR-1995  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: EP 94870106.5  
FILING DATE: 24-JUN-1994  
ATTORNEY/AGENT INFORMATION:  
NAME: SADOFF, B.J.  
REGISTRATION NUMBER: 36,663  
REFERENCE/DOCKET NUMBER: 1487-14  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 703-816-4091  
TELEFAX: 703-816-4100  
INFORMATION FOR SEQ ID NO: 214:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 475 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
US-08-765-332-214

Query Match 19.8%; Score 99; DB 3; Length 475;  
Best Local Similarity 66.8%; Pred. No. 5.6e-25;  
Matches 161; Conservative 0; Mismatches 70; Indels 10; Gaps 1;

QY 92 GGGTCTGTAGCTCAGTGGTTAGAGCGCACCCCTGTATAGGGTGAGGTGCGGCAGTTCGAA 151  
DB 115 GGGCCCTATAGCTCAGCTGGTTAGAGCGCACCCCTGTATAGGGTGAGGTGCGGTTCGAG 174  
QY 152 TCTGCCAGACCCACCAATTTGTCGGA-----TGGCCAGTGTCAAAATGGGCCAT 201  
DB 175 TCCACTTAGGCCACCTTTTGTGATAAACCTTTCTTTTATATGTTAATAAGGGCCCT 234  
QY 202 AGCTACGTGGGAGAGCGCTGTTTGCACGAGAGGTGAGGTTCGATCCCTCCTGG 261  
DB 235 AGCTACGTGGGAGAGCGCTGTTTGCACGAGAGGTGAGGTTCGATCCCGCTAGG 294  
QY 262 CTCACCATCACTCAGATCGCTGAAAGCTCAGAAATCAAGATGCTGTTCAATGTTG 321  
DB 295 CTCACCAAGATAGTTGTTCTTTGAAAACTAGATAAGAAAGTAGTGTAAAAAGACG 354  
QY 322 A 322  
DB 355 A 355

Search completed: February 1, 2003, 04:24:18  
Job time : 27.9431 secs

GenCore version 5.1.3  
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: February 1, 2003, 03:05:22 ; Search time 27.7673 Seconds  
(without alignments) 8073.649 Million cell updates/sec

Title: US-09-931-486-114  
 Perfect score: 499  
 Sequence: 1 ATCGAAGACTTCAGCTCTT.....CAGATTGCTTGGGTTATAT 499

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 396772 seqs, 224632407 residues

Total number of hits satisfying chosen parameters: 793544

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Minimum DB seq length: 0
Maximum DB seq length: 2000000000
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Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 s

Database : Published Applications NA:\*

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2: /cgn2_6/ptodata/1/pubpna/US07_PUBCOMB.seq:
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4: /cgn2_6/ptodata/1/pubpna/US06_PUBCOMB.seq:
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10: /cgn2_6/ptodata/1/pubpna/US09_PUBCOMB.seq:
11: /cgn2_6/ptodata/1/pubpna/US10_NEW_PUB.seq:
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13: /cgn2_6/ptodata/1/pubpna/US60_NEW_PUB.seq:
14: /cgn2_6/ptodata/1/pubpna/US60_PUBCOMB.seq:

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

| Result No. | Score | Query |         |    | ID                 | Description       |
|------------|-------|-------|---------|----|--------------------|-------------------|
|            |       | Match | Length  | DB |                    |                   |
| 1          | 98.8  | 19.5  | 640681  | 10 | US-09-750-988-1    | Sequence 1, Appl  |
| 2          | 97.2  | 19.5  | 582     | 10 | US-09-863-086-87   | Sequence 87, Appl |
| 3          | 97.2  | 19.5  | 590     | 10 | US-09-863-086-88   | Sequence 88, Appl |
| c 4        | 92    | 18.4  | 243     | 10 | US-09-815-242-1358 | Sequence 1358, Ap |
| c 5        | 91.4  | 18.3  | 255     | 10 | US-09-815-242-1377 | Sequence 1377, Ap |
| c 6        | 91.4  | 18.3  | 255     | 10 | US-09-815-242-1402 | Sequence 1402, Ap |
| c 7        | 91.4  | 18.3  | 255     | 10 | US-09-815-242-1415 | Sequence 1415, Ap |
| c 8        | 91.4  | 18.3  | 255     | 10 | US-09-815-242-1423 | Sequence 1423, Ap |
| c 9        | 91.4  | 18.3  | 255     | 10 | US-09-815-242-1431 | Sequence 1431, Ap |
| c 10       | 91.4  | 18.3  | 255     | 10 | US-09-815-242-1454 | Sequence 1454, Ap |
| c 11       | 91.4  | 18.3  | 255     | 10 | US-09-815-242-1473 | Sequence 1473, Ap |
| c 12       | 91.4  | 18.3  | 255     | 10 | US-09-815-242-1475 | Sequence 1475, Ap |
| c 13       | 91.4  | 18.3  | 255     | 10 | US-09-815-242-1544 | Sequence 1544, Ap |
| c 14       | 91.4  | 18.3  | 255     | 10 | US-09-815-242-1638 | Sequence 1638, Ap |
| c 15       | 91.4  | 18.3  | 255     | 10 | US-09-815-242-1638 | Sequence 1638, Ap |
| 16         | 87    | 17.4  | 549     | 10 | US-09-863-086-92   | Sequence 92, Appl |
| 17         | 87    | 17.4  | 603     | 10 | US-09-863-086-85   | Sequence 85, Appl |
| 18         | 87    | 17.4  | 603     | 10 | US-09-863-086-86   | Sequence 86, Appl |
| 19         | 87    | 17.4  | 3309400 | 9  | US-09-738-626-1    | Sequence 1, Appl  |

## ALIGNMENTS

## RESULT 1

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US-09-790-988-1
; Sequence 1, Application US/09790988
; Patent No. US20020127687A1
; GENERAL INFORMATION:
; APPLICANT: SHIGENOBU, SHUJI
; APPLICANT: WATANABE, HIDEMI
; APPLICANT: HATTORI, MASAHIRA
; APPLICANT: SNAKAI, YOSHIYUKI
; TITLE OF INVENTION: GENOME DNA OF
; FILE REFERENCE: 081356/0159
; CURRENT APPLICATION NUMBER: US/09/
; CURRENT FILING DATE: 2001-02-23
; PRIOR APPLICATION NUMBER: JP2000-1
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 640681
; TYPE: DNA
; ORGANISM: Buchnera sp.
US-09-790-988-1

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[illegible]

; Sequence 87, Application US/09863086  
; Patent No. US20020048762a1  
; GENERAL INFORMATION:  
; APPLICANT: Rossau, Rudi  
; TITLE OF INVENTION: HYBRIDIZATION PROBES DERIVED FROM THE SPACER  
; REGION BETWEEN THE 16S A  
; NUMBER OF SEQUENCES: 104  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Merchant, Gould, Smith, Edell, Welter & Schmidt  
; STREET: 3100 No. US20020048762a1west Center, 90 S. 7th Street  
; CITY: Minneapolis  
; STATE: MN  
; COUNTRY: U.S.A.  
; ZIP: 55402  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: DOS  
; SOFTWARE: FastSeq Version 1.5  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/863,086  
; FILING DATE: 22-May-2001  
; CLASSIFICATION: <Unknown>  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 09/312,520  
; FILING DATE: <Unknown>  
; APPLICATION NUMBER: 08/412,614  
; FILING DATE: 29-MAR-1995  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Hillson, Randall A  
; REGISTRATION NUMBER: 31,838  
; REFERENCE/DOCKET NUMBER: 8076.75USC1  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 612/332-5300  
; TELEFAX: 612/332/9081  
; TELEX: <Unknown>  
; INFORMATION FOR SEQ ID NO: 87:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 582 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: Genomic DNA  
; HYPOTHETICAL: NO  
; ANTI-SENSE: NO  
; FRAGMENT TYPE: <Unknown>  
; ORIGINAL SOURCE:  
; SEQUENCE DESCRIPTION: SEQ ID NO: 87:  
US-09-863-086-87

Query Match 19.5%; Score 97.2; DB 10; Length 582;  
Best Local Similarity 75.8%; Pred. No. 3.6e-23;  
Matches 135; Conservative 0; Mismatches 38; Indels 5; Gaps 1;  
QY 92 GGGTCTGTAGCTCAGTTGGTTAGAGCGCACCCCTGTGATAAGGGTGAGTGGCGGAGTTTCGAA 151  
|||||  
Db 98 GGGTCTGTAGCTCAGTGGTTAGAGCACCGCTCTGTGATAAGGGGGGGTGGTTTCGAA 157  
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QY 152 TCTGCCAGACCCACCAAAATTTGCGGGATGCGGAGTGCATCAAAATGGGGCCATAGCTCAGCTG 211  
|||||  
Db 158 TCAACCAAGACCCACCA-----GGTTTCTTGAGAGGGAATGGGGGTGTAGCTCAGCTG 212  
|||||  
QY 212 GGAGAGCGCTGCTTTGCAAGCAGGAGGTGATCGATCCCTCGCTCCACCA 269  
|||||  
Db 213 GGAGAGCGCTGCTTTGCAAGCAGGATGTCATCGGTTTCATCCCGTTCACCTCCACCA 270  
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RESULT 3  
US-09-863-086-88  
; Sequence 88, Application US/09863086  
; Patent No. US20020048762a1  
; GENERAL INFORMATION:  
; APPLICANT: Rossau, Rudi

; TITLE OF INVENTION: HYBRIDIZATION PROBES DERIVED FROM THE SPACER  
; REGION BETWEEN THE 16S A  
; NUMBER OF SEQUENCES: 104  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Merchant, Gould, Smith, Edell, Welter & Schmidt  
; STREET: 3100 No. US20020048762a1west Center, 90 S. 7th Street  
; CITY: Minneapolis  
; STATE: MN  
; COUNTRY: U.S.A.  
; ZIP: 55402  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: DOS  
; SOFTWARE: FastSeq Version 1.5  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/863,086  
; FILING DATE: 22-May-2001  
; CLASSIFICATION: <Unknown>  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 09/312,520  
; FILING DATE: <Unknown>  
; APPLICATION NUMBER: 08/412,614  
; FILING DATE: 29-MAR-1995  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Hillson, Randall A  
; REGISTRATION NUMBER: 31,838  
; REFERENCE/DOCKET NUMBER: 8076.75USC1  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 612/332-5300  
; TELEFAX: 612/332/9081  
; TELEX: <Unknown>  
; INFORMATION FOR SEQ ID NO: 88:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 590 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: Genomic DNA  
; HYPOTHETICAL: NO  
; ANTI-SENSE: NO  
; FRAGMENT TYPE: <Unknown>  
; ORIGINAL SOURCE:  
; SEQUENCE DESCRIPTION: SEQ ID NO: 88:  
US-09-863-086-88

Query Match 19.5%; Score 97.2; DB 10; Length 590;  
Best Local Similarity 75.8%; Pred. No. 3.6e-23;  
Matches 135; Conservative 0; Mismatches 38; Indels 5; Gaps 1;

QY 92 GGGTCTGTAGCTCAGTTGGTTAGAGCGCACCCCTGTGATAAGGGTGAGTGGCGGAGTTTCGAA 151  
|||||  
Db 98 GGGTCTGTAGCTCAGTGGTTAGAGCACCGCTCTGTGATAAGGGGGGTGCTGTTGTTTCGAA 157  
|||||  
QY 152 TCTGCCAGACCCACCAAAATTTGCGGGATGCGGAGTGCATCAAAATGGGGCCATAGCTCAGCTG 211  
|||||  
Db 158 TCAACCAAGACCCACCA-----GGTTTCTTGAGAGGGAATGGGGGTGTAGCTCAGCTG 212  
|||||  
QY 212 GGAGAGCGCTGCTTTGCAAGCAGGAGGTGATCGATCCCTCGCTCCACCA 269  
|||||  
Db 213 GGAGAGCGCTGCTTTGCAAGCAGGATGTCATCGGTTTCGATCCCGTTCACCTCCACCA 270  
|||||

RESULT 4  
US-09-815-242-1358/c  
; Sequence 1358, Application US/09815242  
; Patent No. US20020061569a1  
; GENERAL INFORMATION:  
; APPLICANT: Haselbeck, Robert  
; APPLICANT: Ohlsen, Kari L.  
; APPLICANT: Zyskind, Judith W.  
; APPLICANT: Wall, Daniel  
; APPLICANT: Trawick, John D.

|    | Query Match                                                      | 18.3% | Score 91.4;        | DB 10; | Length 255; |
|----|------------------------------------------------------------------|-------|--------------------|--------|-------------|
|    | Best Local Similarity                                            | 77.0% | Pred. No. 2.le-21; |        |             |
|    | Matches 127; Conservative                                        | 0;    | Mismatches 31;     | Indels | 7; Gaps     |
| QY | 89 ATTGGGTCCTAGCTCAGTGTGGTTAGACGCACCCCTGATAAGGTCGAGGTCGCAGTTC    | 148   |                    |        |             |
|    |                                                                  |       |                    |        |             |
| Dd | 158 AATGGGCGCTATAGCTCAGCTGTGGTTAGACGCACCCCTGATNAGGTCGAGTGGTGTTTC | 99    |                    |        |             |
|    |                                                                  |       |                    |        |             |
| QY | 149 GAATCTGCCACAGACCACCAATTCTCGGGATGGCCAGTGTCAAATGGGGCCATAGCTCAG | 208   |                    |        |             |
|    |                                                                  |       |                    |        |             |
| Dd | 98 GAGTCCACTAGGCCACCATT-----AATTAAATACCTATTGGSGGGCTTAGCTCAG      | 46    |                    |        |             |
|    |                                                                  |       |                    |        |             |
| QY | 209 CTGGGAGAGCCCTGCTTTGCACGAGGATCAGGAGTTCGATC                    | 253   |                    |        |             |
|    |                                                                  |       |                    |        |             |
| b  | 45 CTCGGAGAGCCCTGCTTTGCACGAGGATCAGCGGTTTCGATC                    | 1     |                    |        |             |
|    |                                                                  |       |                    |        |             |

```

RESULT 6
US-09-815-242-1402/c
; Sequence 1402, Application US/09815242
; Patent NO. US20020061569A1
; GENERAL INFORMATION:
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Karl L.
; APPLICANT: Zyskind, Judith W.
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John D.
; APPLICANT: Carr, Grant J.
; APPLICANT: Yamamoto, Robert T.
; APPLICANT: Xu, H. Howard
; TITLE OF INVENTION: Identification of Essential Genes in
; TITLE OF INVENTION: Prokaryotes

```

```

1 FILE REFERENCE: ELITRA.011A
2
3 CURRENT APPLICATION NUMBER: US/09/0815,242
4
5 CURRENT FILING DATE: 2001-03-21
6
7 PRIOR APPLICATION NUMBER: 60/191,078
8
9 PRIOR FILING DATE: 2000-03-21
10
11 PRIOR APPLICATION NUMBER: 60/206,848
12
13 PRIOR FILING DATE: 2000-05-23
14
15 PRIOR APPLICATION NUMBER: 60/207,727
16
17 PRIOR FILING DATE: 2000-05-26
18
19 PRIOR APPLICATION NUMBER: 60/242,578
20
21 PRIOR FILING DATE: 2000-10-23
22
23 PRIOR APPLICATION NUMBER: 60/253,625
24
25 PRIOR FILING DATE: 2000-11-27
26
27 PRIOR APPLICATION NUMBER: 60/257,931
28
29 PRIOR FILING DATE: 2000-12-22
30
31 PRIOR APPLICATION NUMBER: 60/269,308
32
33 PRIOR FILING DATE: 2001-02-16
34
35 NUMBER OF SEQ ID NOS: 14110
36
37 SOFTWARE: FastSeq for Windows Version 4.0
38
39 SEQ ID NO 1402
40
41 LENGTH: 255
42
43 TYPE: DNA
44
45 ORGANISM: Staphylococcus aureus

```

APPLICANT: YAMAMOTO, ROBERT T  
APPLICANT: YAMAMOTO, ROBERT T

;; TITLE OF INVENTION: Identification of Essential Genes in  
;; FILE REFERENCE: ELITRA.011A  
;; CURRENT APPLICATION NUMBER: US/09/815,242  
;; CURRENT FILING DATE: 2001-03-21  
;; PRIOR APPLICATION NUMBER: 60/191,078  
;; PRIOR FILING DATE: 2000-03-21  
;; PRIOR APPLICATION NUMBER: 60/206,848  
;; PRIOR FILING DATE: 2000-05-23  
;; PRIOR APPLICATION NUMBER: 60/207,727  
;; PRIOR FILING DATE: 2000-05-26  
;; PRIOR APPLICATION NUMBER: 60/242,578  
;; PRIOR FILING DATE: 2000-10-23  
;; PRIOR APPLICATION NUMBER: 60/253,625  
;; PRIOR FILING DATE: 2000-11-27  
;; PRIOR APPLICATION NUMBER: 60/257,931  
;; PRIOR FILING DATE: 2000-12-22  
;; PRIOR APPLICATION NUMBER: 60/269,308  
;; PRIOR FILING DATE: 2001-02-16  
;; NUMBER OF SEQ ID NOS: 14110  
;; SOFTWARE: FastSeq for Windows Version 4.0  
;; SEQ ID NO 1431  
;; LENGTH: 255  
;; TYPE: DNA  
;; ORGANISM: Staphylococcus aureus  
US-09-815-242-1431

Query Match 18.3%; Score 91.4; DB 10; Length 255;  
Best Local Similarity 77.0%; Pred. No. 2.1e-21;  
Matches 127; Conservative 0; Mismatches 31; Indels 7; Gaps 1;  
QY 89 ATTGGGTCTAGTCTAGTGGTTAGAGCGCACCCCTGATAAGGTCAGGTCGGCAGTTC 148  
Db 158 AATGGGCTATAGCTAGCTAGCTGGTTAGAGCGCACCCCTGATAAGGTCAGGTCGGTGTTC 99  
QY 149 GAATCTGCCAGACCCACCAATTTGCGGGATGGCCAGTGTCAAAATGGGGCCATAGCTCAG 208  
Db 98 GAGTCCACTTAGGCCACCACTT-----AATTAATACCTATTGTTGGGGCTTACCTCAG 46  
QY 209 CTGGGAGAGCGCTGCTTTGCACGAGGTCAGGAGTTCAGGATTCGATC 253  
Db 45 CTGGGAGAGCGCTGCTTTGCACGAGGTCAGGAGTTCAGGATTCGATC 1

RESULT 10  
US-09-815-242-1454/c  
;; Sequence 1454, Application US/09815242  
;; Patent No. US20020061569A1  
;; GENERAL INFORMATION:  
;; APPLICANT: Haselbeck, Robert  
;; APPLICANT: Ohlsen, Kari L.  
;; APPLICANT: Zyskind, Judith W.  
;; APPLICANT: Wall, Daniel  
;; APPLICANT: Trawick, John D.  
;; APPLICANT: Carr, Grant J.  
;; APPLICANT: Yamamoto, Robert T.  
;; APPLICANT: Xu, H. Howard  
;; TITLE OF INVENTION: Identification of Essential Genes in  
;; FILE REFERENCE: ELITRA.011A  
;; CURRENT APPLICATION NUMBER: US/09/815,242  
;; CURRENT FILING DATE: 2001-03-21  
;; PRIOR APPLICATION NUMBER: 60/191,078  
;; PRIOR FILING DATE: 2000-03-21  
;; PRIOR APPLICATION NUMBER: 60/206,848  
;; PRIOR FILING DATE: 2000-05-23  
;; PRIOR APPLICATION NUMBER: 60/207,727  
;; PRIOR FILING DATE: 2000-05-26  
;; PRIOR APPLICATION NUMBER: 60/242,578  
;; PRIOR FILING DATE: 2000-10-23  
;; PRIOR APPLICATION NUMBER: 60/253,625  
;; PRIOR FILING DATE: 2000-11-27  
;; PRIOR APPLICATION NUMBER: 60/257,931  
;; PRIOR FILING DATE: 2000-12-22  
;; PRIOR APPLICATION NUMBER: 60/269,308  
;; NUMBER OF SEQ ID NOS: 14110  
;; SOFTWARE: FastSeq for Windows Version 4.0  
;; SEQ ID NO 1459  
;; LENGTH: 255  
;; TYPE: DNA  
;; ORGANISM: Staphylococcus aureus  
US-09-815-242-1459

;; PRIOR FILING DATE: 2000-12-22  
;; PRIOR APPLICATION NUMBER: 60/269,308  
;; PRIOR FILING DATE: 2001-02-16  
;; NUMBER OF SEQ ID NOS: 14110  
;; SOFTWARE: FastSeq for Windows Version 4.0  
;; SEQ ID NO 1454  
;; LENGTH: 255  
;; TYPE: DNA  
;; ORGANISM: Staphylococcus aureus  
US-09-815-242-1454

Query Match 18.3%; Score 91.4; DB 10; Length 255;  
Best Local Similarity 77.0%; Pred. No. 2.1e-21;  
Matches 127; Conservative 0; Mismatches 31; Indels 7; Gaps 1;  
QY 89 ATTGGGTCTAGTCTAGTGGTTAGAGCGCACCCCTGATAAGGTCAGGTCGGCAGTTC 148  
Db 158 AATGGGCTATAGCTAGCTAGCTGGTTAGAGCGCACCCCTGATAAGGTCAGGTCGGTGTTC 99  
QY 149 GAATCTGCCAGACCCACCAATTTGCGGGATGGCCAGTGTCAAAATGGGGCCATAGCTCAG 208  
Db 98 GAGTCCACTTAGGCCACCACTT-----AATTAATACCTATTGTTGGGGCTTACCTCAG 46  
QY 209 CTGGGAGAGCGCTGCTTTGCACGAGGTCAGGAGTTCAGGATTCGATC 253  
Db 45 CTGGGAGAGCGCTGCTTTGCACGAGGTCAGGAGTTCAGGATTCGATC 1

RESULT 11  
US-09-815-242-1459/c  
;; Sequence 1459, Application US/09815242  
;; Patent No. US20020061569A1  
;; GENERAL INFORMATION:  
;; APPLICANT: Haselbeck, Robert  
;; APPLICANT: Ohlsen, Kari L.  
;; APPLICANT: Zyskind, Judith W.  
;; APPLICANT: Wall, Daniel  
;; APPLICANT: Trawick, John D.  
;; APPLICANT: Carr, Grant J.  
;; APPLICANT: Yamamoto, Robert T.  
;; APPLICANT: Xu, H. Howard  
;; TITLE OF INVENTION: Identification of Essential Genes in  
;; FILE REFERENCE: ELITRA.011A  
;; CURRENT APPLICATION NUMBER: US/09/815,242  
;; CURRENT FILING DATE: 2001-03-21  
;; PRIOR APPLICATION NUMBER: 60/191,078  
;; PRIOR FILING DATE: 2000-03-21  
;; PRIOR APPLICATION NUMBER: 60/206,848  
;; PRIOR FILING DATE: 2000-05-23  
;; PRIOR APPLICATION NUMBER: 60/207,727  
;; PRIOR FILING DATE: 2000-05-26  
;; PRIOR APPLICATION NUMBER: 60/242,578  
;; PRIOR FILING DATE: 2000-10-23  
;; PRIOR APPLICATION NUMBER: 60/253,625  
;; PRIOR FILING DATE: 2000-11-27  
;; PRIOR APPLICATION NUMBER: 60/257,931  
;; PRIOR FILING DATE: 2000-12-22  
;; PRIOR APPLICATION NUMBER: 60/269,308  
;; NUMBER OF SEQ ID NOS: 14110  
;; SOFTWARE: FastSeq for Windows Version 4.0  
;; SEQ ID NO 1459  
;; LENGTH: 255  
;; TYPE: DNA  
;; ORGANISM: Staphylococcus aureus  
US-09-815-242-1459

Query Match 18.3%; Score 91.4; DB 10; Length 255;  
Best Local Similarity 77.0%; Pred. No. 2.1e-21;  
Matches 127; Conservative 0; Mismatches 31; Indels 7; Gaps 1;  
QY 89 ATTGGGTCTAGTCTAGTGGTTAGAGCGCACCCCTGATAAGGTCAGGTCGGCAGTTC 148









GenCore version 5.1.3  
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OM nucleic - nucleic search, using sw model

Run on: February 1, 2003, 01:09:56 : Search time 931.115 Seconds  
(without alignments)  
8679.427 Million cell updates/sec

Title: US-09-931-486-114  
Perfect score: 499  
Sequence: 1 ATCGAAGACTTCAGCTTCTT.....CAGATTGCTGGGTTATAT 499

Scoring table: IDENTITY\_NUC  
Gapop 10.0, Gapext 1.0

Searched: 16154066 seqs, 8097743376 residues

Total number of hits satisfying chosen parameters: 32308132

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :

EST.\*  
1: em\_estba.\*  
2: em\_esthum.\*  
3: em\_estin.\*  
4: em\_estnu.\*  
5: em\_estov.\*  
6: em\_estpl.\*  
7: em\_estro.\*  
8: em\_hic.\*  
9: gb\_esti.\*  
10: gb\_est2.\*  
11: gb\_hic.\*  
12: gb\_est3.\*  
13: gb\_est4.\*  
14: gb\_est5.\*  
15: em\_estfun.\*  
16: em\_estom.\*  
17: gb\_gss.\*  
18: em\_gss\_hum.\*  
19: em\_gss\_inv.\*  
20: em\_gss\_pln.\*  
21: em\_gss\_vrt.\*  
22: em\_gss\_fun.\*  
23: em\_gss\_mam.\*  
24: em\_gss\_mus.\*  
25: em\_gss\_other.\*  
26: em\_gss\_pro.\*  
27: em\_gss\_rod.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
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| C 1        | 481.8 | 96.6        | 507    | 17    | BH200120    |
| C 2        | 480.2 | 96.2        | 629    | 17    | BH201541    |
| C 3        | 159   | 31.9        | 639    | 17    | AQ509640    |
| C 4        | 111.8 | 22.4        | 319    | 10    | BE092111    |
| C 5        | 86    | 17.2        | 754    | 17    | BH405252    |
| C 6        | 67.8  | 13.6        | 619    | 9     | AA680996    |

|      |      |      |      |    |          |
|------|------|------|------|----|----------|
| C 7  | 67.4 | 13.5 | 593  | 17 | BH400944 |
| C 8  | 67.4 | 13.5 | 760  | 17 | BH393190 |
| C 9  | 65.6 | 13.1 | 6499 | 17 | BH771024 |
| C 10 | 65.4 | 13.1 | 712  | 17 | BH397037 |
| C 11 | 64.4 | 12.9 | 497  | 13 | BI544108 |
| C 12 | 64.4 | 12.9 | 548  | 13 | BI544155 |
| C 13 | 63.6 | 12.7 | 577  | 17 | BH819575 |
| C 14 | 62.8 | 12.6 | 539  | 13 | BI544086 |
| C 15 | 58.6 | 11.7 | 287  | 17 | BH614410 |
| C 16 | 58.4 | 11.7 | 191  | 17 | AZ578476 |
| C 17 | 54.2 | 10.9 | 617  | 9  | AI526132 |
| C 18 | 53.6 | 10.7 | 904  | 17 | BH159957 |
| C 19 | 53.2 | 10.7 | 2149 | 17 | AQ012191 |
| C 20 | 53   | 10.6 | 696  | 17 | BH383241 |
| C 21 | 52   | 10.4 | 216  | 17 | BH169234 |
| C 22 | 51.8 | 10.4 | 608  | 17 | BH375841 |
| C 23 | 51.6 | 10.3 | 579  | 17 | BH375975 |
| C 24 | 51.6 | 10.3 | 938  | 17 | AZ683938 |
| C 25 | 48.8 | 9.8  | 429  | 17 | BH610380 |
| C 26 | 48.6 | 9.7  | 197  | 17 | BH855109 |
| C 27 | 48.6 | 9.7  | 541  | 17 | BH387664 |
| C 28 | 47.8 | 9.6  | 429  | 17 | BH789301 |
| C 29 | 47.6 | 9.5  | 866  | 17 | AZ542405 |
| C 30 | 47.6 | 9.5  | 901  | 17 | AZ531501 |
| C 31 | 47.4 | 9.5  | 432  | 13 | BI941477 |
| C 32 | 47.2 | 9.5  | 704  | 17 | BH427896 |
| C 33 | 47.2 | 9.5  | 750  | 17 | BH646171 |
| C 34 | 47   | 9.4  | 612  | 17 | AQ989869 |
| C 35 | 47   | 9.4  | 963  | 17 | AZ549906 |
| C 36 | 46.4 | 9.3  | 895  | 17 | BH131476 |
| C 37 | 46   | 9.2  | 937  | 17 | BH156063 |
| C 38 | 45.8 | 9.2  | 984  | 17 | BH680408 |
| C 39 | 45.6 | 9.1  | 414  | 12 | BF872471 |
| C 40 | 45.6 | 9.1  | 702  | 17 | BH586090 |
| C 41 | 45.6 | 9.1  | 759  | 17 | BH427885 |
| C 42 | 45.6 | 9.1  | 969  | 17 | BH147834 |
| C 43 | 45.4 | 9.1  | 810  | 17 | AZ679409 |
| C 44 | 45.4 | 9.1  | 820  | 17 | BH159532 |
| C 45 | 45.4 | 9.1  | 822  | 17 | AZ545581 |

## ALIGNMENTS

RESULT 1  
BH200120/c  
LOCUS  
DEFINITION  
Sml-57J2.TF Sml Schistosoma mansoni genomic clone Sml-57J2, DNA  
507 bp  
DNA  
linear  
GSS 24-OCT-2001  
sequence.  
BH200120  
BH200120.1 GI:16370164  
GSS  
Schistosoma mansoni.  
Schistosoma mansoni  
Eukaryota; Metazoa; Platyhelminthes; Trematoda; Digenea;  
Strigeidida; Schistosomatoidea; Schistosomatidae; Schistosoma.  
Shety,J., Simpson,A., Malek,J., Koo,H., LoVerde,P.T. and El-Sayed  
N.M.  
Use of end sequences from Schistosoma mansoni (Puerto Rico strain)  
Sml BAC library for gene discovery and map construction  
Unpublished (2001)  
Other\_GSSs: Sml-57J2.TF  
Contact: Najib M. El-Sayed  
Department of Eukaryotic Genomics  
The Institute for Genomic Research  
9712 Medical Center Dr., Rockville, MD 20850, USA  
Tel: 301 838 0200  
Fax: 301 838 0208  
Email: nelsayed@tigr.org  
lo.edu)  
Seq primer: M13 For  
Class: BAC ends.

BH400944 AG-ND-158  
BH393190 AG-ND-168  
BH771024 LIMGag74  
BH397037 AG-ND-137  
BI544108 S071 Grac  
BI544155 S129 Grac  
BH19575 BACPP13-E  
BI544086 S042 Grac  
BH614410 1C22AG2 S  
BH578476 23h03 Sho  
AI526132 pc3-2 B11  
BH159957 ENTS11TF  
AQ012191 430PIA043  
BH383241 AG-ND-137  
BH169234 SALK\_0008  
BH375841 AG-ND-133  
BH375975 AG-ND-133  
AZ683938 ENTJ28TR  
BH610380 SALK\_0088  
BH55109 SALK\_0866  
BH387664 AG-ND-157  
BH789301 SALK\_0017  
AZ542405 ENTER07TF  
AZ531501 ENTIC155TF  
BI941477 dg07g11.Y  
BH427896 BOHOK30TR  
BH646171 BOME267TF  
AQ989869 RfC00532  
AZ549906 ENTDN46TR  
BH131476 ENTNU96TF  
BH156063 ENTQT49TR  
BH680408 BOMKA39TF  
BF872471 IL3-ET011  
BH586090 BOHOC43TF  
BH427885 BOHOK30TF  
BH147834 ENTQM48TR  
AZ679409 ENTQ08TF  
BH159532 ENTRY12TR  
AZ545581 ENTGE06TR

|    |     |                                                                |     |
|----|-----|----------------------------------------------------------------|-----|
| QY | 1   | ATCGAAGACTTCAGCTTCTTCATTAAGTTCACACAGCAATTCGTTGATTCACCTTCGCGAAA | 60  |
| DB | 485 | ATCGAAGACTTCAGCTTCTTCATTAAGTTCACACAGCAATTCGTTGATTCACCTTCGCGAAA | 426 |
| QY | 61  | CGGATTGGGTTGAGACCCGAGAGTGACGATTGGGCTGTAGCTCAGTTGGTTAGAGCGCA    | 120 |
| DB | 425 | CGGATTGGGTTGAGACCCGAGAGTGACGATTGGGCTGTAGCTCAGTTGGTTAGAGCGCA    | 366 |
| QY | 121 | CCCCGTATAAGGTCGAGTCGGCGAGTTTCGAACTCTGCCAGACCCACCAATTCGTCGGGATG | 180 |
| DB | 365 | CCCCGTATAAGGTCGAGTCGGCGAGTTTCGAACTCTGCCAGACCCACCAATTCGTCGGGATG | 305 |
| QY | 181 | GCCAGTGTCAAATGGGGCCATAGTCTAGCTGGGAGAGCGCTGCTTTCACGCGCAGGAGGT   | 240 |
| DB | 305 | GCCAGTGTCAAATGGGGCCATAGTCTAGCTGGGAGAGCGCTGCTTTCACGCGCAGGAGGT   | 246 |
| QY | 241 | CAGGAGTTCGATCTCTTGGCTCCACATCAACTCAGCATCGCTGGAAGCTCAGAAATG      | 300 |
| DB | 245 | CAGGAGTTCGATCTCTTGGCTCCACATCAACTCAGCATCGCTGGAAGCTCAGAAATG      | 186 |
| QY | 301 | ACACNTGGTAGTTCAAATGTTGATTTCCTGGTCGCGCAGAACCTGTTCTTTAAAAATTT    | 360 |
| DB | 185 | ACACNTGGTAGTTCAAATGTTGATTTCCTGGTCGCGCAGAACCTGTTCTTTAAAAATTT    | 126 |
| QY | 361 | GGGTATGTCATAGAAGTGACTAACAGCGTGTTCCTACTGCACGTTGTTTAATCAAGCGCAAA | 420 |
| DB | 125 | GGGTATGTCATAGAAGTGACTAACAGCGTGTTCCTACTGCACGTTGTTTAATCAAGCGCAAA | 66  |
| QY | 421 | TTTTCGAGGATTCAGCGCGCAATTTTCGGCGAAATGTCGCTTTCACGTTACGAACTCTAACC | 480 |

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Db 65 TTTCGAGTTCAAGCGCGAATTTTCGGCGAATGTCGTTCTACGTTACGAATCTATACCC 6
QY 481 AGATT 485
Db 5 AGATT 1

RESULT 3
AQ509640/c
LOCUS
DEFINITION
  nbx0096P15f CUGI Rice BAC Library Oryza sativa genomic clone
  nbx0096P15f, DNA sequence.
ACCESSION
  AQ509640
VERSION
  AQ509640.1 GI:4733723
KEYWORDS
  GSS.
SOURCE
  Oryza sativa.
  Oryza sativa.
  Oryza sativa.
  Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
  Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
  Ehrhartoideae; Oryzaceae; Oryza.
  1. (bases 1 to 639)
REFERENCE
  Wing,R.A. and Dean,R.A.
  A BAC End Sequencing Framework to Sequence the Rice Genome
  Unpublished (1998)
  Contact: Wing RA
  Clemson University Genomics Institute
  Clemson University
  100 Jordan Hall, Clemson, SC 29634, USA
  Tel: 864 656 7288
  Fax: 864 656 4293
  Email: rwing@clemson.edu
  Seq primer: TAATACGACTCCTATAGGG
  Class: BAC ends
  High quality sequence start: 86
  High quality sequence stop: 304.
  Location/Qualifiers
    1. .639
      /organism="Oryza sativa"
      /strain="Japonica"
      /cultivar="Nipponbare"
      /db_xref="taxon:4530"
      /clone_lib="CUGI Rice BAC Library"
      /tissue_type="Leaf"
      /lab_host="E. coli DH10B"
      /note="Vector: pBelobAC11; Site_1: HindIII; Site_2:
      HindIII; Rice is one of two most popular grains in the
      world. Half of the world population especially those
      inhabiting highly populated areas of the humid tropics
      and subtropics, rely on rice as their primary source of
      carbohydrate. Monocotyledonous rice is a diploid plant
      (2n=24) with a haploid genome equivalent of 431 Mbp
      (Arumuganathan and Earle, 1991). The relatively small
      genome of rice, three times larger than that of
      Arabidopsis, makes it suitable for genomic studies. In
      order to facilitate positional cloning, physical mapping
      and genome sequencing of rice, we have constructed a BAC
      library from Oryza sativa, Nipponbare variety. The
      library contains 36,864 clones with an average insert size
      of 128.5 kb providing 10.9 haploid genome equivalents. The
      deep coverage allows the isolation a particular sequence
      with a probability of 99.9 %. Two high density filters,
      each containing 18,432 clones (doubly spotted), represent
      the whole library for colony screening."
      158 a 175 c 148 g 156 t 2 others
BASE COUNT
ORIGIN
  Query Match 31.9%; Score 159; DB 17; Length 639;
  Best Local Similarity 71.2%; Pred. No. 3.7e-39;
  Matches 327; Conservative 0; Mismatches 85; Indels 47; Gaps 7;
  QY 33 CACGAATTGCTGATTCACTTGCAGAAAGCGATTGGGTTGAGA-----CCCGAGACTGAC 87
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Db 639 CACGAATTGCTTTATTTCACGTATAGAAAGACAAATTGAGTTAGATAGACTCAAGTAAGAC 580
QY 88 GATTGGGTCTGTAGCTCAGTTGGTTAGAGCGCACCCCTGATAGGGTGAGTGGCGAGTT 147
  |||||
Db 579 GATTGGGTCTGTAGCTCAGTTGGTTAGAGCGCACCCCTGATAGGGTGAGTGGCGAGTT 520
  |||||
QY 148 CGAATCTGCCAGACCCACCAATTTGTCGGGATGCCAGTGTCAAAATGGGCGCATAGCTCA 207
  |||||
Db 519 CGAATCTGCCAGACCCACCA-----TCGATGGGGCCATAGCTCA 478
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QY 208 GCTGGGAGAGCGCTGTTTGCAGCGAGGAGTTCAGAGTTTCGATCTCTCTTGGCTCCAC 267
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Db 477 GCTGGGAGAGCGCTGCTTGCAGCGAGGAGTTCAGAGTTTCGATCTCTCTTGGCTCCAC 418
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QY 268 CATC-----AACTCAGCATCGCTGAAGCTCAGAAATGAACATT-GGTA 310
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Db 417 CATCTCCACCCCTGTGCGATAACACGATGCTTGAAGAGCTCAGAAAGTGAAGTTCCTT 358
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QY 311 GTTCAATGTTGATTCTGGTCTTTGCGCCAGAACTGTTCTTTAAAAATTTGGGTATGTGA 370
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Db 357 GCGGAATCTGACITCTGGTCTTTG-ATCAGAACTGTTCTTTAAAAATTTGGGAAAGTGA 299
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QY 371 TAGAAGT-----GACTAACAGCGTGTTCACCTGCAGCTGTGTAATCAAGGCAAAATTTGC 425
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Db 298 TAGAAGTAGACACATTTGACTGTTTTCACCTGCGAGTTCGATGTCGTAAGGTAATAATCTTGC 239
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QY 426 GAGTTCAAGCGCGAATTTTCGGCG-ATGTCGCTCTTTCAC 463
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Db 238 GAATCAAGCGCAAGTTTTCGGCGAATGTCGCTCTTTCAC 200
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RESULT 4
LOCUS
DEFINITION
  IL2-BT0733-240400-073-G03 BT0733 Homo sapiens cDNA, mRNA sequence.
ACCESSION
  BE092111
VERSION
  BE092111.1 GI:8482563
KEYWORDS
  EST.
SOURCE
  human.
  ORGANISM
    Homo sapiens
    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
    Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
    1 (bases 1 to 319)
    Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R.,
    Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F.,
    Goldman,G.H., Carvalho,A.F., Matsukuma,A., Bala,G.S., Simpson,D.H.,
    Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare
    ,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and
    Simpson,A.J.
    Shotgun sequencing of the human transcriptome with ORF expressed
    sequence tags
    Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
    20202663
    Contact: Simpson A.J.G.
    Laboratory of Cancer Genetics
    Ludwig Institute for Cancer Research
    Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
    Brazil
    Tel: +55-11-2704922
    Fax: +55-11-2707001
    Email: asimpson@ludwig.org.br
    This sequence was derived from the FAPESP/LICR Human Cancer Genome
    project. This entry can be seen in the following URL
    (http://www.ludwig.org.br/scripts/gethtml2.pl?tl=et2-IL2-BT0733-240
    400-073-G03&t3=2000-04-24&t4=1)
    Seq primer: puc 18 forward
    High quality sequence stop: 298.
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        /db_xref="taxon:9606"
        /clone_lib="BT0733"
        /dev_stage="Adult"

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Best Local Similarity 68.6%; Pred. No. 2.9e-10;
Matches 129; Conservative 0; Mismatches 40; Indels 19; Gaps 2;

QY 103 TCAGTTGGTTAGAGCGCACCCCTGATAGAGGTGAGGTGCGGATCTGGAATCTGCCAGAC 162
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Db 518 TCAGTTGGTTAGAGCGCACCCCTGATAGAGGTGAGGTGCGGATCTGGAATCTGCCAGAC 459

QY 163 CCACCAATGTG-----GGGATGCCAGTGTCAATGCGGCGCATAGCT 205
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Db 458 CTACCAAAATTCGACGGCAAAATTTGAAGAGGTTTAACTACATGCTATGGGTTATAGCT 399

QY 206 CAGCTGGGAGAGCGCTGCTTTGCA--CGCAGGAGGTGAGGATTCGATCCTCCTTGGCT 263
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Db 398 CAGCTGGGAGAGCGCTGCTTTGCA--CGCAGGAGGTGAGGATTCGATCCTCCTTGGCT 339

QY 264 CCACCATC 271
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Db 338 CCACCATC 331

RESULT 7
BH400944/c
LOCUS BH400944
DEFINITION AG-ND-158022.TF ND-TAM Anopheles gambiae genomic clone AG-ND-158022
, DNA sequence.
ACCESSION BH400944
VERSION BH400944.1 GI:17347147
KEYWORDS GSS.
SOURCE African malaria mosquito.
ORGANISM Anopheles gambiae
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea;
Anopheles.
REFERENCE 1 (bases 1 to 593)
AUTHORS Shetty,J., Malek,J., Koo,H., Collins,F., Gardner,M. and Loftus,B.J.
TITLE Direct Submission of BAC-end sequences from Anopheles gambiae
JOURNAL Unpublished (2001)
COMMENT Other GSSs: AG-ND-158022.TF
Contact: Brendan J Loftus
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 0208
Fax: 301 838 3543
Email: bjloftus@tigr.org
This clone is from an A. gambiae BAC library (ND-TAM) provided by
F.H. Collins and sequenced by The Institute for Genomic Research
(TIGR). The BAC library was generated from A. gambiae PEST strain
DNA. All DNA was extracted from newly hatched first instar larvae
to minimize the inclusion of DNA from microorganisms that inhabit
the gut. The DNA is derived from mixed sexes of larvae. The BAC
library was constructed at Texas A&M University BAC Center
University, College Station, Texas 77843-2123, USA using a HindIII
partial digest.
Seq primer: M13 For
Class: BAC ends.

FEATURES
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Location/Qualifiers
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/strain="PEST"
/db_xref="taxon:7165"
/clone="AG-ND-158022"
/clone_lib="ND-TAM"
/note="Vector: pECBAC1; Site_1: 199 t"

BASE COUNT 119 a 157 c 118 g 199 t
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Best Local Similarity 71.9%; Pred. No. 3.8e-10;
Matches 123; Conservative 0; Mismatches 31; Indels 17; Gaps 2;

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Db 569 GTAGCTCAGTTGGTTAGAGCGCTACACTGATATGTAGAGGTGCGGATCTGGAATCTGCC 510

QY 158 CAGACCCCAATTTGCGGGATGGCCAGTGTCAATGGGCGCATAGCTCAGCTGGG-AGA 216
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Db 509 CGAGACTACTAATTGA-----AAAAGGGGAATTAGCTCAGCTGGCTAGA 466

QY 217 GGCCTGCTTTTCACGACGAGGTGAGGATTCGATCCTCCTTGGCTCCAC 267
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Db 514 CGAGACTACTAATTGA-----AAAAGGGGAATTAGCTCAGCTGGCTAGA 471

QY 217 GGCCTGCTTTTCACGACGAGGTGAGGATTCGATCCTCCTTGGCTCCAC 267
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Db 470 GGCCTGCTTTTCACGACGAGGTGAGGATTCGACTCCCTTATTTCAC 420

RESULT 8
BH393190/c
LOCUS BH393190
DEFINITION AG-ND-168H12.TR ND-TAM Anopheles gambiae genomic clone AG-ND-168H12
, DNA sequence.
ACCESSION BH393190
VERSION BH393190.1 GI:17339331
KEYWORDS GSS.
SOURCE African malaria mosquito.
ORGANISM Anopheles gambiae
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea;
Anopheles.
REFERENCE 1 (bases 1 to 760)
AUTHORS Shetty,J., Malek,J., Koo,H., Collins,F., Gardner,M. and Loftus,B.J.
TITLE Direct Submission of BAC-end sequences from Anopheles gambiae
JOURNAL Unpublished (2001)
COMMENT Other GSSs: AG-ND-168H12.TF
Contact: Brendan J Loftus
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 0208
Fax: 301 838 3543
Email: bjloftus@tigr.org
This clone is from an A. gambiae BAC library (ND-TAM) provided by
F.H. Collins and sequenced by The Institute for Genomic Research
(TIGR). The BAC library was generated from A. gambiae PEST strain
DNA. All DNA was extracted from newly hatched first instar larvae
to minimize the inclusion of DNA from microorganisms that inhabit
the gut. The DNA is derived from mixed sexes of larvae. The BAC
library was constructed at Texas A&M University BAC Center
University, College Station, Texas 77843-2123, USA using a HindIII
partial digest.
Seq primer: M13 Rev
Class: BAC ends.

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1..760
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/strain="PEST"
/db_xref="taxon:7165"
/clone="AG-ND-168H12"
/clone_lib="ND-TAM"
/note="Vector: pECBAC1; Site_1: HindIII"

BASE COUNT 171 a 187 c 139 g 263 t
ORIGIN
Query Match      13.5%; Score 67.4; DB 17; Length 760;
Best Local Similarity 71.9%; Pred. No. 4.4e-10;
Matches 123; Conservative 0; Mismatches 31; Indels 17; Gaps 2;

QY 98 GTAGCTCAGTTGGTTAGAGCGCACCCCTGATAGAGGTGAGGTGCGGATCTGGAATCTGCC 157
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Db 569 GTAGCTCAGTTGGTTAGAGCGCTACACTGATATGTAGAGGTGCGGATCTGGAATCTGCC 510

QY 158 CAGACCCCAATTTGCGGGATGGCCAGTGTCAATGGGCGCATAGCTCAGCTGGG-AGA 216
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 509 CGAGACTACTAATTGA-----AAAAGGGGAATTAGCTCAGCTGGCTAGA 466

QY 217 GGCCTGCTTTTCACGACGAGGTGAGGATTCGATCCTCCTTGGCTCCAC 267
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

```







\_\_\_\_\_

library"  
/tissue\_type="gametophyte thalli"  
/note="Vector: pMD 18-T; Site\_1: Ecor V with a T hang;  
Wild type Gracilaria lemaneiformis were harvested from  
Zhanshan Bay, Qingdao (China). After rinsed with boiled  
seawater, younger thalli were cut and washed every 3-4  
days until 1 month, when thalli were cultivated in

|         |     |              |    |            |     |        |    |      |    |
|---------|-----|--------------|----|------------|-----|--------|----|------|----|
| Matches | 67; | Conservative | 0; | Mismatches | 14; | Indels | 0; | Gaps | 0; |
|---------|-----|--------------|----|------------|-----|--------|----|------|----|





GenCore version 5.1.3  
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OM nucleic - nucleic search, using sw model

Run on: February 1, 2003, 01:06:21 ; Search time 963.563 Seconds  
(without alignments)  
14135.156 Million cell updates/sec

Title: US-09-931-486-115  
Perfect score: 468  
Sequence: 1 ATCGAGGACATCAGCTGTCT.....CAGATTGCTGGGTTATAT 468

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 2054640 seqs, 14551402878 residues

Total number of hits satisfying chosen parameters: 4109280

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

GenEmbl:\*\*  
1: gb\_ba:\*\*  
2: gb\_htg:\*\*  
3: gb\_in:\*\*  
4: gb\_om:\*\*  
5: gb\_ov:\*\*  
6: gb\_pat:\*\*  
7: gb\_ph:\*\*  
8: gb\_pl:\*\*  
9: gb\_pr:\*\*  
10: gb\_ro:\*\*  
11: gb\_sts:\*\*  
12: gb\_sy:\*\*  
13: gb\_un:\*\*  
14: gb\_vi:\*\*  
15: em\_ba:\*\*  
16: em\_fun:\*\*  
17: em\_hum:\*\*  
18: em\_in:\*\*  
19: em\_mu:\*\*  
20: em\_om:\*\*  
21: em\_or:\*\*  
22: em\_ov:\*\*  
23: em\_pat:\*\*  
24: em\_ph:\*\*  
25: em\_pl:\*\*  
26: em\_ro:\*\*  
27: em\_sts:\*\*  
28: em\_un:\*\*  
29: em\_vi:\*\*  
30: em\_htg\_hum:\*\*  
31: em\_htg\_inv:\*\*  
32: em\_htg\_other:\*\*  
33: em\_htg\_mus:\*\*  
34: em\_htg\_pln:\*\*  
35: em\_htg\_rod:\*\*  
36: em\_htg\_mam:\*\*  
37: em\_htg\_vrt:\*\*  
38: em\_sy:\*\*  
39: em\_hgo\_hum:\*\*  
40: em\_hgo\_mus:\*\*  
41: em\_hgo\_other:\*\*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match % | Length | DB | ID        | Description        |
|------------|-------|---------------|--------|----|-----------|--------------------|
| 1          | 468   | 100.0         | 468    | 6  | A48048    | A48048 Sequence 11 |
| 2          | 468   | 100.0         | 468    | 6  | ARI77093  | ARI77093 Sequence  |
| 3          | 468   | 100.0         | 468    | 6  | AX191056  | AX191056 Sequence  |
| 4          | 297.8 | 63.6          | 527    | 1  | AF127584  | AF127584 Pseudomon |
| 5          | 296   | 63.2          | 527    | 1  | AF127586  | AF127586 Pseudomon |
| 6          | 290.8 | 62.1          | 526    | 1  | AF127583  | AF127583 Pseudomon |
| 7          | 288.4 | 61.6          | 521    | 1  | AF364306  | AF364306 Pseudomon |
| 8          | 288.4 | 61.6          | 521    | 1  | AF364307  | AF364307 Pseudomon |
| 9          | 286.4 | 61.2          | 523    | 1  | AF364308  | AF364308 Pseudomon |
| 10         | 285.2 | 60.9          | 541    | 1  | AF127582  | AF127582 Pseudomon |
| 11         | 283.6 | 60.6          | 541    | 1  | AF127580  | AF127580 Pseudomon |
| 12         | 278.4 | 59.5          | 543    | 1  | AF127590  | AF127590 Pseudomon |
| 13         | 277.6 | 59.3          | 526    | 1  | AF127585  | AF127585 Pseudomon |
| 14         | 276.4 | 59.1          | 540    | 1  | AF127581  | AF127581 Pseudomon |
| 15         | 275.8 | 58.9          | 584    | 1  | AF127570  | AF127570 Alcanivor |
| 16         | 275.8 | 58.9          | 584    | 1  | AF127571  | AF127571 Alcanivor |
| 17         | 274.4 | 58.6          | 539    | 1  | AF127578  | AF127578 Pseudomon |
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| 19         | 273.8 | 58.5          | 5679   | 1  | AF134704  | AF134704 Pseudomon |
| 20         | 273.6 | 58.5          | 525    | 1  | AF127591  | AF127591 Pseudomon |
| 21         | 273.6 | 58.5          | 567    | 1  | PSERGDNNA | L06304 Pseudomonas |
| 22         | 273.6 | 58.5          | 567    | 1  | PSERGDNNA | L06306 Pseudomonas |
| 23         | 272.2 | 58.2          | 488    | 1  | PCI279242 | AJ279242 Pseudomon |
| 24         | 267.8 | 57.2          | 588    | 6  | BD011675  | BD011675 Method fo |
| 25         | 267.8 | 57.2          | 588    | 23 | E49505    | E49505 Method for  |
| 26         | 265.4 | 56.7          | 555    | 1  | AF148208  | AF148208 Pseudomon |
| 27         | 262.4 | 56.1          | 462    | 1  | PAG279243 | AJ279243 Pseudomon |
| 28         | 262   | 56.0          | 543    | 1  | AF127588  | AF127588 Pseudomon |
| 29         | 261.2 | 55.8          | 562    | 1  | PSERGDNAB | L06307 Pseudomonas |
| 30         | 259.6 | 55.5          | 562    | 1  | PSERGDNAB | L06305 Pseudomonas |
| 31         | 258.4 | 55.2          | 522    | 1  | AF127587  | AF127587 Pseudomon |
| 32         | 257.4 | 55.0          | 631    | 1  | AF422499  | AF422499 Unculture |
| 33         | 257.4 | 55.0          | 631    | 1  | AF422501  | AF422501 Unculture |
| 34         | 252.2 | 51.8          | 4958   | 1  | AF134705  | AF134705 Pseudomon |
| 35         | 239.8 | 51.2          | 553    | 1  | D87087    | D87087 Pseudomonas |
| 36         | 231   | 49.4          | 667    | 1  | AY119683  | AY119683 Pseudomon |
| 37         | 226.8 | 48.5          | 564    | 1  | D86357    | D86357 Pseudomonas |
| 38         | 225.8 | 48.2          | 557    | 1  | AF127589  | AF127589 Pseudomon |
| 39         | 221.6 | 47.4          | 529    | 1  | PST251904 | AJ251904 Pseudomon |
| 40         | 221.6 | 47.4          | 529    | 1  | PST390587 | AJ390587 Pseudomon |
| 41         | 220.4 | 47.1          | 521    | 1  | PAB439389 | AJ439389 Pseudomon |
| 42         | 219.6 | 46.9          | 578    | 1  | D86378    | D86378 Pseudomonas |
| 43         | 219.2 | 46.8          | 528    | 1  | PAB439391 | AJ439391 Pseudomon |
| C 44       | 219.2 | 46.8          | 1176   | 1  | AE004949  | AE004949 Pseudomon |
| C 45       | 219.2 | 46.8          | 12065  | 1  | AE004883  | AE004883 Pseudomon |

ALIGNMENTS

RESULT 1  
A48048  
LOCUS  
DEFINITION  
ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM  
REFERENCE  
AUTHORS  
TITLE  
JOURNAL

A48048  
Sequence 115 from Patent WO9600298.  
A48048  
A48048.1 GI:2301910  
unidentified.  
unidentified.  
unclassified.  
1 (bases 1 to 468)  
James G., Rossal, R. and van, H.H.  
SIMULTANEOUS DETECTION, IDENTIFICATION AND DIFFERENTIATION OF  
EUBACTERIAL TAXA USING A HYBRIDIZATION ASSAY  
Patent: WO 9600298-A 115 04-JAN-1996;

468 bp  
linear  
PAT 07-MAR-1997

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INNOGENETICS NV (BE)
Other publication AU 2924695 960119.
Location/Qualifiers
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/organism="unidentified"
/db_xref="taxon:32644"
BASE COUNT 117 a 101 c 117 g 133 t
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Query Match 100.0%; Score 468; DB 6; Length 468;
Best Local Similarity 100.0%; Pred. No. 5.5e-122;
Matches 468; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 181 CAGCTGGGAGAGCGCTGCTTCGACGAGGAGGTTCAGCGGTCGATCCCGCTGGCTCC 240
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DB 361 ACAGCACTTTCAGTGTGTGTTCAGGCTAAGGTAAAATTTCTGAGTAATTAACAAGTTT 420
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DB 421 TCGCGAAATGTTGCTTCACAGTATACCAAGATTCGTTGGGGTTATAT 468

RESULT 3
AX191056
LOCUS
DEFINITION Sequence 115 from Patent EP1091004.
ACCESSION AX191056
VERSION AX191056.1 GI:15149701
KEYWORDS
SOURCE unidentified.
ORGANISM unclassified.
REFERENCE 1 (bases 1 to 468)
AUTHORS James G., Rossau, R. and Van Heuverswyn, H.
TITLE Simultaneous detection, identification and differentiation of
eubacterial taxa using a hybridization assay
JOURNAL Patent: EP 1091004-A 115 11-APR-2001;
INNOGENETICS N.V. (BE)
FEATURES
source Location/Qualifiers
BASE COUNT 117 a 101 c 117 g 133 t
ORIGIN
Query Match 100.0%; Score 468; DB 6; Length 468;
Best Local Similarity 100.0%; Pred. No. 5.5e-122;
Matches 468; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATCGAGGACATCAGCTGCTCATAAGCTCCACACGAGGTTCAGCGGTCGATCCCGCTGGCTCC 60
DB 1 ATCGAGGACATCAGCTGCTCATAAGCTCCACACGAGGTTCAGCGGTCGATCCCGCTGGCTCC 60
QY 61 CGATTAGGTTAGCAACCTTCGATTGGGTCTGTAGCTCAGTTGGTTAGAGCGCACCCCTGA 120
DB 61 CGATTAGGTTAGCAACCTTCGATTGGGTCTGTAGCTCAGTTGGTTAGAGCGCACCCCTGA 120
QY 121 TAAGGTGAGGTGGCGAGTTCGAATTCGCCAGCACCCACCAATTTGCTGGGGCCATAGCT 180
DB 121 TAAGGTGAGGTGGCGAGTTCGAATTCGCCAGCACCCACCAATTTGCTGGGGCCATAGCT 180
QY 181 CAGCTGGGAGAGCGCTGCTTCGACGAGGAGGTTCAGCGGTCGATCCCGCTGGCTCC 240
DB 181 CAGCTGGGAGAGCGCTGCTTCGACGAGGAGGTTCAGCGGTCGATCCCGCTGGCTCC 240
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DB 301 TCTGAACCTTATCAGAAATCGTCTTTAAAATTTGGGTATGTGATAGAAAGATAGACTGG 360
QY 361 ACAGCACTTTCAGTGTGTGTTCAGGCTAAGGTAAAATTTCTGAGTAATTAACAAGTTT 420
DB 361 ACAGCACTTTCAGTGTGTGTTCAGGCTAAGGTAAAATTTCTGAGTAATTAACAAGTTT 420
QY 421 TCGCGAAATGTTGCTTCACAGTATACCAAGATTCGTTGGGGTTATAT 468
DB 421 TCGCGAAATGTTGCTTCACAGTATACCAAGATTCGTTGGGGTTATAT 468

RESULT 2
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LOCUS
DEFINITION Sequence 115 from patent US 6312903.
ACCESSION ARI77093
VERSION ARI77093.1 GI:17919448
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 468)
AUTHORS James G., Rossau, R. and Van Heuverswyn, H.
TITLE Simultaneous detection, identification and differentiation of
eubacterial taxa using a hybridization assay
JOURNAL Patent: US 6312903-A 115 06-NOV-2001;
FEATURES
source Location/Qualifiers
BASE COUNT 117 a 101 c 117 g 133 t
ORIGIN
Query Match 100.0%; Score 468; DB 6; Length 468;
Best Local Similarity 100.0%; Pred. No. 5.5e-122;
Matches 468; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATCGAGGACATCAGCTGCTCATAAGCTCCACACGAGGTTCAGCGGTCGATCCCGCTGGCTCC 60
DB 1 ATCGAGGACATCAGCTGCTCATAAGCTCCACACGAGGTTCAGCGGTCGATCCCGCTGGCTCC 60
QY 61 CGATTAGGTTAGCAACCTTCGATTGGGTCTGTAGCTCAGTTGGTTAGAGCGCACCCCTGA 120
DB 61 CGATTAGGTTAGCAACCTTCGATTGGGTCTGTAGCTCAGTTGGTTAGAGCGCACCCCTGA 120
QY 121 TAAGGTGAGGTGGCGAGTTCGAATTCGCCAGCACCCACCAATTTGCTGGGGCCATAGCT 180
DB 121 TAAGGTGAGGTGGCGAGTTCGAATTCGCCAGCACCCACCAATTTGCTGGGGCCATAGCT 180
QY 181 CAGCTGGGAGAGCGCTGCTTCGACGAGGAGGTTCAGCGGTCGATCCCGCTGGCTCC 240
DB 181 CAGCTGGGAGAGCGCTGCTTCGACGAGGAGGTTCAGCGGTCGATCCCGCTGGCTCC 240
QY 241 ACCACCCCGCTTCCAGTTCGAAATTCGCAAGCTTAGAAATGAATATTCGCGTCGAATATGATT 300
DB 241 ACCACCCCGCTTCCAGTTCGAAATTCGCAAGCTTAGAAATGAATATTCGCGTCGAATATGATT 300
QY 301 TCTGAACCTTATCAGAAATCGTCTTTAAAATTTGGGTATGTGATAGAAAGATAGACTGG 360
DB 301 TCTGAACCTTATCAGAAATCGTCTTTAAAATTTGGGTATGTGATAGAAAGATAGACTGG 360
QY 361 ACAGCACTTTCAGTGTGTGTTCAGGCTAAGGTAAAATTTCTGAGTAATTAACAAGTTT 420
DB 361 ACAGCACTTTCAGTGTGTGTTCAGGCTAAGGTAAAATTTCTGAGTAATTAACAAGTTT 420
QY 421 TCGCGAAATGTTGCTTCACAGTATACCAAGATTCGTTGGGGTTATAT 468
DB 421 TCGCGAAATGTTGCTTCACAGTATACCAAGATTCGTTGGGGTTATAT 468
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|                                                 |     |                                                                                                                                                                                                                          |     |
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| Best Local Similarity 80.6%; Pred. No. 1.2e-71; |     | Matches 403; Conservative 0; Mismatches 62; Indels 35; Gaps 4;                                                                                                                                                           |     |
| QY                                              | 61  | CGATTAGGTTAGCAACCTTCGATTGGTCTGTAGCTCAGTTGGTTAGAGCGCACCCCTGA                                                                                                                                                              | 120 |
| Db                                              | 75  | CGATAAG--AAGCAGGCCGAAATTTGGTCTGTAGCTCAGTTGGTTAGAGCGCACCCCTGA                                                                                                                                                             | 132 |
| QY                                              | 121 | TAAGGGTGAAGTGGGAGTTCGAATCTGCCAGACACCCACCAATTTGCT-----168                                                                                                                                                                 |     |
| Db                                              | 133 | TAA--GTGAGGTGGGAGTTCGAATCTGCCAGACACCCACCAATTTGCTGGGATCCT                                                                                                                                                                 | 190 |
| QY                                              | 169 | -----GGGGCCATAGCTCAGCTGGGAGAGCGGCTGCCCTGCACGAGGAGTTCAG                                                                                                                                                                   | 218 |
| Db                                              | 191 | GTAGCAATACGGGCCATAGCTCAGCTGGGAGAGCGGCTGCCCTGCACGAGGAGTTCAG                                                                                                                                                               | 250 |
| QY                                              | 219 | CGGTTCCATCCCGTGGCTCCACCCCGCTGCCCTGCACGAGTTCGAAGCTTAGAATGA                                                                                                                                                                | 278 |
| Db                                              | 251 | CGGTTCCATCCCGTGGCTCCACCCACTGCTCTCTGATGTTATTAAGCTTAGAATGA                                                                                                                                                                 | 310 |
| QY                                              | 279 | ATATTC-----CGCTCGAATATTGATTTCTGAACCTTTATCAGAATCGTTCTTTAA                                                                                                                                                                 | 328 |
| Db                                              | 311 | GCATTCCATCGTATGGTGGTGAATGTTGATTTCTAGCTTTGACTAGATCGTTCTTTAA                                                                                                                                                               | 370 |
| QY                                              | 329 | AAATTGGGTATGTAGTAAAGATAGACTGGACAGCACTTTCACTGGTGTGTTCCAGG                                                                                                                                                                 | 388 |
| Db                                              | 371 | AAATTGGGTATGTAGTAAAGATAGACTGGATGATCTTCACTGGTGTGTTATTCAGG                                                                                                                                                                 | 430 |
| QY                                              | 389 | CTAAGTAAATTTGTCAG--TAATTACAAATTTTCGGCGAATGTTGCTCTTCACAGTATA                                                                                                                                                              | 446 |
| Db                                              | 431 | CTAAGTAAATTTGTCAGTTTATCGGAATTTTCGGCGAATGTTGCTCTTCACAGTATA                                                                                                                                                                | 490 |
| QY                                              | 447 | ACCAGATTGCTGGGGTTATAT 468                                                                                                                                                                                                |     |
| Db                                              | 491 | ACCAGATTGCTGGGGTTATAT 512                                                                                                                                                                                                |     |
| RESULT 6                                        |     |                                                                                                                                                                                                                          |     |
| AF127583                                        |     | 526 bp DNA linear BCT 10-MAR-2001                                                                                                                                                                                        |     |
| LOCUS                                           |     |                                                                                                                                                                                                                          |     |
| DEFINITION                                      |     | Pseudomonas gingeri strain pf2 16S ribosomal RNA gene, partial sequence; internal transcribed spacer 1, complete sequence; trna-ile and trna-ala genes, complete sequence; and 23S ribosomal RNA gene, partial sequence. |     |
| ACCESSION                                       |     | AF127583.1 GI:13270381                                                                                                                                                                                                   |     |
| VERSION                                         |     |                                                                                                                                                                                                                          |     |
| KEYWORDS                                        |     | Pseudomonas gingeri.                                                                                                                                                                                                     |     |
| SOURCE                                          |     | Bacteria; Proteobacteria; gamma subdivision; Pseudomonadaceae; Pseudomonas.                                                                                                                                              |     |
| REFERENCE                                       |     | 1 (bases 1 to 526)                                                                                                                                                                                                       |     |
| AUTHORS                                         |     | Kwon, S.W. and Cheon, M.S.                                                                                                                                                                                               |     |
| TITLE                                           |     | Direct Submission                                                                                                                                                                                                        |     |
| JOURNAL                                         |     | Submitted (11-FEB-1999) Division of Molecular Genetics, National Institute of Agricultural Science and Technology, Seodun-dong 249, Suwon, Kyunggi-do 441-707, Republic of Korea                                         |     |
| FEATURES                                        |     | Location/Qualifiers                                                                                                                                                                                                      |     |
| source                                          |     | 1..526                                                                                                                                                                                                                   |     |
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|                                                 |     | /strain="pf2"                                                                                                                                                                                                            |     |
|                                                 |     | /db_xref="taxon:117681"                                                                                                                                                                                                  |     |
|                                                 |     | /note="(J.M. Wells)"                                                                                                                                                                                                     |     |
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| misc_RNA                                        |     | 12..511                                                                                                                                                                                                                  |     |
|                                                 |     | /product="internal transcribed spacer 1"                                                                                                                                                                                 |     |
| trRNA                                           |     | 97..169                                                                                                                                                                                                                  |     |
|                                                 |     | /product="trna-ile"                                                                                                                                                                                                      |     |
| trRNA                                           |     | 203..275                                                                                                                                                                                                                 |     |
|                                                 |     | /product="trna-Ala"                                                                                                                                                                                                      |     |
| rRNA                                            |     | 512..>526                                                                                                                                                                                                                |     |
|                                                 |     | /product="23S ribosomal RNA"                                                                                                                                                                                             |     |
| BASE COUNT                                      |     | 140 a 107 c 134 g 145 t                                                                                                                                                                                                  |     |
| ORIGIN                                          |     |                                                                                                                                                                                                                          |     |
| Query Match                                     |     | 62.1%; Score 290.8; DB 1; Length 526;                                                                                                                                                                                    |     |

|                                                 |     |                                                                                                                                |     |
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| Best Local Similarity 80.6%; Pred. No. 1.2e-71; |     | Matches 403; Conservative 0; Mismatches 62; Indels 35; Gaps 4;                                                                 |     |
| QY                                              | 1   | ATCGACACATCAGCTGCTCTATAAGCTCCACACAGCAATTCGTTGATTCATTGAAGAAGA                                                                   | 60  |
| Db                                              | 15  | ATCGACACATCAGCTGCTCTATAAGTTCCACACAGCAATTCGTTGATTCATTGAAGAAGA                                                                   | 74  |
| QY                                              | 61  | CGATTAGGTTAGCAACCTTCGATTGGTCTGTAGCTCAGTTGGTTAGAGCGCACCCCTGA                                                                    | 120 |
| Db                                              | 75  | CGATAAG--AAGCAGGCCGAAATTTGGTCTGTAGCTCAGTTGGTTAGAGCGCACCCCTGA                                                                   | 132 |
| QY                                              | 121 | TAAGGGTGAAGTGGGAGTTCGAATCTGCCAGACACCCACCAATTTG-----166                                                                         |     |
| Db                                              | 133 | TAAGGGTGAAGTGGGAGTTCGAATCTGCCAGACACCCACCAATTTGTTGGGAACCGCT                                                                     | 192 |
| QY                                              | 167 | -----CTGGGGCCATAGCTCAGCTGGGAGAGCGGCTGCCCTGCACGAGGAGTTCAG                                                                       | 218 |
| Db                                              | 193 | GTAGAAATACGGGGCCATAGCTCAGCTGGGAGAGCGGCTGCCCTGCACGAGGAGTTCAG                                                                    | 252 |
| QY                                              | 219 | CGGTTCCATCCCGTGGCTCCACCCCGCTTGCACAGCACTTTGCAGTTTGTCAAGCTTAGAATGA                                                               | 278 |
| Db                                              | 253 | CGGTTCCATCCCGTGGCTCCACCACTTAAGTCTTCTGTCT--TCAAGCTTAGAATGA                                                                      | 311 |
| QY                                              | 279 | ATATTC-----CGCTCGAATATTGATTTCTGAACCTTTATCAGAATCGTTCTTTAA                                                                       | 328 |
| Db                                              | 312 | GCATTCCATCGATGTGATGGTGAATGTTGATTTCTAGTCTTTGATTAGTCTGTTCTTAA                                                                    | 371 |
| QY                                              | 329 | AAATTGGGTATGTAGTAAAGATAGACTGGACAGCACTTTCACTGGTGTGTTCCAGG                                                                       | 388 |
| Db                                              | 372 | AAATTGGGTATGTAGTAAAGATAGACTGAACGTTACTTTCACTGGTAACGGATCAGG                                                                      | 431 |
| QY                                              | 389 | CTAAGTAAATTTGTGAGTAATTACAGTTTTCGGCGAATGTTGCTCTTCACAGTATAAC                                                                     | 448 |
| Db                                              | 432 | CTAAGTAAATTTGTAGTAATTTCGGAATTTTCGGCGAATGTTGCTCTTCACAGTATAAC                                                                    | 491 |
| QY                                              | 449 | CAGATTGCTGGGGTTATAT 468                                                                                                        |     |
| Db                                              | 492 | CAGATTGCTGGGGTTATAT 511                                                                                                        |     |
| RESULT 7                                        |     |                                                                                                                                |     |
| AF364306                                        |     | 521 bp DNA linear BCT 02-MAY-2001                                                                                              |     |
| LOCUS                                           |     |                                                                                                                                |     |
| DEFINITION                                      |     | Pseudomonas tolaasii LMG 6641 internal transcribed spacer 1, complete sequence.                                                |     |
| ACCESSION                                       |     | AF364306                                                                                                                       |     |
| VERSION                                         |     | AF364306.1 GI:13926167                                                                                                         |     |
| KEYWORDS                                        |     | Pseudomonas tolaasii.                                                                                                          |     |
| SOURCE                                          |     | Bacteria; Proteobacteria; gamma subdivision; Pseudomonadaceae; Pseudomonas.                                                    |     |
| REFERENCE                                       |     | 1 (bases 1 to 521)                                                                                                             |     |
| AUTHORS                                         |     | Munsch, P. and Alatosava, T.                                                                                                   |     |
| TITLE                                           |     | ITS 1 internal transcribed spacer                                                                                              |     |
| JOURNAL                                         |     | Unpublished                                                                                                                    |     |
| REFERENCE                                       |     | 2 (bases 1 to 521)                                                                                                             |     |
| AUTHORS                                         |     | Munsch, P. and Alatosava, T.                                                                                                   |     |
| TITLE                                           |     | Direct Submission                                                                                                              |     |
| JOURNAL                                         |     | Submitted (28-MAR-2001) REDEC of Kaiaani, Biotechnology Laboratory, University of Oulu, Salmelantie 43, Sotkamo 88600, Finland |     |
| FEATURES                                        |     | Location/Qualifiers                                                                                                            |     |
| source                                          |     | 1..521                                                                                                                         |     |
|                                                 |     | /organism="Pseudomonas tolaasii"                                                                                               |     |
|                                                 |     | /strain="LMG 6641"                                                                                                             |     |
|                                                 |     | /db_xref="taxon:29442"                                                                                                         |     |
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| BASE COUNT                                      |     | 136 a 107 c 130 g 148 t                                                                                                        |     |
| ORIGIN                                          |     |                                                                                                                                |     |



Query Match 61.6%; Score 288.4; DB 1; Length 521;  
 Best Local Similarity 79.8%; Pred. No. 5.9e-71;  
 Matches 410; Conservative 0; Mismatches 56; Indels 48; Gaps 4;

QY 1 ATCGACGACATCAGCTGCTCATAAGCTCCACACGAATGCTTGATTCATTGAAGAAGA 60  
 DB 10 ATCGACGACATCAGCTGCTCATAAGCTCCACACGAATGCTTGATTCATTGAAGAAGA 69  
 QY 61 CGATTAGGTAGCAACCTTCGATTCGGTCTGTAGCTCAGTTGGTTAGAGCGCACCCCTGA 120  
 DB 70 CGATAAG--AAGCAGCCGAAATTTGGTCTGTAGCTCAGTTGGTTAGAGCGCACCCCTGA 127  
 QY 121 TAAGGCTGAGGTCGGCAGTTCCGAATCTGCCAGACCCACCAATTTGCT----- 168  
 DB 128 TAAGGCTGAGGTCGGCAGTTCCGAATCTGCCAGACCCACCAATTTGCTGGGAAACGCC 187  
 QY 169 -----GGGCCATAGCTCAGCTGGGAGAGCGCTGCCCTGCACGAGGAGTCA 217  
 DB 188 TGTAGAAATACGGGGCCATAGCTCAGCTGGGAGAGCGCTGCCCTGCACGAGGAGTCA 247  
 QY 218 GCGGTTCCATCCCGCTTGGCTCCACACCCCGCTTGCAGTTTGTCAAGCTTAGAAATG 277  
 DB 248 GCGGTTCCATCCCGCTTGGCTCCACACCCCGCTTGCAGTTTGTCAAGCTTAGAAATG 307  
 QY 278 AATATTC-----CGTCCGAATATTGATTTCTGAACCTTTATCAGAATCGTCTTTA 327  
 DB 308 AGCATTCATCAGTGTGATGTTGATTTCTAGTCTTTGATTAGATCGTCTTTA 367  
 QY 328 AAAATTTGGGTATGTATAGAAAGATAGCTGGACAGCACTTCTACTGCTGTGTTCAG 387  
 DB 368 AAAATTTGGGTATGTATAGAAAGATAGCTGAAGCTTACTTCTACTGTTAACGGATCAG 427  
 QY 388 GCTAAGTAAATTTGTCAGT-----AATTACAAGTTTTCGGGAAATGTTGT 434  
 DB 428 GCTAAGTAAATTTGTCAGTCTTCTAGTTGAGAAATTCGAATTTTCGGGAAATGTTGT 487  
 QY 435 CTTACAGTATAACCAAGATTCCTGGGTTTATAT 468  
 DB 488 CTTACAGTATAACCAAGATTCCTGGGTTTATAT 521

RESULT 8  
 AF364307  
 LOCUS Pseudomonas tolaasii LMG 521 bp DNA linear BCT 02-MAY-2001  
 DEFINITION complete sequence.  
 ACCESSION AF364307  
 VERSION AF364307.1 GI:13926168  
 KEYWORDS Pseudomonas tolaasii.  
 SOURCE Pseudomonas tolaasii.  
 ORGANISM Bacteria; Proteobacteria; gamma subdivision; Pseudomonadaceae; Pseudomonas.  
 REFERENCE 1 (bases 1 to 521)  
 AUTHORS Munsch, P. and Alatossava, T.  
 TITLE ITS 1 internal transcribed spacer  
 JOURNAL Unpublished  
 REFERENCE 2 (bases 1 to 521)  
 AUTHORS Munsch, P. and Alatossava, T.  
 TITLE Direct Submission  
 JOURNAL Submitted (28-MAR-2001) REDEC of Kajaani, Biotechnology Laboratory, University of Oulu, Salmelantie 43, Sotkamo 88600, Finland  
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BASE COUNT 136 a 107 c 130 g 148 t  
 ORIGIN determined"

Query Match 61.6%; Score 288.4; DB 1; Length 521;  
 Best Local Similarity 79.8%; Pred. No. 5.9e-71;  
 Matches 410; Conservative 0; Mismatches 56; Indels 48; Gaps 4;

QY 1 ATCGACGACATCAGCTGCTCATAAGCTCCACACGAATGCTTGATTCATTGAAGAAGA 60  
 DB 10 ATCGACGACATCAGCTGCTCATAAGCTCCACACGAATGCTTGATTCATTGAAGAAGA 69  
 QY 61 CGATTAGGTAGCAACCTTCGATTCGGTCTGTAGCTCAGTTGGTTAGAGCGCACCCCTGA 120  
 DB 70 CGATAAG--AAGCAGCCGAAATTTGGTCTGTAGCTCAGTTGGTTAGAGCGCACCCCTGA 127  
 QY 121 TAAGGCTGAGGTCGGCAGTTCCGAATCTGCCAGACCCACCAATTTGCT----- 168  
 DB 128 TAAGGCTGAGGTCGGCAGTTCCGAATCTGCCAGACCCACCAATTTGCTGGGAAACGCC 187  
 QY 169 -----GGGCCATAGCTCAGCTGGGAGAGCGCTGCCCTGCACGAGGAGTCA 217  
 DB 188 TGTAGAAATACGGGGCCATAGCTCAGCTGGGAGAGCGCTGCCCTGCACGAGGAGTCA 247  
 QY 218 GCGGTTCCATCCCGCTTGGCTCCACACCCCGCTTGCAGTTTGTCAAGCTTAGAAATG 277  
 DB 248 GCGGTTCCATCCCGCTTGGCTCCACACCCCGCTTGCAGTTTGTCAAGCTTAGAAATG 307  
 QY 278 AATATTC-----CGTCCGAATATTGATTTCTGAACCTTTATCAGAATCGTCTTTA 327  
 DB 308 AGCATTCATCAGTGTGATGTTGATTTCTAGTCTTTGATTAGATCGTCTTTA 367  
 QY 328 AAAATTTGGGTATGTATAGAAAGATAGCTGGACAGCACTTCTACTGCTGTGTTCAG 387  
 DB 368 AAAATTTGGGTATGTATAGAAAGATAGCTGAAGCTTACTTCTACTGTTAACGGATCAG 427  
 QY 388 GCTAAGTAAATTTGTCAGT-----AATTACAAGTTTTCGGGAAATGTTGT 434  
 DB 428 GCTAAGTAAATTTGTCAGTCTTCTAGTTGAGAAATTCGAATTTTCGGGAAATGTTGT 487  
 QY 435 CTTACAGTATAACCAAGATTCCTGGGTTTATAT 468  
 DB 488 CTTACAGTATAACCAAGATTCCTGGGTTTATAT 521

RESULT 9  
 AF364308  
 LOCUS Pseudomonas tolaasii PS 3a internal transcribed spacer 1, complete  
 DEFINITION sequence.  
 ACCESSION AF364308  
 VERSION AF364308.1 GI:13926169  
 KEYWORDS Pseudomonas tolaasii.  
 SOURCE Pseudomonas tolaasii.  
 ORGANISM Bacteria; Proteobacteria; gamma subdivision; Pseudomonadaceae; Pseudomonas.  
 REFERENCE 1 (bases 1 to 523)  
 AUTHORS Munsch, P. and Alatossava, T.  
 TITLE ITS 1 internal transcribed spacer  
 JOURNAL Unpublished  
 REFERENCE 2 (bases 1 to 523)  
 AUTHORS Munsch, P. and Alatossava, T.  
 TITLE Direct Submission  
 JOURNAL Submitted (28-MAR-2001) REDEC of Kajaani, Biotechnology Laboratory, University of Oulu, Salmelantie 43, Sotkamo 88600, Finland  
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1..523
/feature="contains tRNA-Ala and tRNA-Ile; spans not
determined"
137 a 106 c 129 g 151 t

BASE COUNT 137 a 106 c 129 g 151 t
ORIGIN

Query Match 61.2%; Score 286.4; DB 1; Length 523;
Best Local Similarity 79.5%; Pred. No. 2.2e-70;
Matches 410; Conservative 0; Mismatches 56; Indels 50; Gaps 4;

QY 1 ATCGACGACATCAGCTGTCTCTAATAGCTCCACACGAAATTCCTGATTCATTTGAAGAAGA 60
Db 10 ATCGACGACATCAGCTGTCTCTAATAGCTCCACACGAAATTCCTGATTCATTTGAAGAAGA 69
QY 61 CGATTAGGTTAGCAACCTTCGATGGTCTGTAGCTCAGTGGTGTAGAGCGACCCCTGA 120
Db 70 CGATAAG--AAGCAGCCGGAATTCGATGGTCTGTAGCTCAGTGGTGTAGAGCGACCCCTGA 127
QY 121 TAAGGGTGAGGTCGGCAGTTCGAATCTGCCAGACCCACCAATTTGCT----- 168
Db 128 TAAGGGTGAGGTCGGCAGTTCGAATCTGCCAGACCCACCAATTTGCTGGGAAGGCC 187
QY 169 -----GGGGCCATAGCTCAGCTGGGAGAGCGCTGCCTTGCACCGAGAGTCA 217
Db 188 TGTAAGAAATACGGGGCCATAGCTCAGCTGGGAGAGCGCTGCCTTGCACCGAGAGTCA 247
QY 218 GCGGTTTCGATCCCGCTTGGCTCCACACCCCGCTTGGCAGTTTGTCAAAGCTTAGAATG 277
Db 248 ACGGTTTCGATCCCGCTTGGCTCCACACCTACTGCTTCTAGCTTATGAAAGCTTAGAATG 307
QY 278 AATATTC-----GCGTCAATATTCGATTTCTGAACTTTATCAGAAATCGTCTTTA 327
Db 308 AGCATTCATCAGCTGATGGTGAATCTGATTTCTAGCTTTGATTTAGATCGTCTTTA 367
QY 328 AATATTCGATTCGATTAAGAGATAGCTGCACAGCAGCTTTCACCTGGTGTGTGTCAG 387
Db 368 AATATTCGATTCGATTAAGAGATAGCTGCACAGCAGCTTTCACCTGGTGAACGGATCAG 427
QY 388 GCTAAGGTAAATTTGTTG-----AGTAAATACAAAGTTTTCGGGGAATGTT 432
Db 428 GCTAAGGTAAATTTGTTGACTTACTCAGTTTTCGATTTATCGAATTTTCGGGGAATGTT 487
QY 433 GTCTTCAGATATAACAGATTCGTTGGGTTATAT 468
Db 488 GTCTTCAGATATAACAGATTCGTTGGGTTATAT 523

RESULT 10
AF127582 541 bp DNA linear BCT 10-MAR-2001
LOCUS
DEFINITION
Pseudomonas reactans strain H22 16S ribosomal RNA gene, partial
sequence; internal transcribed spacer 1, complete sequence;
tRNA-Ile and tRNA-Ala genes, complete sequence; and 23S ribosomal
RNA gene, partial sequence.
AF127582 GI:13270380
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
Pseudomonas reactans.
Bacteria; Proteobacteria; gamma subdivision; Pseudomonadaceae;
Pseudomonas.
1 (bases 1 to 541)
Kwon, S.W. and Cheon, M.S.
Direct Submission
Submitted (11-FEB-1999) Division of Molecular Genetics, National
Institute of Agricultural Science and Technology, Seodun-dong 249,
Suwon, Kyunggi-do 441-707, Republic of Korea
Location/Qualifiers
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97..170
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204..276
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144 a 111 c 135 g 151 t

BASE COUNT 144 a 111 c 135 g 151 t
ORIGIN

Query Match 60.9%; Score 285.2; DB 1; Length 541;
Best Local Similarity 79.4%; Pred. No. 4.8e-70;
Matches 408; Conservative 0; Mismatches 58; Indels 48; Gaps 4;

QY 1 ATCGACGACATCAGCTGTCTCTAATAGCTCCACACGAAATTCCTGATTCATTTGAAGAAGA 60
Db 15 ATCGACGACATCAGCTGTCTCTAATAGCTCCACACGAAATTCCTGATTCATTTGAAGAAGA 74
QY 61 CGATTAGGTTAGCAACCTTCGATGGTCTGTAGCTCAGTGGTGTAGAGCGACCCCTGA 120
Db 75 CGATAAG--AAGCAGCCGGAATTCGATGGTCTGTAGCTCAGTGGTGTAGAGCGACCCCTGA 132
QY 121 TAAGGGTGAGGTCGGCAGTTCGAATCTGCCAGACCCACCAATTTT----- 165
Db 133 TAAGGGTGAGGTCGGCAGTTCGAATCTGCCAGACCCACCAATTTT----- 192
QY 166 -----GCTGGGCCATAGCTCAGCTGGGAGAGCGCTGCCTTGCACCGAGAGTCA 217
Db 193 TGTAAGAAATATGGGGCCATAGCTCAGCTGGGAGAGCGCTGCCTTGCACCGAGAGTCA 252
QY 218 GCGGTTTCGATCCCGCTTGGCTCCACACCCCGCTTGGCAGTTTGTCAAAGCTTAGAATG 277
Db 253 ACGGTTTCGATCCCGCTTGGCTCCACCACTACTGCTTCTCGGTTATGAAAGCTTAGAATG 312
QY 278 AATATTC-----GCGTCAATATTCGATTTCTGAACTTTATCAGAAATCGTCTTTA 327
Db 313 AGCATTCATCAGTGTGATGGTGAATCTGATTTCTAGCTTTGATTTAGATCGTCTTTA 372
QY 328 AATATTCGATTCGATTAAGAGATAGCTGCACAGCAGCTTTCACCTGGTGTGTGTCAG 387
Db 373 AATATTCGATTCGATTAAGAGATAGCTGCACAGCAGCTTTCACCTGGTGAACGGATCAG 432
QY 388 GCTAAGGTAAATTTGTTGAGT-----AATTAAGTTTTCGGGGAATGTTGT 434
Db 433 GCTAAGGTAAATTTGTTGAGTTCCTTAGTGAAGAAATTCGAATTTTCGGGGAATGTTGT 492
QY 435 CTTCACAGTATAACAGATTCCTTGGGTTATAT 468
Db 493 CTTCACAGTATAACAGATTCCTTGGGTTATAT 526

RESULT 11
AF127580 541 bp DNA linear BCT 10-MAR-2001
LOCUS
DEFINITION
Pseudomonas reactans strain pf1 16S ribosomal RNA gene, partial
sequence; internal transcribed spacer 1, complete sequence;
tRNA-Ile and tRNA-Ala genes, complete sequence; and 23S ribosomal
RNA gene, partial sequence.
AF127580 GI:13270378
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
Pseudomonas reactans.
Bacteria; Proteobacteria; gamma subdivision; Pseudomonadaceae;
Pseudomonas.
1 (bases 1 to 541)
Kwon, S.W. and Cheon, M.S.
Direct Submission
Submitted (11-FEB-1999) Division of Molecular Genetics, National
Institute of Agricultural Science and Technology, Seodun-dong 249,
Suwon, Kyunggi-do 441-707, Republic of Korea
Location/Qualifiers
1..541
/organism="Pseudomonas reactans"
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FEATURES
source
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Institute of Agricultural Science and Technology, Seodun-dong 249,  
Suwon, Kyunggi-do 441-707, Republic of Korea

# FEATURES

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12. 526  
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97. 170  
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204. 276  
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527. 541  
/product="23S ribosomal RNA"  
146 a 110 c 134 g 151 t

Query Match 60.6%; Score 283.6; DB 1; Length 541;  
Best Local Similarity 79.2%; Pred. No. 1.4e-69;  
Matches 407; Conservative 0; Mismatches 59; Indels 48; Gaps 4;  
Qy 1 ATCGACGACATCAGCTGCTCATAGCTCCACACAGAAATGCTTGATTCATTGAAGAAGA 60  
Db 15 ATCGACGACATCAGCTGCTCATAGCTCCACACAGAAATGCTTGATTCATTGAAGAAGA 74  
Qy 61 CGATTAGTTAGCAACCTTCGATGGGTCTGTAGCTAGCTAGCTAGCTAGCTAGCTAGCT 120  
Db 75 CGATAAG--AAGCAGCCGCGAAATGGGTCTGTAGCTAGCTAGCTAGCTAGCTAGCT 132  
Qy 121 TAAGGGTGAGGTGCGCAGTTCGAATCTGCCAGACCCACCAATTT----- 165  
Db 133 TAAGGGTGAGGTGCGCAGTTCGAATCTGCCAGACCCACCAATTTTGTGTTGGGAACGCC 192  
Qy 166 -----GCTGGGGCCATAGCTCAGCTGGGAGAGCGCTGCTTGCACGAGGAGTCA 217  
Db 193 TGTAGAAATATGGGGCCATAGCTCAGCTGGGAGAGCGCTGCTTGCACGAGGAGTCA 252  
Qy 218 GCGGTTGATCCCGCTGGCTCCACCGCCGCTGGCCAGTTCGCAAGCTTAGAAATG 277  
Db 253 ACGGTTCGATCCCGCTGGCTCCACCGCCGCTGGCCAGTTCGCAAGCTTAGAAATG 312  
Qy 278 AATATTC-----GCTGCGAATATGATTTCTGAACCTTATCAGAAATCGTCTTTA 327  
Db 313 AGCATTCATCAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 372  
Qy 328 AAAATTTGGGTATGTAGAAAGATAGCTGGACAGCACTTCTCACTGGTGTGTTTCAAG 387  
Db 373 AAAATTTGGGTATGTAGAAAGATAGCTGGACAGCACTTCTCACTGGTGTGTTTCAAG 432  
Qy 388 GCTAAGTAAATTTGTGAGT-----AATTACAGTTTTCGGCGAATGTTGT 434  
Db 433 GCTAAGTAAATTTGTGAGTCTCTTAATGAGAAATTCGAATTTTCGGCGAATGTTGT 492  
Qy 435 CTTACAGTATAACAGATGCTTGGGGTTATAT 468  
Db 493 CTTACAGTATAACAGATGCTTGGGGTTATAT 526

RESULT 12  
AF127590  
LOCUS  
DEFINITION  
Pseudomonas reactans strain ATCC14340 16S ribosomal RNA gene,  
partial sequence; internal transcribed spacer 1, complete sequence;  
rRNA-Ile and rRNA-Ala genes, complete sequence; and 23S ribosomal  
RNA gene, partial sequence.  
ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
AF127590.1 GI:13270388  
Pseudomonas reactans.

# ORGANISM

Pseudomonas reactans  
Bacteria; Proteobacteria; gamma subdivision; Pseudomonadaceae;  
Pseudomonas.

REFERENCE  
1 (bases 1 to 543)  
AUTHORS  
Kwon,S.W. and Cheon,M.S.  
TITLE  
Direct Submission  
JOURNAL  
Submitted (11-FEB-1999) Division of Molecular Genetics, National  
Institute of Agricultural Science and Technology, Seodun-dong 249,  
Suwon, Kyunggi-do 441-707, Republic of Korea

# FEATURES

Source  
1. 543  
/organism="Pseudomonas reactans"  
/strain="ATCC14340"  
/db\_xref="ATCC:14340"  
/db\_xref="taxon:117680"  
1. 11  
/product="16S ribosomal RNA"  
12. 528  
/product="internal transcribed spacer 1"  
97. 170  
/product="rRNA-Ile"  
204. 276  
/product="rRNA-Ala"  
529. 543  
/product="23S ribosomal RNA"  
147 a 109 c 133 g 154 t

Query Match 59.5%; Score 278.4; DB 1; Length 543;  
Best Local Similarity 78.5%; Pred. No. 4.1e-68;  
Matches 405; Conservative 0; Mismatches 61; Indels 50; Gaps 4;  
Qy 1 ATCGACGACATCAGCTGCTCATAGCTCCACACAGAAATGCTTGATTCATTGAAGAAGA 60  
Db 15 ATCGACGACATCAGCTGCTCATAGCTCCACACAGAAATGCTTGATTCATTGAAGAAGA 74  
Qy 61 CGATTAGTTAGCAACCTTCGATGGGTCTGTAGCTAGCTAGCTAGCTAGCTAGCTAGCT 120  
Db 75 CGATAA--CAAGCAGCCGCGAAATGGGTCTGTAGCTAGCTAGCTAGCTAGCTAGCT 132  
Qy 121 TAAGGGTGAGGTGCGCAGTTCGAATCTGCCAGACCCACCAATTTTGTGTTGGGAACGCC 165  
Db 133 TAAGGGTGAGGTGCGCAGTTCGAATCTGCCAGACCCACCAATTTTGTGTTGGGAACGCC 192  
Qy 166 -----GCTGGGGCCATAGCTCAGCTGGGAGAGCGCTGCTTGCACGAGGAGTCA 217  
Db 193 TGTAGAAATATGGGGCCATAGCTCAGCTGGGAGAGCGCTGCTTGCACGAGGAGTCA 252  
Qy 218 GCGGTTGATCCCGCTGGCTCCACCGCCGCTGGCCAGTTCGCAAGCTTAGAAATG 277  
Db 253 ACGGTTCGATCCCGCTGGCTCCACCGCCGCTGGCCAGTTCGCAAGCTTAGAAATG 312  
Qy 278 AATATTC-----GCTGCGAATATGATTTCTGAACCTTATCAGAAATCGTCTTTA 327  
Db 313 AGCATTCATCAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 372  
Qy 328 AAAATTTGGGTATGTAGAAAGATAGCTGGACAGCACTTCTCACTGGTGTGTTTCAAG 387  
Db 373 AAAATTTGGGTATGTAGAAAGATAGCTGGACAGCACTTCTCACTGGTGTGTTTCAAG 432  
Qy 388 GCTAAGTAAATTTGTGAGT-----TGAGTAATTAACAGTTTTCGGCGAATGTT 432  
Db 433 GCTAAGTAAATTTGTGAGTTACTCAGTTTGTAGTATTATCGAATTTTCGGCGAATGTT 492  
Qy 433 GCTCTCAGTATAACAGATGCTTGGGGTTATAT 468  
Db 493 GCTCTCAGTATAACAGATGCTTGGGGTTATAT 528

RESULT 13  
AF127585  
LOCUS  
DEFINITION  
Pseudomonas fluorescens strain LMG5939 16S ribosomal RNA gene,  
linear BCT 10-MAR-2001

partial sequence; internal transcribed spacer 1, complete sequence;  
trna-ile and trna-ala genes, complete sequence; and 23S ribosomal  
RNA gene, partial sequence.

ACCESSION AF127585.1 GI:13270383  
VERSION AF127585.1  
KEYWORDS Pseudomonas fluorescens.  
SOURCE Bacteria; Proteobacteria; gamma subdivision; Pseudomonadaceae;  
ORGANISM Pseudomonas.

REFERENCE 1 (bases 1 to 526)  
AUTHORS Kwon,S.W. and Cheon,M.S.  
TITLE Direct Submission  
JOURNAL Submitted (11-FEB-1999) Division of Molecular Genetics, National  
Institute of Agricultural Science and Technology, Seodun-dong 249,  
Suwon, Kyunggi-do 441-707, Republic of Korea

FEATURES  
source  
1..526  
/organism="Pseudomonas fluorescens"  
/strain="LMG5939"  
/db\_xref="taxon:294"  
/note="biotype: F"

trna <1..11  
/product="16S ribosomal RNA"

misc\_RNA 12..511  
/product="internal transcribed spacer 1"

trna 97..168  
/product="trna-ile"

trna 202..274  
/product="trna-ala"

rRNA 512..526  
/product="23S ribosomal RNA"

BASE COUNT 136 a 108 c 135 g 147 t

ORIGIN

Query Match 59.3%; Score 277.6; DB 1; Length 526;

Best Local Similarity 81.5%; Pred. No. 6.9e-68;

Matches 409; Conservative 0; Mismatches 54; Indels 39; Gaps 6;

QY 1 ATCGACGACATCAGTGTCTCATAAGCTCCACACGAAATTCGTTGATTCAATGAAGA 60

DB 15 ATCGACGACATCAGTGTCTCATAAGCTCCACACGAAATTCGTTGATTCAATGAAGA 74

QY 61 CGATTAGGTTAGCAACCTTCGATTGGGTCTGTAGCTCAGTTGGTTAGAGCGACCCCTGA 120

DB 75 CGATAAG--AAGCAGCCGAAATTTGGTCTGTAGCTCAGTTGGTTAGAGCGACCCCTGA 132

QY 121 TAAGGTTAGGTCGGCAGTTGCAATCTGCCACGACCCACCAATTTGCT----- 168

DB 133 TAA--GTGAGGTCGGCAGTTGCAATCTGCCACGACCCACCAATTTGCTGGGAAAGGCC 190

QY 169 -----GGGGCCATAGCTCAGCTGGGAGAGCGCTTGCACGAGGAGTCA 217

DB 191 TGTAAGAAATACGGGGCCATAGCTCAGCTGGGAGAGCGCTTGCACGAGGAGTCA 250

QY 218 GCGGTTGATCCGCTGGCTCCACACCGCTTGCAGTTTGTCAAGCTTAGAATG 277

DB 251 ACGGTTGATCCGCTGGCTCCACACCGCTTGCAGTTTGTCAAGCTTAGAATG 310

QY 278 AATATT-----CGCTCGAATATTGATTTCTGACATTTATCAGAACTGTTTAA 328

DB 311 AGCAATCCATCGTGACGATGTGAATGTTGATTTCTAGTCTTGTATGATCGTTCTTAA 370

QY 329 AATATTTGGGTATGTAGAAAGATAGACTGGACAGCACTTTCACCTGGTGTGTTTCAAG 388

DB 371 AATATTTGGGTATGTAGAAAGATAGACTGGACAGCACTTTCACCTGGTGTGTTTCAAG 429

QY 389 CTAAAGTAAATTTGTGAG--TAATTAACAAGTTTTCGGCGAAATGTTCTTCAAGTATA 446

DB 430 CTAAAGTAAATTTGTGAGTTTATCGCGAAATTTTCGGCGAAATGTTCTTCAAGTATA 489

QY 447 ACCAGATTGCTGGGGTTATAT 468

DB 490 ACCAGATTGCTGGGGTTATAT 511

RESULT 14

LOCUS AF127581

DEFINITION

Pseudomonas reactans strain H3 16S ribosomal RNA gene, partial  
sequence; internal transcribed spacer 1, complete sequence;  
trna-ile and trna-ala genes, complete sequence; and 23S ribosomal  
RNA gene, partial sequence.

ACCESSION AF127581.1 GI:13270379

VERSION AF127581.1

KEYWORDS Pseudomonas reactans.

SOURCE Pseudomonas reactans

ORGANISM Bacteria; Proteobacteria; gamma subdivision; Pseudomonadaceae;

REFERENCE 1 (bases 1 to 540)

AUTHORS Kwon,S.W. and Cheon,M.S.

TITLE Direct Submission

JOURNAL Submitted (11-FEB-1999) Division of Molecular Genetics, National

Institute of Agricultural Science and Technology, Seodun-dong 249,

Suwon, Kyunggi-do 441-707, Republic of Korea

FEATURES Location/Qualifiers

source 1..540

/organism="Pseudomonas reactans"

/strain="H3"

/db\_xref="taxon:117680"

/note="(J.M. Wells)"

trna <1..11

/product="16S ribosomal RNA"

misc\_RNA 12..525

/product="internal transcribed spacer 1"

trna 97..170

/product="trna-ile"

trna 204..275

/product="trna-ala"

rRNA 526..540

/product="23S ribosomal RNA"

BASE COUNT 144 a 109 c 137 g 150 t

ORIGIN

Query Match 59.1%; Score 276.4; DB 1; Length 540;

Best Local Similarity 79.8%; Pred. No. 1.5e-67;

Matches 409; Conservative 0; Mismatches 56; Indels 49; Gaps 5;

QY 1 ATCGACGACATCAGCTGTCTCATAAGCTCCACACGAAATTCGTTGATTCAATGAAGA 60

DB 15 ATCGACGACATCAGCTGTCTCATAAGCTCCACACGAAATTCGTTGATTCAATGAAGA 74

QY 61 CGATTAGGTTAGCAACCTTCGATTGGGTCTGTAGCTCAGTTGGTTAGAGCGACCCCTGA 120

DB 75 CGATAAG--AAGCAGCCGAAATTTGGTCTGTAGCTCAGTTGGTTAGAGCGACCCCTGA 132

QY 121 TAAGGTTAGGTCGGCAGTTGCAATCTGCCACGACCCACCAATTTTGTGTTGGGAAAGGCC 165

DB 133 TAAGGTTAGGTCGGCAGTTGCAATCTGCCACGACCCACCAATTTTGTGTTGGGAAAGGCC 192

QY 166 -----GCTGGGGCCATAGCTCAGCTGGGAGAGCGCTTGCCTTGCACGAGGAGTCA 217

DB 193 TGTAAGAAATATGGGGCCATAGCTCAGCTGGGAGAGCGCTTGCACGAGGAGTCA 251

QY 218 GCGGTTGATCCGCTGGCTCCACACCGCTTGCAGTTTGTCAAGCTTAGAATG 277

DB 252 ACGGTTGATCCGCTGGCTCCACACCGCTTGCAGTTTGTCAAGCTTAGAATG 311

QY 278 AATATT-----CGCTCGAATATTGATTTCTGAACTTTATCAGAACTGTTCTTTA 327

DB 312 AGCAATCCATCAATGTGATGTTGATTTCTAGTCTTGTATGATCGTTCTTTA 371

QY 328 AATATTTGGGTATGTAGAAAGATAGACTGGACAGCACTTTCACCTGGTGTGTTTCAAG 387

DB 372 AATATTTGGGTATGTAGAAAGATAGACTGGACAGCACTTTCACCTGGTGTGTTTCAAG 431

QY 388 GCTAAGTAAATTTGTGAGT-----AATTACAAGTTTTCGCGGAATGTTGT 434  
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Db 432 GCTAAGTAAATTTGTGAGTTCCTAGTTGAGAAATTCGAATTTTCGCGGAATGTCGT 491  
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QY 435 CTTACAGTATAACCAAGATTCGTTGGGTTATAT 468  
|||||  
Db 492 CTTACAGTATAACCAAGATTCGTTGGGTTATAT 525  
|||||

RESULT 15  
AF197570  
LOCUS  
DEFINITION  
Alcanivorax borkumensis strain LE4 16S ribosomal RNA gene, partial  
sequence; internal transcribed spacer 1, complete sequence;  
tRNA-Ile and tRNA-Ala genes, complete sequence; and 23S ribosomal  
RNA gene, partial sequence.

ACCESSION  
AF197570  
VERSION  
AF197570.1 GI:11640606  
KEYWORDS  
Alcanivorax borkumensis.  
SOURCE  
Alcanivorax borkumensis.  
ORGANISM  
Alcanivorax borkumensis.  
Bacteria; Proteobacteria; gamma subdivision;  
Alcanivorax/Fundibacter group; Alcanivorax.  
REFERENCE  
1 (bases 1 to 584)  
Wang, W.F. and Tan, H.M.  
Sequencing of 16S-23S ISR of rRNA from Alcanivorax borkumensis LE4  
Unpublished  
2 (bases 1 to 584)  
Wang, W.F. and Tan, H.M.  
Direct Submission  
TITLE  
Submitted (21-OCT-1999) Department of Microbiology, National  
University of Singapore, 10 Kent Ridge Crescent, Singapore 119260,  
Singapore

FEATURES  
source  
1..584  
/organism="Alcanivorax borkumensis"  
/strain="LE4"  
/db\_xref="taxon:59754"  
<1..64  
/product="16S ribosomal RNA"  
65..578  
/product="internal transcribed spacer 1"  
148..221  
/product="tRNA-Ile"  
255..327  
/product="tRNA-Ala"  
579..584  
/product="23S ribosomal RNA"  
BASE COUNT 153 a 124 c 148 g 159 t

Query Match 58.9%; Score 275.8; DB 1; Length 584;  
Best Local Similarity 78.3%; Pred No. 2.3e-67;  
Matches 403; Conservative 0; Mismatches 62; Indels 50; Gaps 4;

QY 1 ATCGACGACATCAGTGTCTCATAGCTCCACAGAAATTCGTTGATTCATTGAAGAAGA 60  
|||||  
Db 67 ATCGACGACATCAGTGTCTCATAGCTCCACAGAAATTCGTTGATTCATTGAAGAAGA 126  
|||||  
QY 61 CGATTAGGTAGCAACCTTCGTTGGGTTCTGTAGTCTAGTTCGTTAGAGCGCACCCCTGA 120  
|||||  
Db 127 CG-AAAAGAGACGCCCGGAATTCGTTGGGTTCTGTAGTCTAGTTCGTTAGAGCGCACCCCTGA 183  
|||||  
QY 121 TAAGGTGAGGTGCGGAGTTCGAATCTGCCAGACCCACCAATTTGCT----- 168  
|||||  
Db 184 TAAGGTGAGGTGCGGAGTTCGAATCTGCCAGACCCACCAATTTGCTGGGAACGCC 243  
|||||  
QY 169 -----GGGCCCATAGCTAGCTGGGAGAGCGGCTGCTTCGACGAGGAGGTCA 217  
|||||  
Db 244 TGTAAGAAATACGGGGCCATAGCTCAACTGGGAGAGCGGCTGCCCTTGACGAGGAGGTCA 303  
|||||  
QY 218 GCGGTTGATCCCGGTTGGCTCCACCACCCCGCTTGCCAGTTTGTCAAAGCTTAGAAATG 277  
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Search completed: February 1, 2003, 03:05:14  
Job Time : 965.563 secs

Db 304 GCGGTTGATCCCGCTTGGCTCCACCACTACTGCTCTGTATATAAGCTTAGAAATG 363  
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QY 278 AATATTC-----GCGTCGAATATGATTTCTGAACCTTATCAGAATCGTCTTTA 327  
|||||  
Db 364 AGCATTCATCAATCCGATGGTGAATGTTGATTTCTAGTCTTTGACTAGTTCTTTA 423  
|||||  
QY 328 AAAATTTGGGTATGTGATAGAAAAGATAGACTGGACAGCACCTTTCACCTGGTGTGTTCAG 387  
|||||  
Db 424 AAAATTTGGGTATGTGATAGAAAAGATAGACTGAAACGTTACTTTTCACTGGTAACGATCAC 483  
|||||  
QY 388 GCTAAGGTAAATTTG-----TGACTAATTACAAGTTTTCGCGGAATGTTG 433  
|||||  
Db 484 GCTAAGGTAAATTTGAGTTCCTCAATTTGAGTATATTCGAATTTTCGCGGAATGTCG 543  
|||||  
QY 434 TCTTCACAGTATAACCAAGATTCGTTGGGTTATAT 468  
|||||  
Db 544 TCTTCACAGTATAACCAAGATTCGTTGGGTTATAT 578  
|||||



GenCore version 5.1.3  
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OM nucleic - nucleic search, using sw model

Run on: January 31, 2003, 19:23:36 ; Search time 110.822 Seconds  
(without alignments)  
9510.154 Million cell updates/sec

Title: US-09-931-486-115

Perfect score: 468

Sequence: 1 ATGACGACATCAGCTGTCT.....CAGATGCTGGGGTTATAT 468

Scoring table: IDENTITY\_NUC

Gapop 10.0 , Gapext 1.0

Searched: 2185239 seqs, 1125999159 residues

Total number of hits satisfying chosen parameters: 4370478

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

1: N\_Geneseq\_101002.\*  
2: /SIDS2/gcgdata/geneseq/geneseq-emb1/NA1980.DAT.\*  
3: /SIDS2/gcgdata/geneseq/geneseq-emb1/NA1981.DAT.\*  
4: /SIDS2/gcgdata/geneseq/geneseq-emb1/NA1982.DAT.\*  
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24: /SIDS2/gcgdata/geneseq/geneseq-emb1/NA2001B.DAT.\*  
25: /SIDS2/gcgdata/geneseq/geneseq-emb1/NA2002.DAT.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

| Result No. | Score | Match | Length | DB | ID       | Description         |
|------------|-------|-------|--------|----|----------|---------------------|
| 1          | 468   | 100.0 | 468    | 17 | AAT11846 | P. putida LMG 2232  |
| 2          | 267.8 | 57.2  | 588    | 22 | AAI69774 | 16S/23S rRNA spacer |
| 3          | 216   | 46.2  | 471    | 17 | AAT11842 | P. aeruginosa UZG   |
| 4          | 205.2 | 43.8  | 504    | 17 | AAT11844 | P. stutzeri LMG 23  |
| 5          | 198.4 | 42.4  | 499    | 17 | AAT11845 | P. alcaligenes LMG  |
| 6          | 178   | 38.0  | 520    | 17 | AAT11843 | P. pseudocaligenes  |
| 7          | 110.8 | 23.7  | 640681 | 24 | ABA92787 | Buchnera sp. genom  |
| 8          | 109   | 23.3  | 603    | 12 | AAQ14102 | N.gonorrhoeae stra  |
| 9          | 105.2 | 22.5  | 400    | 18 | AAV78022 | Staphylococcus aur  |

|   |    |       |      |         |    |           |
|---|----|-------|------|---------|----|-----------|
| c | 10 | 105.2 | 22.5 | 400     | 18 | AAV77902  |
|   | 11 | 105.2 | 22.5 | 1311    | 18 | AAV77852  |
|   | 12 | 104.8 | 22.4 | 664     | 12 | AAQ14106  |
|   | 13 | 104.4 | 22.3 | 808     | 17 | AAT11889  |
|   | 14 | 104.4 | 22.3 | 808     | 17 | AAT11890  |
|   | 15 | 104.4 | 22.3 | 809     | 17 | AAT11891  |
| c | 16 | 104.2 | 22.3 | 400     | 18 | AAV77984  |
|   | 17 | 102.8 | 22.0 | 335     | 12 | AAQ14103  |
|   | 18 | 102.8 | 22.0 | 20844   | 21 | AAAB1460  |
| c | 19 | 102.8 | 22.0 | 172325  | 21 | AAAF21613 |
|   | 20 | 102.8 | 22.0 | 349980  | 21 | AAAF21544 |
|   | 21 | 102.8 | 22.0 | 349980  | 21 | AAAF21607 |
| c | 22 | 102.8 | 22.0 | 349980  | 21 | AAAF21611 |
|   | 23 | 102.8 | 22.0 | 349980  | 21 | AAAF21612 |
| c | 24 | 102.8 | 22.0 | 837096  | 21 | AAAB1489  |
|   | 25 | 102.8 | 22.0 | 1437668 | 21 | AAAB1490  |
|   | 26 | 102.6 | 21.9 | 1396    | 22 | AAH55089  |
| c | 27 | 101   | 21.6 | 2839    | 22 | AAH54998  |
|   | 28 | 101   | 21.6 | 3444    | 22 | AAH54992  |
|   | 29 | 101   | 21.6 | 4429    | 22 | AAH54300  |
|   | 30 | 100.8 | 21.5 | 549     | 12 | AAQ14109  |
| c | 31 | 100.4 | 21.5 | 351     | 18 | AAV78405  |
|   | 32 | 99.4  | 21.2 | 498     | 12 | AAQ14107  |
| c | 33 | 99.4  | 21.2 | 269223  | 22 | AAFP28554 |
|   | 34 | 96    | 20.5 | 470     | 17 | AAT11898  |
|   | 35 | 94.6  | 20.2 | 479     | 22 | AAT171400 |
| c | 36 | 93    | 19.9 | 243     | 23 | AAH48781  |
|   | 37 | 92.4  | 19.7 | 255     | 23 | AAH48800  |
| c | 38 | 92.4  | 19.7 | 255     | 23 | AAH48825  |
|   | 39 | 92.4  | 19.7 | 255     | 23 | AAH48838  |
| c | 40 | 92.4  | 19.7 | 255     | 23 | AAH48846  |
|   | 41 | 92.4  | 19.7 | 255     | 23 | AAH48854  |
| c | 42 | 92.4  | 19.7 | 255     | 23 | AAH48877  |
|   | 43 | 92.4  | 19.7 | 255     | 23 | AAH48882  |
| c | 44 | 92.4  | 19.7 | 255     | 23 | AAH48896  |
|   | 45 | 92.4  | 19.7 | 255     | 23 | AAH48898  |

#### ALIGNMENTS

RESULT 1  
AAT11846  
ID AAT11846 standard; DNA; 468 BP.  
XX  
AC AAT11846;  
XX  
DT 03-SEP-1996 (first entry)  
XX  
DE P. putida LMG 2232 16S-23S rRNA spacer region.  
XX  
KW Probe; detection; identification; microorganism; amplify;  
KW 16S-23S rRNA spacer region; respiratory tract; universal;  
KW species-specific; ss.  
XX  
OS Pseudomonas putida.  
XX  
PN WO9600298-A1.  
XX  
PD 04-JAN-1996.  
XX  
PF 23-JUN-1995; 95WO-EP02452.  
XX  
PR 07-APR-1995; 95EP-0870032.  
XX  
PR 24-JUN-1994; 94EP-0870106.  
XX  
PA (INNO-) INNOGENETICS NV.  
XX  
PI Jannes G, Rossau R, Van Heuverswyn H;  
XX  
DR WPI; 1996-068882/07.  
XX  
PT Novel hybridisation assay for the detection of eubacteria - esp

OS *Pseudomonas* a

*Pseudomonas aeruginosa*.



PN W09600298-AL.  
 XX 04-JAN-1996.  
 XX 23-JUN-1995; 95WO-EP02452.  
 XX 07-APR-1995; 95EP-0870032.  
 XX 24-JUN-1994; 94EP-0870106.  
 XX (INNO-) INNOGENETICS NV.  
 XX Jannes G, Rossau R, Van Heuverswyn H;  
 XX WPI; 1996-068882/07.  
 XX Novel hybridisation assay for the detection of eubacteria - esp  
 PT Mycobacterium, comprises amplifying the 16S-23S rRNA spacer region  
 XX Claim 2; Fig 36; 248pp; English.  
 XX The sequences given in AAT11791-857 represent the 16S-23S rRNA spacer  
 CC regions derived from various microorganisms. These sequences were  
 CC used in the method of the invention for the detection and identification  
 CC of at least one or more microorganisms. The method comprises amplifying  
 CC the 16S-23S rRNA spacer region and hybridising one or more of the probes  
 CC given in AAT34011-77 to the amplified sequence. These probes were  
 CC specifically used to detect microorganisms in samples originating from  
 CC the respiratory tract. This spacer region is derived from *Pseudomonas*  
 CC *aeruginosa* UZG 5669.  
 XX Sequence 471 BP; 116 A; 103 C; 120 G; 132 T; 0 other;  
 SQ  
 Query Match 46.28; Score 216; DB 17; Length 471;  
 Best Local Similarity 74.98; Pred. No. 6e-59;  
 Matches 370; Conservative 0; Mismatches 75; Indels 49; Gaps 6;  
 QY 1 ATCGACGACATFAGCTGTCTCATAAGCTCCACACAGCAATTCGTTGATTGAAGAAGA 60  
 Db 1 ATCGAAGATCCCGCTCTTCTCATAAGCTCCACACAGCAATTCGTTGATTGAAGAAGA 59  
 QY 61 CGATTAGGTAGCAACCTTCGATTGGGTCTGTAGCTCAGTTGGTTAGAGCCACCCCTGA 120  
 Db 60 -----CGATTGGGTCTGTAGCTCAGTTGGTTAGAGCCACCCCTGA 100  
 QY 121 TAAGGGTCAGTGGCGAGTTTGAATCTGCCAGACCCACCAATTT-----164  
 Db 101 TAAGGGTCAGTGGCGAGTTTGAATCTGCCAGACCCACCAATTTGGTGTGCTGCGTG 160  
 QY 165 -----TCTGGGGCCATAGCTAGCTGGGAGCGCCTGCTTCACGAGGAGGTGAGC 219  
 Db 161 ATCGATACGGGGCCATAGCTAGCTGGGAGCGCCTGCTTCACGAGGAGGTGAGC 220  
 QY 220 GGTTCGATCCCGTTGCTCCACACCCGCTTCCAGTTTGTCAAAGCTTAGAAATGAA 279  
 Db 221 AGTTCGATCTCTCTGGCTCCACCATC---TAAACCAATCTGCGAAAGCTCAGAAATGAA 277  
 QY 280 TATTCG-CGTGCAATATTGATTCTGAACTTT--ATCAGAAATCGTTCTTTAAATAATTTGG 336  
 Db 278 TGTTCGTGGATGAACATTGATTCTGTCTTTGCACCAACAGCTGCTTTAAATAATTCGG 337  
 QY 337 GTATGTCATAGAAGATAGACTGGACAGCACTTTCACTGTGTGTGTTCAAGGCTAAGGTA 396  
 Db 338 GTATGTCATAGAAGATAGACTGAATGATCTCTTTCACTGTGTGATCAAGTCAAGGTA 397  
 QY 397 AAATTTCGTGAGT--AATTACAAAGTTTTCGGCGAATGTGTTCTTCACAGTATAACCAATT 454  
 Db 398 AAATTTCGTGAGTTCAGCGCGAATTTTCGGCGAATGTGTTCTTCACAGTATAACCAATT 457  
 QY 455 GCTTGGGGTTATAT 468  
 Db 458 GCTTGGGGTTATAT 471

RESULT 4  
 AAT11844  
 ID AAT11844 standard; DNA; 504 BP.  
 XX  
 AC AAT11844;  
 XX  
 DT 03-SEP-1996 (first entry)  
 XX  
 DE P. stutzeri LMG 2333 16S-23S rRNA spacer region.  
 XX  
 KW Probe; detection; identification; microorganism; amplification;  
 KW 16S-23S rRNA spacer region; respiratory tract; universal;  
 KW species-specific; ss.  
 XX  
 OS *Pseudomonas stutzeri*.  
 XX  
 PN W09600298-AL.  
 XX  
 PD 04-JAN-1996.  
 XX  
 PF 23-JUN-1995; 95WO-EP02452.  
 XX  
 PR 07-APR-1995; 95EP-0870032.  
 PR 24-JUN-1994; 94EP-0870106.  
 XX  
 PA (INNO-) INNOGENETICS NV.  
 XX  
 PI Jannes G, Rossau R, Van Heuverswyn H;  
 XX  
 DR WPI; 1996-068882/07.  
 XX  
 PT Novel hybridisation assay for the detection of eubacteria - esp  
 PT Mycobacterium, comprises amplifying the 16S-23S rRNA spacer region  
 XX  
 PS Claim 2; Fig 38; 248pp; English.  
 XX  
 CC The sequences given in AAT11791-857 represent the 16S-23S rRNA spacer  
 CC regions derived from various microorganisms. These sequences were  
 CC used in the method of the invention for the detection and identification  
 CC of at least one or more microorganisms. The method comprises amplifying  
 CC the 16S-23S rRNA spacer region and hybridising one or more of the probes  
 CC given in AAT34011-77 to the amplified sequence. These probes were  
 CC specifically used to detect microorganisms in samples originating from  
 CC the respiratory tract. This spacer region is derived from *Pseudomonas*  
 CC *stutzeri* LMG 2333.  
 XX  
 SQ Sequence 504 BP; 119 A; 111 C; 137 G; 137 T; 0 other;  
 Query Match 43.88; Score 205.2; DB 17; Length 504;  
 Best Local Similarity 74.78; Pred. No. 1.8e-55;  
 Matches 378; Conservative 0; Mismatches 88; Indels 40; Gaps 8;  
 QY 1 ATCGACGACATFAGCTGTCTCATAAGCTCCACACAGCAATTCGTTGATTGAAGAAGA 59  
 Db 1 ATCGAAGATCCCGCTCTTCTCATAAGCTCCACACAGCAATTCGTTGATTGAAGAAGA 60  
 QY 60 ACGATTAGGTAGCAACCTTT-----CGATTGGGTCTGTAGCTCAGTTGGTTAGAGCGCA 113  
 Db 61 GCGATTGGGTTAGACCCCGAGAGTAACGATTGGGTCTGTAGCTCAGTTGGTTAGAGCGCA 120  
 QY 114 CCCCTGATAAGGGTGGAGTTCGCGAGTTCGAAATCTGCCAGACCCACCAATTTGCTGGGGC 173  
 Db 121 CCCCTGATAAGGGTGGAGTTCGCGAGTTCGAAATCTGCCAGACCCACCAATTTGCTGGGGC 179  
 QY 174 CATAGCTCAGCTGGAGAGCGCTTCGCTTGCACGAGGAGGTTCAGCGGTTTCGATCCCGCT 233  
 Db 180 CATAGCTCAGCTGGAGAGCGCTTCGCTTGCACGAGGAGGTTCAGCGGTTTCGATCCCGCT 239  
 QY 234 TGGCTCCACC-----ACCCCGCTTGGCAGTTTGTTCAAAGCTTAGAA 274  
 Db 240 TGGCTCCACCATTAACTCTAGTTCGCCGAAAGCTCAGAAATGAGTGTTCACGAGTATGAGG 299  
 QY 275 ATGAATATTCGCGTCGAATATTGATTCTGAACTTT--ATCAGAAATCGTTCTTTAAATAAT 332

```

Db 300 TTGATGCGCTGGTGAACATGATTTCTGGACTTGGCCAGAGACTGTTCTTTAAAT 359
QY 333 TTGGTATGTGATAGAAAGATAGACTGGACAGCACTTTCACCTGGTGTGGTTCAGGCTAA 392
Db 360 TTGGGTATGTGATAGAAAGTAGA-CGGATGTGTGCTTTTCACTGGCAGCATGTCCGCTCAA 418
QY 393 GGTAAATTTTGGAGTAAT--TACAAGTTTTCGGGGAATGTGTTCCACAGTA----- 444
Db 419 GGTAAATTTTGGGTGTCTCTATGCAATTTTCCGGCAATGTCTTCACCTTATAGAC 478
QY 445 --TAACACAGATTGCTTGGGGTTATAT 468
Db 479 AGTAACACAGATTGCTTGGGGTTATAT 504

RESULT 5
AAT11845
ID AAT11845 standard; DNA; 499 BP.
XX
AC AAT11845;
XX
DT 03-SEP-1996 (first entry)
XX
DE P. alcaligenes LMG 1224 16S-23S rRNA spacer region.
XX
KW Probe; detection; identification; microorganism; amplify;
KW 16S-23S rRNA spacer region; respiratory tract; universal;
KW species-specific; ss.
XX
OS Pseudomonas alcaligenes.
XX
PN WO9600298-A1.
XX
PD 04-JAN-1996.
XX
PF 23-JUN-1995; 95WO-EF02452.
XX
PR 07-APR-1995; 95EP-0870032.
PR 24-JUN-1994; 94EP-0870106.
XX
PA (INNO-) INNOGENETICS NV.
XX
PI Jannes G, Rossau R, Van Heuverswyn H;
XX
WPI; 1996-068882/07.
XX
PT Novel hybridisation assay for the detection of eubacteria - esp
PT Mycobacterium, comprises amplifying the 16S-23S rRNA spacer region
XX
PS Claim 2; Fig 39; 248pp; English.
XX
CC The sequences given in AAT11791-857 represent the 16S-23S rRNA spacer
CC regions derived from various microorganisms. These sequences were
CC used in the method of the invention for the detection and identification
CC of at least one or more microorganisms. The method comprises amplifying
CC the 16S-23S rRNA spacer region and hybridising one or more of the probes
CC given in AAT34011-77 to the amplified sequence. These probes were
CC specifically used to detect microorganisms in samples originating from
CC the respiratory tract. This spacer region is derived from Pseudomonas
CC alcaligenes LMG 1224.
XX
SQ Sequence 499 BP; 123 A; 109 C; 130 G; 137 T; 0 other;
Query Match 42.4%; Score 198.4; DB 17; Length 499;
Best Local Similarity 72.08; Pred. No. 2.7e-53;
Matches 367; Conservative 0; Mismatches 96; Indels 41; Gaps 7;

QY 1 ATCGACGACATCAGCTGCTCTAAGCTCCACACGAAATGCTTGAATTCATTGAAGAAGA 60
Db 1 ATCGAAGACTTCAGCTTCTTCATAAGTCCACACGAAATGCTTGAATTCAGTTCGGAAGA 60
QY 61 CGATTAGGTAGCAACCTT-----CGATTGGGTCTGTAGCTCAGTGTGTTAGACGCA 113

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Db 61 GCGATTGGGTTGAGACCCGAGAGTGCAGATTTGGGTCTGTAGCTCAGTTGTTAGACGCGCA 120
QY 114 CCCTGATAAGGTCAGGTCGCGAGTTCCGAATCTGCCAGAGCCACCAATTTGC----- 167
Db 121 CCCCTGATAAGGTCAGGTCGCGAGTTCCGAATCTGCCAGAGCCACCAATTTGCGGATG 180
QY 168 -----TGGGGCCATAGCTCAGCTGGGAGAGCCGCTTGCCTTGCACGAGAGGT 215
Db 181 GCCAGTGTCAAAATGGGCCATAGCTCAGCTGGGAGAGCGCTGCTTTGCACGAGAGGT 240
QY 216 CAGCGGTTGCATCCCGCTTGGCTCCACACCCGCTTGCAGTTTGTCAAAGCTTAGAAA 275
Db 241 CAGGAGTTCGATCCTCTTGGCTCCACCA--TCAACTCAGATCGCTGAAAGCTCAGAAA 298
QY 276 TGAATATTTCG-CGTGGAATATTGATTTCTGAACCTT--ATCAGAAATCGTTCTTTAAAT 332
Db 299 TGAACATTGGTAGTTCATGTTGATTTCTGGTCTTTGCGCCAGCAACTGTTCTTTAAAT 358
QY 333 TTGGGTATGTGATAGAAAGATAGACTGGACAGCACTTTCACCTGGTGTGTTTCAGGCTAA 392
Db 359 TTGGGTATGTGATAGA---AGTGACTAACACAGCGTGTTCACCTGCACGTTGTTAATCAAG 415
QY 393 GGTAAATTTTGTGAGTAATTAACAAGTTTTCGGGGAATGTGTTCTTCTCAC-----AGTA 444
Db 416 CAAAATTTGCGAGTTCAAGCGCAATTTTCGGCAATGTGCTTTCACGTTACGATCTA 475
QY 445 TAACACAGATTGCTTGGGGTTATAT 468
Db 476 TAACACAGATTGCTTGGGGTTATAT 499

RESULT 6
AAT11843
ID AAT11843 standard; DNA; 520 BP.
XX
AC AAT11843;
XX
DT 03-SEP-1996 (first entry)
XX
DE P. pseudoalcaligenes LMG 1225 16S-23S rRNA spacer region.
XX
KW Probe; detection; identification; microorganism; amplify;
KW 16S-23S rRNA spacer region; respiratory tract; universal;
KW species-specific; ss.
XX
OS Pseudomonas pseudoalcaligenes.
XX
PN WO9600298-A1.
XX
PD 04-JAN-1996.
XX
PF 23-JUN-1995; 95WO-EF02452.
XX
PR 07-APR-1995; 95EP-0870032.
PR 24-JUN-1994; 94EP-0870106.
XX
PA (INNO-) INNOGENETICS NV.
XX
PI Jannes G, Rossau R, Van Heuverswyn H;
XX
WPI; 1996-068882/07.
XX
PT Novel hybridisation assay for the detection of eubacteria - esp
PT Mycobacterium, comprises amplifying the 16S-23S rRNA spacer region
XX
PS Claim 2; Fig 37; 248pp; English.
XX
CC The sequences given in AAT11791-857 represent the 16S-23S rRNA spacer
CC regions derived from various microorganisms. These sequences were
CC used in the method of the invention for the detection and identification
CC of at least one or more microorganisms. The method comprises amplifying
CC the 16S-23S rRNA spacer region and hybridising one or more of the probes
CC given in AAT34011-77 to the amplified sequence. These probes were
CC specifically used to detect microorganisms in samples originating from
CC the respiratory tract. This spacer region is derived from Pseudomonas
CC alcaligenes LMG 1224.
XX
SQ Sequence 499 BP; 123 A; 109 C; 130 G; 137 T; 0 other;
Query Match 42.4%; Score 198.4; DB 17; Length 499;
Best Local Similarity 72.08; Pred. No. 2.7e-53;
Matches 367; Conservative 0; Mismatches 96; Indels 41; Gaps 7;

QY 1 ATCGACGACATCAGCTGCTCTAAGCTCCACACGAAATGCTTGAATTCATTGAAGAAGA 60
Db 1 ATCGAAGACTTCAGCTTCTTCATAAGTCCACACGAAATGCTTGAATTCAGTTCGGAAGA 60
QY 61 CGATTAGGTAGCAACCTT-----CGATTGGGTCTGTAGCTCAGTGTGTTAGACGCA 113

```

CC given in AAT34011-77 to the amplified sequence. These probes were  
 CC specifically used to detect microorganisms in samples originating from  
 CC the respiratory tract. This spacer region is derived from *Pseudomonas*  
 CC *pseudocaligenes* LMG 1225.

XX  
 SQ Sequence 520 BP; 126 A; 109 C; 134 G; 151 T; 0 other;  
 Query Match 38.0%; Score 178; DB 17; Length 520;  
 Best Local Similarity 71.1%; Pred. No. 9.8e-47;  
 Matches 371; Conservative 0; Mismatches 95; Indels 56; Gaps 8;  
 QY 1 ATCGACGACATCAGCTGTCTCATAGCTCCACACAAATGCTGATTCATTGAGAAGA 60  
 DB 1 ATCGAAGACATCAGCTTCTCATAGTATCCACACAAATGCTGATTCATTGAGAAGA 60  
 QY 61 CGATTAGGTAGCACACCTTCGAT-TGGGTCCTAGCTAGTCTAGTGGTAGAGCCACCCCTG 119  
 DB 61 AATGCTGTAAACGCGCGCTGTTATAGGTCCTAGCTAGTGGTAGAGCCACCCCTG 120  
 QY 120 ATAAGGTTGAGTCCGAGTTCGAATCTGCCAGACCCACCAATTTGCT----- 168  
 DB 121 ATAAAGGTTGAGTCCGAGTTCGAATCTGCCAGACCCACCAATTTGCT----- 168  
 QY 169 -----GGGCCATPAGCTAGCTGGGAGAGCGCTGCTTGCAGCAGGAGGTGACGGGTTTC 224  
 DB 181 ATACGGGGCCATAGCTCAGCTGGGAGAGCGCTGCTTGCAGCAGGAGGTGACGGGTTTC 240  
 QY 225 GATCCCGCTTGGCTCCACACCC-----CGCTTGCAGTGTGTCAAAGCTTAGAATG 277  
 DB 241 GATCCCGCTTGGCTCCACACCTCTCGTGTGCGGTGAGTGTAAAGAGTTTCAGAAATG 300  
 QY 278 A-----ATATTCGGGTGCAATATTGATTTCTGAACTT-----TATCAGAA 317  
 DB 301 ATGCGGCTTACGGTTTGCTGCTTGAGTCTGATTTCTGGCTTTTGACCGGTACGAA 360  
 QY 318 TCGTCTTTAAATTTGGGTATGTATGATAGAAAGATGAGTGGACGACCTTTCACTGGT 377  
 DB 361 TCGTCTTTAAATTTGGGTATGTATGATAGAAAGATGAGTGGACGACCTTTCACTGGT 418  
 QY 378 GTGCTTCAGGCTAAGTAAATTTGTGAGT-----AATTACAAGTTTTCGGCGAATGTTG 433  
 DB 419 AATTGATCTGTCAGGTAAATTTGTGAGTTCCTCAAGACGCAATTTTCGGCGAATGTCG 478  
 QY 434 TCTTCAC-----AGTAAACCAAGATGCTTGGGGTTATAT 468  
 DB 479 TCTTCACGATTGACAGACAGTAAACCAAGATGCTTGGGGTTATAT 520

## RESULT 7

ABA92787  
 ID ABA92787 standard; DNA; 640681 BP.

XX ABA92787;  
 AC

XX 27-MAR-2002 (first entry)  
 DT

XX Buchnera sp. genomic DNA SEQ ID NO:1.  
 DE

XX Buchnera; cockroach-symbiotic bacterium; cockroach extermination;  
 KW circular; ds.  
 KW

XX Buchnera sp.  
 OS

XX JP2001292771-A.  
 PN

XX 23-OCT-2001.  
 PD

XX 07-APR-2000; 2000JP-0107160.  
 PF

XX 07-APR-2000; 2000JP-0107160.  
 PR

XX (RIKA ) RIKAGAKU KENKYUSHO.  
 PA

XX

DR WPI; 2002-126043/17.

XX A genomic DNA of cockroach-symbiotic bacterium -  
 PT

PS Claim 1; Page 16-230; 237pp; Japanese.  
 XX

CC The present invention describes a gene (I) derived from *Buchnera* sp.  
 CC containing the DNA (a) or (b), (a) has a fully defined base pair  
 CC sequence selected from a table of sequences found in the *Buchnera* sp.  
 CC genomic DNA of ABA92787 given in the specification or is a DNA selected  
 CC from complementary DNA sequences, and (b) is a DNA which hybridises with  
 CC the DNA (a) and encodes a protein. Also described are: (1) a recombinant  
 CC vector (II) containing (1); (2) a transformant (III) containing (II);  
 CC (3) a genomic DNA of *Buchnera* sp. containing the sequence given in  
 CC ABA92787; (4) a plasmid derived from *Buchnera* sp. containing DNA (c) or  
 CC or ABB92788 and (d) is a plasmid which hybridises with a DNA; and (5) a  
 CC method for the preparation of a protein in which (III) is cultured and  
 CC the expression protein of the objective protein is collected from the  
 CC resultant culture. The DNA is useful for developing agricultural  
 CC chemicals for exterminating cockroaches. The present sequence represents  
 CC the specifically claimed *Buchnera* sp. genomic DNA sequence, from the  
 CC present invention.

SQ Sequence 640681 BP; 237522 A; 83822 C; 84757 G; 234580 T; 0 other;

Query Match 23.7%; Score 110.8; DB 24; Length 640681;  
 Best Local Similarity 79.0%; Pred. No. 1.3e-23;  
 Matches 147; Conservative 0; Mismatches 32; Indels 7; Gaps 1;

QY 63 ATTAGGTTAGCAACCTTCGATTCGGTCTGTAGCTCAGTGGTTAGAGCGCACCCCTGATA 122  
 DB 275618 ATTATCTATAAATAAATAATAGAGGCTTGTAGCTCAGATGGTTAGAGCGCACCCCTGATA 122

QY 123 AGGGTGAGGTGCGGCGAGTTCGAATCTGCCAGACCCACCC-----AATTTGCTGGGCGCA 175  
 DB 275678 AGGGTGAGGTGCGGTTCAATTCACCTCAGGCTACCAATAAATAATCATCTGGGGCTA 275737

QY 176 TAGCTCAGCTGGGAGAGCGCCCTGCTTGCACGAGGAGTTCAGTCCGATCCCGCTTG 235  
 DB 275738 TAGCTCAGCTGGGAGAGCGCCCTGCTTGCACGAGGAGTTCAGTCCGATCCCGCTTG 235

QY 236 GCTCCA 241  
 DB 275798 GCTCCA 275803

## RESULT 8

AAQ14102  
 ID AAQ14102 standard; DNA; 603 BP.

XX AAQ14102;  
 AC

XX 10-JAN-1992 (first entry)  
 DT

XX N.gonorrhoeae strain NCTC 8375 16S to 23S rRNA gene spacer region.  
 DE

XX rRNA gene; ribosomal RNA; probe; ss.  
 KW

XX *Neisseria gonorrhoeae* NCTC 8375.  
 OS

XX EP452596-A.  
 PN

XX 23-OCT-1991.  
 PD

XX 18-APR-1990; 90EP-0401054.  
 PF

XX 18-APR-1990; 90EP-0401054.  
 PR

XX (INNO-) INNOGENETICS NV SA.  
 PA

XX Rossau R, Van Heuverswijn H;  
 PI

XX



FT FT /\*tag= a  
FT FT /note= "these bases represent a line of missing text in  
FT FT the sequence listing in the specification. They  
FT FT are included to maintain the nucleotide numbering  
FT FT given in the specification for this DNA sequence"

EP786519-A2.

30-JUL-1997.

07-JAN-1997; 97EP-0100117.

05-JAN-1996; 96US-0009861.

(HUMA-) HUMAN GENOME SCI INC.

Barash SC, Choi GH, Dillon PJ, Fannon MR, Kunsch CA;

Rosen CA;

WPI; 1997-374922/35.

Polynucleotide(s) and proteins derived from Staphylococcus aureus -  
stored on computer readable medium and used in the production of  
anti-S.aureus vaccines

Claim 1; Page 2600; 3271pp; English.

This sequence represents one of 5191 Staphylococcus aureus DNA sequences  
of the invention. The DNA sequences are recorded on a computer readable  
medium, preferably selected from a floppy or hard disk, random access  
memory (RAM), read-only memory (ROM) or CD-ROM. Homology searches using  
the S.aureus DNA sequences allows putative functions to be assigned so  
that protein-encoding or regulatory regions of commercial, therapeutic or  
industrial importance can be obtained. Specifically, sequences which are  
likely to encode antigens have been identified and these polypeptides can  
be used in a vaccine composition against S.aureus infection. The  
polypeptides can also be used in a kit for the immunodetection of  
S.aureus in a sample. S.aureus is implicated in numerous human diseases,  
including cellulitis, eyelid infections, scalded skin syndrome, toxic shock  
syndrome, etc. Organisms transformed with the DNA sequences can be used  
for recombinant production of the polypeptides. The new DNA sequences  
(and their fragments) are useful as primers or probes for isolating  
homologues of any of the S.aureus DNA sequences contained on the  
computer readable medium.

Sequence 400 BP; 105 A; 82 C; 66 G; 107 T; 40 other;

Query Match 22.5%; Score 105.2; DB 18; Length 400;  
Best Local Similarity 67.9%; Pred. No. 1.9e-23;  
Matches 167; Conservative 0; Mismatches 68; Indels 11; Gaps 1;

QY 10 ATCAGCTGTCTCATAGCTCCACAGCAATTCCTTGATTCATTGAAGAGACGATTAGT 69

DB 348 ACATCTTCTTTCAGAAGATGCGGAATAACGTGACATATTTGATTCAGTTTGAATGTTG 289

QY 70 TAGCAACCTTCGATTTGGTCTGTAGCTCAGTTGGTTAGAGCCGCCCTGATAAGGGTGA 129

DB 288 TTCAATCAAAATTAATGGGCTATACCTCAGCTGGTTAGAGCCGCCCTGATAAGGGTGA 229

QY 130 GGTGGGAGTTCGAATCTGCCAGACCCACCAAT-----TTGCTGGGGCCATAG 178

DB 228 GGTGGGAGTTCGAATCTGCCAGACCCACCAAT-----TTGCTGGGGCCATAG 169

QY 179 CTCAGCTGGGAGAGCGCTGCTTCACGAGGAGGTTCAGCGGTTCGATCCGCTGGCT 238

DB 168 CTCAGCTGGGAGAGCGCTGCTTCACGAGGAGGTTCAGCGGTTCGATCCGCTGGCT 109

QY 239 CCACCA 244

DB 108 CCACCA 103

RESULT 11

AAV77852

ID AAV77852 standard; DNA; 1311 BP.

XX AC AAV77852;

XX DT 16-MAR-1999 (first entry)

XX DE Staphylococcus aureus contig SEQ ID #3541.

XX KW Computer readable medium; vaccine; S.aureus infection; immunodetection;  
XX KW cellulitis; eyelid infection; food poisoning; osteomyelitis; therapy;  
XX KW skin infection; surgical wound infection; scalded skin syndrome;  
XX KW toxic shock syndrome; ds.

XX OS Staphylococcus aureus.

XX PN EP786519-A2.

XX PD 30-JUL-1997.

XX PF 07-JAN-1997; 97EP-0100117.

XX PR 05-JAN-1996; 96US-0009861.

XX PA (HUMA-) HUMAN GENOME SCI INC.

XX PI Barash SC, Choi GH, Dillon PJ, Fannon MR, Kunsch CA;

XX PI Rosen CA;

XX DR WPI; 1997-374922/35.

XX PT Polynucleotide(s) and proteins derived from Staphylococcus aureus -  
XX PT stored on computer readable medium and used in the production of  
XX PT anti-S.aureus vaccines

XX PS Claim 1; Page 2576; 3271pp; English.

XX CC This sequence represents one of 5191 Staphylococcus aureus DNA sequences  
XX CC of the invention. The DNA sequences are recorded on a computer readable  
XX CC medium, preferably selected from a floppy or hard disk, random access  
XX CC memory (RAM), read-only memory (ROM) or CD-ROM. Homology searches using  
XX CC the S.aureus DNA sequences allows putative functions to be assigned so  
XX CC that protein-encoding or regulatory regions of commercial, therapeutic or  
XX CC industrial importance can be obtained. Specifically, sequences which are  
XX CC likely to encode antigens have been identified and these polypeptides can  
XX CC be used in a vaccine composition against S.aureus infection. The  
XX CC polypeptides can also be used in a kit for the immunodetection of  
XX CC S.aureus in a sample. S.aureus is implicated in numerous human diseases,  
XX CC including cellulitis, eyelid infections, scalded skin syndrome, toxic shock  
XX CC syndrome, etc. Organisms transformed with the DNA sequences can be used  
XX CC for recombinant production of the polypeptides. The new DNA sequences  
XX CC (and their fragments) are useful as primers or probes for isolating  
XX CC homologues of any of the S.aureus DNA sequences contained on the  
XX CC computer readable medium.

SQ Sequence 1311 BP; 380 A; 264 C; 328 G; 334 T; 5 other;

Query Match 22.5%; Score 105.2; DB 18; Length 1311;  
Best Local Similarity 67.9%; Pred. No. 3.5e-23;  
Matches 167; Conservative 0; Mismatches 68; Indels 11; Gaps 1;

QY 10 ATCAGCTGTCTCATAGCTCCACAGCAATTCCTTGATTCATTGAAGAGACGATTAGT 69

DB 590 AACATCTTCTTTCAGAAGATGCGGAATAACGTGACATATTTGATTCAGTTTGAATGTTG 649

QY 70 TAGCAACCTTCGATTTGGTCTGTAGCTCAGTTGGTTAGAGCCGCCCTGATAAGGGTGA 129

DB 650 TTCATCAAAATTAATGGGCTATACCTCAGCTGGTTAGAGCCGCCCTGATAAGGGTGA 709

QY 130 GGTGGGAGTTCGAATCTGCCAGACCCACCAAT-----TTGCTGGGGCCATAG 178

Db 710 GGTGGTGGTTCGAGTCCACTAGGCCACCATTAAATTAATACCTATTTGGGGCTTAG 769  
QY 179 CTGAGCTGGGAGAGCGCTGCTTGCACGAGGAGGTCAGCGTTCGATCCGCTTGGCT 238  
Db 770 CTGAGCTGGGAGAGCGCTGCTTGCACGAGGAGGTCAGCGTTCGATCCGCTAGTCT 829  
QY 239 CCACCA 244  
Db 830 CCACCA 835  
RESULT 12  
AAQ14106  
ID AAQ14106 standard; DNA: 664 BP.  
XX  
AC AAQ14106;  
XX  
DT 10-JAN-1992 (first entry)  
XX  
DE N.meningitidis NCTC 10025 16S to 23S rRNA gene spacer region.  
XX  
KW rRNA gene; ribosomal RNA; probe; ss.  
XX  
OS Neisseria meningitidis NCTC 10025.  
XX  
PN EP452596-A.  
XX  
PD 23-OCT-1991.  
XX  
PF 18-APR-1990; 90EP-0401054.  
XX  
PR 18-APR-1990; 90EP-0401054.  
XX  
PA (INNO-) INNOGENETICS NV SA.  
XX  
PI Rossau R, Van Heuverswijn H;  
XX  
DR WPI; 1991-311940/43.  
XX  
PT Hybridisation probes for detecting non-viral microorganisms -  
PT derived from spacer region between 16S and 23S rRNA genes, for  
PT detecting e.g. BORDETELLA PERTUSSIS, NEISSERIA GONORRHOEA  
XX  
PS Disclosure; Fig 3; 4lpp; English.  
XX  
CC This sequence is the non-coding strand of the 16S-23S rRNA gene  
CC spacer region; the 5'-end is proximal to the 16S rRNA gene and the 3'-  
CC -end proximal to the 23S rRNA gene. A set of probes was designed  
CC based on this sequence which was specific for N.meningitidis. A kit  
CC is provided for detection of this species using the probes.  
XX  
SQ Sequence 664 BP; 235 A; 123 C; 154 G; 152 T; 0 other;  
Query Match 22.4%; Score 104.8; DB 12; Length 664;  
Best Local Similarity 82.5%; Pred. No. 3.3e-23;  
Matches 132; Conservative 0; Mismatches 27; Indels 1; Gaps 1;  
QY 85 GGGTCTGTAGTCTAGTGGTTAGAGCGCACCCCTGATAAGGTTGAGTTCGGCAGTTCGAA 144  
Db 100 GGGTTGTAGTCTAGTGGTTAGAGCACACGCTTGATAAGCGTGGGGTCGGAGGTTCAAG 159  
QY 145 TCTGCCAGACCCACCAATTGCTGGGGCCATAGCTAGCTGGGAGAGCGCTGCTTGC 204  
Db 160 TCTCCAGAGACCCACCA-GAACGGGGGGCATAGCTAGTGGTAGAGCACCTGCTTGC 218  
QY 205 ACGAGGAGGTCAGCGTTCGATCCCGCTTGGCTCCACCA 244  
Db 219 AAGCAGGGGTCATCGGTTCGATCCCGCTTGGCTCCACCA 258  
RESULT 13  
AAT11889  
ID AAT11889 standard; DNA: 808 BP.

XX  
AC AAT11889;  
XX  
DT 03-SEP-1996 (first entry)  
XX  
DE Brucella melitensis NIDO Biovar 1 16S-23S rRNA spacer region.  
XX  
KW Probe; detection; identification; microorganism; amplify;  
KW 16S-23S rRNA spacer region; food; universal;  
KW species-specific; ss.  
XX  
OS Brucella melitensis.  
XX  
PN WO9600298-A1.  
XX  
PD 04-JAN-1996.  
XX  
PF 23-JUN-1995; 95WO-EP02452.  
XX  
PR 07-APR-1995; 95EP-0870032.  
PR 24-JUN-1994; 94EP-0870106.  
XX  
PA (INNO-) INNOGENETICS NV.  
XX  
PI Jannes G, Rossau R, Van Heuverswijn H;  
XX  
DR WPI; 1996-068882/07.  
XX  
PT Novel hybridisation assay for the detection of eubacteria - esp  
PT Mycobacterium, comprises amplifying the 16S-23S rRNA spacer region  
XX  
PS Claim 5; Fig 56; 248pp; English.  
XX  
CC The sequences given in AAT11889-905 represent the 16S-23S rRNA spacer  
CC regions derived from various microorganisms. These sequences were  
CC used in the method of the invention for the detection and identification  
CC of at least one or more microorganisms. The method comprises amplifying  
CC the 16S-23S rRNA spacer region and hybridising one or more probes to  
CC the amplified sequence. These probes were specifically used to detect  
CC microorganisms in samples originating from food. This spacer region is  
CC derived from Brucella melitensis NIDO Biovar 1.  
XX  
SQ Sequence 808 BP; 178 A; 181 C; 236 G; 211 T; 2 other;  
Query Match 22.3%; Score 104.4; DB 17; Length 808;  
Best Local Similarity 79.0%; Pred. No. 4.9e-23;  
Matches 139; Conservative 0; Mismatches 31; Indels 6; Gaps 1;  
QY 84 TGGGTCTGTAGTCTAGTGGTTAGAGCGCACCCCTGATAAGGTTGAGTTCGGCAGTTCGA 143  
Db 279 TGGGTCTGTAGTCTAGTGGTTAGAGCACACGCTTGATAAGCGTGGGTTCGGAGGTTCAA 338  
QY 144 ATCTGCCAGACCCACCAATTGCT-----GGGCCATAGCTAGCTGGGAGAGCGCT 197  
Db 339 GTCTCTCCAGGCCACCAAGTTACTTGATGAGGGCCGTAGCTAGCTGGGAGAGCACCT 398  
QY 198 GCCTTGCACGAGGAGTTCAGGGTTCGATCCCGCTTGGCTCCACCCCGCTTG 253  
Db 399 GCTTGTGAAGCAGGGGGTTCGCTGCTGATCCCGTCCGGCTCCACCATCATGTTGG 454  
RESULT 14  
AAT11890  
ID AAT11890 standard; DNA: 808 BP.  
XX  
AC AAT11890;  
XX  
DT 03-SEP-1996 (first entry)  
XX  
DE Brucella suis NIDO Biovar 1 16S-23S rRNA spacer region.  
XX  
KW Probe; detection; identification; microorganism; amplify;  
KW 16S-23S rRNA spacer region; food; universal;

KW species-specific; ss.

XX Brucella suis.

XX WO9600298-Al.

XX 04-JAN-1996.

XX 23-JUN-1995; 95WO-EP02452.

XX 07-APR-1995; 95EP-0870032.

XX 24-JUN-1994; 94EP-0870106.

XX (INNO-) INNOGENETICS NV.

XX Jannes G, Rossau R, Van Heuverswyn H;

XX WPI; 1996-068882/07.

XX Novel hybridisation assay for the detection of eubacteria - esp  
PT Mycobacterium, comprises amplifying the 16S-23S rRNA spacer region

XX Claim 5; Fig 57; 248pp; English.

XX The sequences given in AAT11889-905 represent the 16S-23S rRNA spacer  
CC regions derived from various microorganisms. These sequences were  
CC used in the method of the invention for the detection and identification  
CC of at least one or more microorganisms. The method comprises amplifying  
CC the 16S-23S rRNA spacer region and hybridising one or more probes to  
CC the amplified sequence. These probes were specifically used to detect  
CC microorganisms in samples originating from food. This spacer region is  
CC derived from Brucella suis NIDO Biovar 1.

XX Sequence 808 BP; 177 A; 181 C; 237 G; 210 T; 3 other;

XX Query Match 22.3%; Score 104.4; DB 17; Length 808;  
XX Best Local Similarity 79.0%; Pred. No. 4.9e-23;  
XX Matches 139; Conservative 0; Mismatches 31; Indels 6; Gaps 1;QY 84 TGGGCTGTAGCTCAGTGTGGTTAGAGCGCACACCGCTTGTATAGCGTGGGGTCGGAGGTTCAA 143  
DB 279 TGGGCTGTAGCTCAGTGTGGTTAGAGCGCACACCGCTTGTATAGCGTGGGGTCGGAGGTTCAA 338QY 144 ATCTGCCAGACCCACCAATTGCT-----GGGGCCATAGCTCAGCTGGGAGAGCGCCT 197  
DB 339 GTCTCCAGGCGCCACCAAGTTACTTGTATGAGGGGCGGTAGCTCAGCTGGGAGAGCACCT 398QY 198 GCCTTCACGAGGAGGTGAGCGGTTGATCCCGCTTGGCTCCACCAACCCGCTTG 253  
DB 399 GCTTTGCAAGCAGGGGGTGTGCGGTTGATCCCGCTTGGCTCCACCAACCATCATGTTGG 454XX Search completed: February 1, 2003, 01:41:23  
XX Job time : 343.822 secs

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XX 07-APR-1995; 95EP-0870032.

XX 24-JUN-1994; 94EP-0870106.

XX (INNO-) INNOGENETICS NV.

XX Jannes G, Rossau R, Van Heuverswyn H;

XX WPI; 1996-068882/07.

XX Novel hybridisation assay for the detection of eubacteria - esp  
PT Mycobacterium, comprises amplifying the 16S-23S rRNA spacer region

XX Claim 5; Fig 79; 248pp; English.

XX The sequences given in AAT11889-905 represent the 16S-23S rRNA spacer  
CC regions derived from various microorganisms. These sequences were  
CC used in the method of the invention for the detection and identification  
CC of at least one or more microorganisms. The method comprises amplifying  
CC the 16S-23S rRNA spacer region and hybridising one or more probes to  
CC the amplified sequence. These probes were specifically used to detect  
CC microorganisms in samples originating from food. This spacer region is  
CC derived from Brucella abortus NIDO Tulya biovar 3.

XX Sequence 809 BP; 179 A; 181 C; 236 G; 211 T; 2 other;

XX Query Match 22.3%; Score 104.4; DB 17; Length 809;  
XX Best Local Similarity 79.0%; Pred. No. 4.9e-23;  
XX Matches 139; Conservative 0; Mismatches 31; Indels 6; Gaps 1;QY 84 TGGGCTGTAGCTCAGTGTGGTTAGAGCGCACACCGCTTGTATAGCGTGGGGTCGGAGGTTCAA 143  
DB 280 TGGGCTGTAGCTCAGTGTGGTTAGAGCGCACACCGCTTGTATAGCGTGGGGTCGGAGGTTCAA 339QY 144 ATCTGCCAGACCCACCAATTGCT-----GGGGCCATAGCTCAGCTGGGAGAGCGCCT 197  
DB 340 GTCTCCAGGCGCCACCAAGTTACTTGTATGAGGGGCGGTAGCTCAGCTGGGAGAGCACCT 399QY 198 GCCTTCACGAGGAGGTGAGCGGTTGATCCCGCTTGGCTCCACCAACCCGCTTG 253  
DB 400 GCTTTGCAAGCAGGGGGTGTGCGGTTGATCCCGCTTGGCTCCACCAACCATCATGTTGG 455XX Search completed: February 1, 2003, 01:41:23  
XX Job time : 343.822 secs

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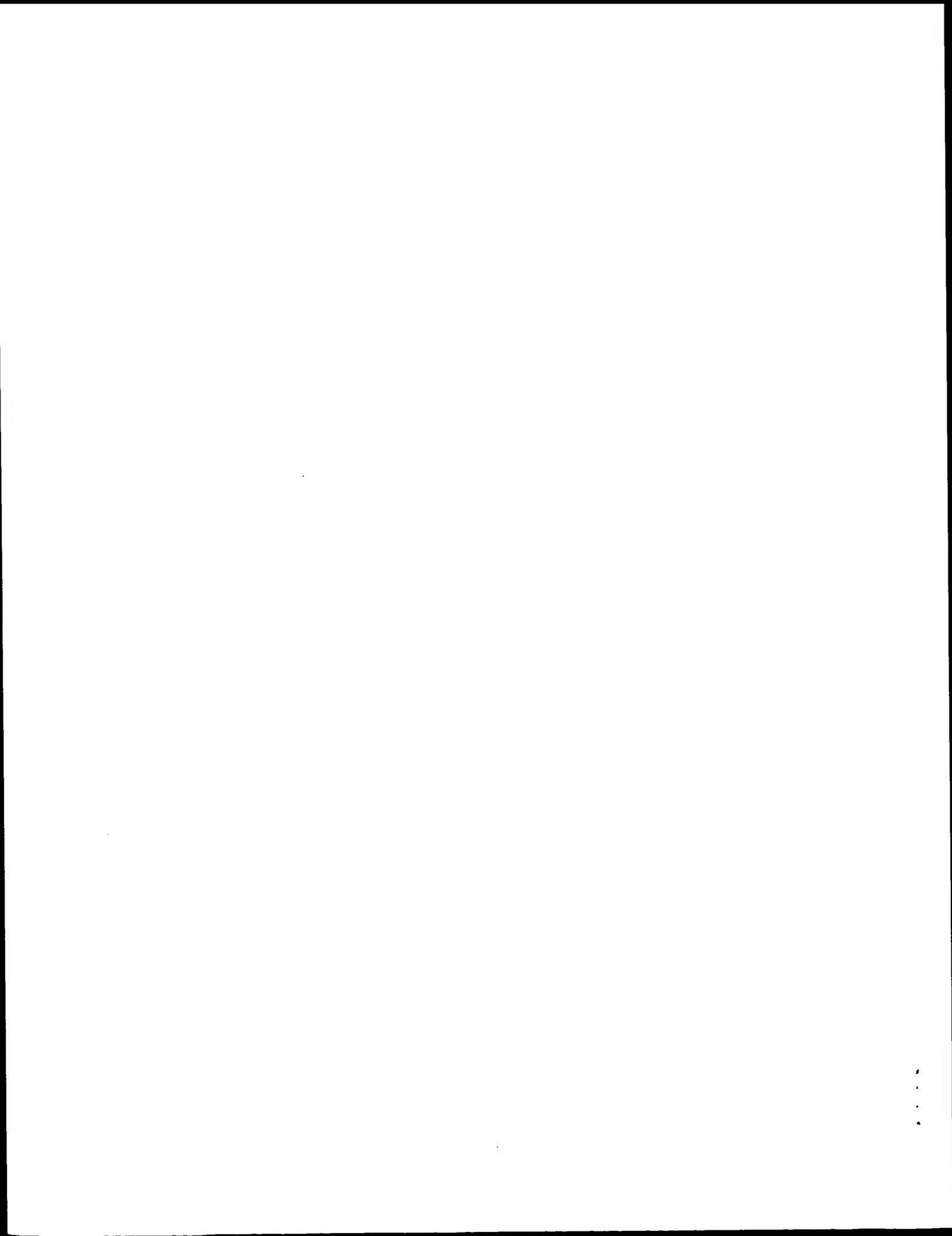
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GenCore version 5.1.3  
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OM nucleic - nucleic search, using sw model

Run on: February 1, 2003, 01:17:06 ; Search time 24.3314 Seconds  
(without alignments)  
5898.736 Million cell updates/sec

Title: US-09-931-486-115

Perfect score: 468

Sequence: 1 ATCGACGACATCAGCTGTCT.....CAGATTGCTGGGGTTATAT 468

Scoring table: IDENTITY\_NUC

Gapop 10.0 , Gapext 1.0

Searched: 441362 seqs, 15338381 residues

Total number of hits satisfying chosen parameters: 882724

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued\_Patents\_NA.\*

1: /cgn2.6/ptodata/1/ina/5A-COMB.seq.\*  
2: /cgn2.6/ptodata/1/ina/5B-COMB.seq.\*  
3: /cgn2.6/ptodata/1/ina/6A-COMB.seq.\*  
4: /cgn2.6/ptodata/1/ina/6B-COMB.seq.\*  
5: /cgn2.6/ptodata/1/ina/PCTUS-COMB.seq.\*  
6: /cgn2.6/ptodata/1/ina/backfiles1.seq.\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

| Result<br>No. | Score | % Query |        | DB | ID                | Description       |
|---------------|-------|---------|--------|----|-------------------|-------------------|
|               |       | Match   | Length |    |                   |                   |
| 1             | 468   | 100.0   | 468    | 3  | US-08-765-332-115 | Sequence 115, App |
| 2             | 468   | 100.0   | 468    | 4  | US-09-448-894-115 | Sequence 115, App |
| 3             | 216   | 46.2    | 471    | 3  | US-08-765-332-111 | Sequence 111, App |
| 4             | 216   | 46.2    | 471    | 4  | US-09-448-894-111 | Sequence 111, App |
| 5             | 205.2 | 43.8    | 504    | 3  | US-08-765-332-113 | Sequence 113, App |
| 6             | 205.2 | 43.8    | 504    | 4  | US-09-448-894-113 | Sequence 113, App |
| 7             | 198.4 | 42.4    | 499    | 3  | US-08-765-332-114 | Sequence 114, App |
| 8             | 198.4 | 42.4    | 499    | 4  | US-09-448-894-114 | Sequence 114, App |
| 9             | 178   | 38.0    | 520    | 3  | US-08-765-332-112 | Sequence 112, App |
| 10            | 178   | 38.0    | 520    | 4  | US-09-448-894-112 | Sequence 112, App |
| 11            | 109   | 23.3    | 603    | 1  | US-08-412-614-85  | Sequence 85, App  |
| 12            | 109   | 23.3    | 603    | 1  | US-08-412-614-86  | Sequence 86, App  |
| 13            | 109   | 23.3    | 603    | 2  | US-08-635-761-85  | Sequence 85, App  |
| 14            | 109   | 23.3    | 603    | 2  | US-08-635-761-86  | Sequence 86, App  |
| 15            | 109   | 23.3    | 603    | 4  | US-09-312-520-85  | Sequence 85, App  |
| 16            | 109   | 23.3    | 603    | 4  | US-09-312-520-86  | Sequence 86, App  |
| 17            | 104.8 | 22.4    | 664    | 1  | US-08-412-614-89  | Sequence 89, App  |
| 18            | 104.4 | 22.3    | 808    | 3  | US-08-765-332-131 | Sequence 131, App |
| 19            | 104.4 | 22.3    | 808    | 3  | US-08-765-332-132 | Sequence 132, App |
| 20            | 104.4 | 22.3    | 808    | 4  | US-09-448-894-131 | Sequence 131, App |
| 21            | 104.4 | 22.3    | 808    | 4  | US-09-448-894-132 | Sequence 132, App |
| 22            | 104.4 | 22.3    | 809    | 3  | US-08-765-332-154 | Sequence 154, App |
| 23            | 104.4 | 22.3    | 809    | 4  | US-09-448-894-154 | Sequence 154, App |
| 24            | 100.8 | 21.5    | 549    | 1  | US-08-412-614-92  | Sequence 92, App  |
| 25            | 100.8 | 21.5    | 549    | 2  | US-08-635-761-92  | Sequence 92, App  |
| 26            | 100.8 | 21.5    | 549    | 4  | US-09-312-520-92  | Sequence 92, App  |
| 27            | 99.4  | 21.2    | 498    | 1  | US-08-412-614-90  | Sequence 90, App  |

28 99.4 21.2 498 2 US-08-635-761-90 Sequence 90, App  
29 99.4 21.2 498 4 US-09-312-520-90 Sequence 90, App  
30 96 20.5 470 3 US-08-765-332-195 Sequence 195, App  
31 96 20.5 470 4 US-09-448-894-195 Sequence 195, App  
32 89 19.0 582 1 US-08-412-614-87 Sequence 87, App  
33 89 19.0 582 2 US-08-635-761-87 Sequence 87, App  
34 89 19.0 582 4 US-09-312-520-87 Sequence 88, App  
35 89 19.0 590 1 US-08-412-614-88 Sequence 88, App  
36 89 19.0 590 2 US-08-635-761-88 Sequence 88, App  
37 89 19.0 590 4 US-09-312-520-88 Sequence 88, App  
38 88.4 18.9 463 3 US-08-765-332-215 Sequence 215, App  
39 88.4 18.9 463 4 US-09-448-894-215 Sequence 215, App  
40 88.4 18.9 475 3 US-08-765-332-214 Sequence 214, App  
41 88.4 18.9 475 4 US-09-448-894-214 Sequence 214, App  
42 87 18.6 654 2 US-08-635-761-89 Sequence 89, App  
43 87 18.6 654 4 US-09-312-520-89 Sequence 89, App  
44 78.6 16.8 363 3 US-08-765-332-119 Sequence 119, App  
45 78.6 16.8 363 4 US-09-448-894-119 Sequence 119, App

## ALIGNMENTS

RESULT 1  
US-08-765-332-115  
; Sequence 115, Application US/08765332  
; Patent No. 6025132  
; GENERAL INFORMATION:  
; APPLICANT: JANNES, GEERT  
; APPLICANT: ROSSAU, RUDI  
; APPLICANT: VAN HEUVERSWYN, HUGO  
; TITLE OF INVENTION: SIMULTANEOUS DETECTION, IDENTIFICATION  
; TITLE OF INVENTION: AND DIFFERENTIATION OF EUBACTERIAL TAXA USING A  
; TITLE OF INVENTION: HYBRIDIZATION ASSAY  
; NUMBER OF SEQUENCES: 216  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: NIXON & VANDERHYE P.C.  
; STREET: 1100 NORTH GLEBE ROAD, 8TH FLOOR  
; CITY: WASHINGTON  
; STATE: D.C.  
; COUNTRY: USA  
; ZIP: 22201  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/765,332  
; FILING DATE: 23-DEC-1996  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: WO PCT/EP95/02452  
; FILING DATE: 23-JUN-1995  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: EP 95870032.0  
; FILING DATE: 07-APR-1995  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: EP 94870106.5  
; FILING DATE: 24-JUN-1994  
; ATTORNEY/AGENT INFORMATION:  
; NAME: SADOFF, B.J.  
; REGISTRATION NUMBER: 36,663  
; REFERENCE/DOCKET NUMBER: 1487-14  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 703-816-4100  
; TELEFAX: 703-816-4100  
; INFORMATION FOR SEQ ID NO: 115:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 468 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear

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; MOLECULE TYPE: cdna
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
US-08-765-332-115

Query Match 100.0%; Score 468; DB 3; Length 468;
Best Local Similarity 100.0%; Pred. No. 9.4e-152;
Matches 468; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ATCGACGACATCAGCTGCTCATAGCTCCACACGAAATTCCTTGATTCATTGAAGAAGA 60
Db 1 ATCGACGACATCAGCTGCTCATAGCTCCACACGAAATTCCTTGATTCATTGAAGAAGA 60
Qy 61 CGATTAGCTTACCAACCTTCGATGGGCTCTAGCTAGTGGTGTAGAGCGCACCCCTGA 120
Db 61 CGATTAGCTTACCAACCTTCGATGGGCTCTAGCTAGTGGTGTAGAGCGCACCCCTGA 120
Qy 121 TAAGGCTGAGTCGCGAGTTCGAATCTGCCAGACCCACCAATTTGCTGGGGCCATAGCT 180
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Qy 181 CAGCTGGGAGAGCGCTGCCCTTCGACGAGGAGTTCAGCGTTCGATCCCGCTTGGCTCC 240
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Db 301 TCTGAACCTTATCAGATCGTTCTTAAATAATTTGGGATGATGATAGAAAGATAGACTGG 360
Qy 361 ACAGCACTTTCAGTGGTGTGTTCAAGCTAAGGTAAATTTGTGAGTAATTACAGTTT 420
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Qy 421 TCGGCAATGTTGTTCTTCACAGTATAACAGATTTCCTGGGGTTATAT 468
Db 421 TCGGCAATGTTGTTCTTCACAGTATAACAGATTTCCTGGGGTTATAT 468

RESULT 3
US-08-765-332-111
; Sequence 111, Application US/08765332
; Patent No. 6025132
; GENERAL INFORMATION:
; APPLICANT: JANNES, GEERT
; APPLICANT: ROSSAU, RUDI
; APPLICANT: VAN HEUVERSWYN, HUGO
; TITLE OF INVENTION: SIMULTANEOUS DETECTION, IDENTIFICATION
; AND DIFFERENTIATION OF EUBACTERIAL TAXA USING A
; HYBRIDIZATION ASSAY

APPLICATION NUMBER: 08/765,332
FILING DATE: <Unknown>
APPLICATION NUMBER: EP 95870032.0
FILING DATE: 07-APR-1995
APPLICATION NUMBER: EP 94870106.5
FILING DATE: 24-JUN-1994
ATTORNEY/AGENT INFORMATION:
NAME: SADOFF, B.J.
REGISTRATION NUMBER: 36,663
REFERENCE/DOCKET NUMBER: 1487-14
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-816-4091
TELEFAX: 703-816-4100
INFORMATION FOR SEQ ID NO: 115:
SEQUENCE CHARACTERISTICS:
LENGTH: 468 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cdna
HYPOTHETICAL: NO
ANTI-SENSE: NO
SEQUENCE DESCRIPTION: SEQ ID NO: 115:
US-09-448-894-115

Query Match 100.0%; Score 468; DB 4; Length 468;
Best Local Similarity 100.0%; Pred. No. 9.4e-152;
Matches 468; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ATCGACGACATCAGCTGCTCATAGCTCCACACGAAATTCCTTGATTCATTGAAGAAGA 60
Db 1 ATCGACGACATCAGCTGCTCATAGCTCCACACGAAATTCCTTGATTCATTGAAGAAGA 60
Qy 61 CGATTAGCTTACCAACCTTCGATGGGCTCTAGCTAGTGGTGTAGAGCGCACCCCTGA 120
Db 61 CGATTAGCTTACCAACCTTCGATGGGCTCTAGCTAGTGGTGTAGAGCGCACCCCTGA 120
Qy 121 TAAGGCTGAGTCGCGAGTTCGAATCTGCCAGACCCACCAATTTGCTGGGGCCATAGCT 180
Db 121 TAAGGCTGAGTCGCGAGTTCGAATCTGCCAGACCCACCAATTTGCTGGGGCCATAGCT 180
Qy 181 CAGCTGGGAGAGCGCTGCCCTTCGACGAGGAGTTCAGCGTTCGATCCCGCTTGGCTCC 240
Db 181 CAGCTGGGAGAGCGCTGCCCTTCGACGAGGAGTTCAGCGTTCGATCCCGCTTGGCTCC 240
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Db 241 ACCACCCGCTTGGCAGTTTGTCAAAGCTTAGAAATGAATATTCGCGTCGAATATTGATT 300
Qy 301 TCTGAACCTTATCAGATCGTTCTTAAATAATTTGGGATGATGATAGAAAGATAGACTGG 360
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Db 361 ACAGCACTTTCAGTGGTGTGTTCAAGCTAAGGTAAATTTGTGAGTAATTACAGTTT 420
Qy 421 TCGGCAATGTTGTTCTTCACAGTATAACAGATTTCCTGGGGTTATAT 468
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RESULT 2
US-09-448-894-115
; Sequence 115, Application US/09448894
; Patent No. 6312903
; GENERAL INFORMATION:
; APPLICANT: JANNES, GEERT
; APPLICANT: ROSSAU, RUDI
; APPLICANT: VAN HEUVERSWYN, HUGO
; TITLE OF INVENTION: SIMULTANEOUS DETECTION, IDENTIFICATION
; AND DIFFERENTIATION OF EUBACTERIAL TAXA USING A
; HYBRIDIZATION ASSAY

NUMBER OF SEQUENCES: 216
CORRESPONDENCE ADDRESS:
ADDRESS: NIXON & VANDERHUYE P.C.
STREET: 1100 NORTH GLEBE ROAD, 8TH FLOOR
CITY: WASHINGTON
STATE: D.C.
COUNTRY: USA
ZIP: 22201
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/448,894
FILING DATE: 29-NOV-1999
CLASSIFICATION: <Unknown>
07-APR-1995
24-JUN-1994
PRIOR APPLICATION DATA:
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; NUMBER OF SEQUENCES: 216
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: NIXON & VANDERHYE P.C.
; STREET: 1100 NORTH GLEBE ROAD, 8TH FLOOR
; CITY: WASHINGTON
; STATE: D.C.
; COUNTRY: USA
; ZIP: 22201
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/765,332
; FILING DATE: 23-DEC-1996
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: WO PCT/EP95/02452
; FILING DATE: 23-JUN-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: EP 95870032.0
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; APPLICATION NUMBER: EP 94870106.5
; FILING DATE: 24-JUN-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: SADOFF, B.J.
; REGISTRATION NUMBER: 36,663
; REFERENCE/DOCKET NUMBER: 1487-14
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 703-816-4100
; TELEFAX: 703-816-4100
; INFORMATION FOR SEQ ID NO: 111:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 471 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; US-08-765-332-111

Query Match 46.2%; Score 216; DB 3; Length 471;
Best Local Similarity 74.9%; Pred. No. 8.4e-65;
Matches 370; Conservative 0; Mismatches 75; Indels 49; Gaps 6;

QY 1 ATCGACGACATCAGCTGTCTCATAAGCTCCACACGAAATTCGTTGATTGATTGAAGAAGA 60
Db 1 ATCGAAGATCCGGCTTCTTCATAAGCTCCACACGAAATTCGTTGATTGATTGATTGAAGA- 59

QY 61 CGATTAGTTAGCAACCTTCGATTGGTGTGCTAGCTCAGTTGGTTAGAGCCACCCCTGA 120
Db 60 -----CGATTGGTGTGCTAGCTCAGTTGGTTAGAGCCACCCCTGA 100

QY 121 TAAGGGTGAGTCCGGCAGTTTCGAATCTGCCAGACCCACCAAT- 164
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QY 165 -----TGCCTGGGGCCATAGCTCAGCTGGGAGAGCGCTGCTTGCACGAGGAGGTGAGC 219
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QY 280 TATTCC- -CGTCCGATATTGATTCTGAACCTT- -ATCAGAACTGCTCTTAAATAATTGG 336
Db 278 TGTTCGTGGATGACATTTGATTCTTGTCTTGCACACGAACTGCTCTTAAATAATTGG 337

QY 337 GTATGTGATAGAAAGATAGACTGGACAGCACTTTTCACTGGTGTGTTCAAGGCTTAAGGTA 396
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QY 397 AAATTTGTGAGT- -AATTACAAAGTTTTCGGCGAAATGTTGTTCTTCACAGTATACCAAGATT 454
Db 398 AAATTTGCGAGTTCAAGCGCAATTTTCGGCGAAATGTTGTTCTTCACAGTATACCAAGATT 457
QY 455 GCTTGGGGTTATAT 468
Db 456 GCTTGGGGTTATAT 471

RESULT 4
US-09-448-894-111
; Sequence 111, Application US/09448894
; Patent No. 6312903
; GENERAL INFORMATION:
; APPLICANT: JANNES, GEERT
; ROSSAU, RUDI
; VAN HEUVERSWYN, HUGO
; TITLE OF INVENTION: SIMULTANEOUS DETECTION, IDENTIFICATION
; AND DIFFERENTIATION OF EUBACTERIAL TAXA USING A
; HYBRIDIZATION ASSAY
; NUMBER OF SEQUENCES: 216
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: NIXON & VANDERHYE P.C.
; STREET: 1100 NORTH GLEBE ROAD, 8TH FLOOR
; CITY: WASHINGTON
; STATE: D.C.
; COUNTRY: USA
; ZIP: 22201
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/448,894
; FILING DATE: 29-NOV-6312903-1999
; CLASSIFICATION: <Unknown>
; 07-APR-1995
; 24-JUN-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/765,332
; FILING DATE: <Unknown>
; APPLICATION NUMBER: EP 95870032.0
; FILING DATE: 07-APR-1995
; APPLICATION NUMBER: EP 94870106.5
; FILING DATE: 24-JUN-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: SADOFF, B.J.
; REGISTRATION NUMBER: 36,663
; REFERENCE/DOCKET NUMBER: 1487-14
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 703-816-4091
; TELEFAX: 703-816-4100
; INFORMATION FOR SEQ ID NO: 111:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 471 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; SEQUENCE DESCRIPTION: SEQ ID NO: 111:
US-09-448-894-111

Query Match 46.2%; Score 216; DB 4; Length 471;
Best Local Similarity 74.9%; Pred. No. 8.4e-65;
Matches 370; Conservative 0; Mismatches 75; Indels 49; Gaps 6;

QY 1 ATCGACGACATCAGCTGTCTCATAAGCTCCACACGAAATTCGTTGATTGATTGAAGAAGA 60
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Db 1 ATCGAAGATCCGGCTCTTCTATAGCTCCACAGCAATGCTTGATTCACCTGGTTAGA- 59  
Qy 61 CGATTAGGTACCAACCTTCGATTGGTCTAGCTCAGTTGTTAGAGCGCACCCCTCA 120  
Db 60 -----CGATTGGGTCTAGCTCAGTTGTTAGAGCGCACCCCTCA 100  
Qy 121 TAAGGGTGGGTCGAGTTCGAATCTGCCAGACCCACCAAT----- 164  
Db 101 TAAGGGTGGGTCGAGTTCGAATCTGCCAGACCCACCAATTTGTTGGTGTGCGTG 160  
Qy 165 -----TGTGGGGCCATAGCTCAGCTGGAGAGCGGCTTGCACGAGAGGTGACG 219  
Db 161 ATCCGATACGGGGCCATAGCTCAGCTGGAGAGCGGCTTGCACGAGAGGTGACG 220  
Qy 220 GGTTCGATCCCGCTGGCTCCACGACCCCGCTTGCACGAGTTCGAAGCTTGAAGTAA 279  
Db 221 AGTTCGATCCCTTGGGTCCACCATC-----TAAACAAATCGTGAAGCTCAGAAATGAA 277  
Qy 280 TATTCG-CGTCAATATTGATTCTGAACCTT--ATCAGAATCGTTCTTTAAAAATTTGG 336  
Db 278 TGTTCGTGATGAACATGATTCTGGTCTTGCACGAGACTGTTCTTTAAAAATTCGG 337  
Qy 337 GTATGTATAGAAATAGACTGGACAGCACTTTCACCTGGTGTGTTTCAGGCTAAGTA 396  
Db 338 GTATGTATAGAAATGAAGACTGAATGATCTCTTTCACCTGGTGTATCAAGTCAAGTA 397  
Qy 397 AATTTGTGAGT--AATTACAAGTTTTCGGCGAATGTTCTTTCACGATATACAGATT 454  
Db 398 AATTTGGGAGTTCAAGCGCGAATTTTCGGCGAATGTTCTTTCACGATATACAGATT 457  
Qy 455 GCTTGGGGTTATAT 468  
Db 458 GCTTGGGGTTATAT 471

## RESULT 5

US-08-765-332-113  
; Sequence 113, Application US/08765332  
; Patent No. 6025132  
; GENERAL INFORMATION:  
; APPLICANT: JANNES, GEERT  
; APPLICANT: ROSSAU, RUDI  
; APPLICANT: VAN HEUVERSWYN, HUGO  
; TITLE OF INVENTION: SIMULTANEOUS DETECTION, IDENTIFICATION  
; AND DIFFERENTIATION OF EUBACTERIAL TAXA USING A  
; TITLE OF INVENTION: HYBRIDIZATION ASSAY  
; NUMBER OF SEQUENCES: 216  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: NIXON & VANDERHUYE P.C.  
; STREET: 1100 NORTH GLEBE ROAD, 8TH FLOOR  
; CITY: WASHINGTON  
; STATE: D.C.  
; COUNTRY: USA  
; ZIP: 22201  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/765.332  
; FILING DATE: 23-DEC-1996  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: WO PCT/EP95/02452  
; FILING DATE: 23-JUN-1995  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: EP 95870032.0  
; FILING DATE: 07-APR-1995  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: EP 94870106.5  
; FILING DATE: 24-JUN-1994

; ATTORNEY/AGENT INFORMATION:  
; NAME: SADOFF, B.J.  
; REGISTRATION NUMBER: 36,663  
; REFERENCE/DOCKET NUMBER: 1487-14  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 703-816-4091  
; TELEFAX: 703-816-4100  
; INFORMATION FOR SEQ ID NO: 113:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 504 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: cDNA  
; HYPOTHETICAL: NO  
; ANTI-SENSE: NO  
US-08-765-332-113

Query Match 43.8%; Score 205.2; DB 3; Length 504;  
Best Local Similarity 74.7%; Pred. No. 4.7e-61;  
Matches 378; Conservative 0; Mismatches 88; Indels 40; Gaps 8;  
Qy 1 ATCGAGCATCAGCTGCTCATAGCTCCACAGCAATGCTTGATTCAT-TTGAAGAAG 59  
Db 1 ATCGAAGACACCGGCTTCGTCATAAGCTCCACAGCAATGCTTGATTCACCTGCGAAG 60  
Qy 60 ACGATTAGGTAGCAACCTT-----CGATTGGGTCTAGCTCAGTTGGTTAGAGCGCA 113  
Db 61 GCGATTGGTTAGACCCGAGAGTAACGATTGGGTCTGTAGCTCAGTTGGTTAGAGCGCA 120  
Qy 114 CCCCTGATAAGGGTGAGGTCGGCAGTTCCGAATCTGCCAGACCCACCAATTTGCTGGGGC 173  
Db 121 CCCCTGATAAGGGTGAGGTCGGCAGTTCCGAATCTGCCAGACCCACCAATTTGCTGGGGC 179  
Qy 174 CATAGCTAGCTGGAGAGCGGCTGCTTGCACGAGGAGGTCAGGGGTCGATCCCGCT 233  
Db 180 CATAGCTAGCTGGAGAGCGGCTGCTTGCACGAGGAGGTCAGGGGTCGATCCCGCT 239  
Qy 234 TGGCTCCAC-----ACCCCGCTTCCAGTTTGTCAAAGCTTAGAA 274  
Db 240 TGGCTCCACCATTAATCTAGTCGGCGAAGCTCAGAAATGAGTGTTCACGAGATGAGG 299  
Qy 275 ATGAATATTCGGTCCGAATATTGATTTCTGAACCTT--ATCAGAATCGTTCTTTAAAAAT 332  
Db 300 TTGATTGCTGGGTTCGAACATTTCTGACTTTTGGCTGCGCCAGCAACTGTTCTTTAAAAAT 359  
Qy 333 TTGGGTATGTATAGAAATAGACTGGACAGCACTTTTCACCTGGTGTGTTTCAGGCTAA 392  
Db 360 TTGGGTATGTATAGAAATAGACTGGACAGCACTTTTCACCTGGTGTGTTTCAGGCTAA 418  
Qy 393 GGTAAATTTGTGAGTAAT---TACAAGTTTTCGGCGAATGTTCTTTCACAGTA----- 444  
Db 419 GGTAAATTTGTGAGTAATTTCTCTATGCAAAATTTTCGGCGAATGTTCTTTCACGTTATAGAC 478  
Qy 445 --TAACCAAGATTGCTTGGGGTTATAT 468  
Db 479 AGTAACCAAGATTGCTTGGGGTTATAT 504

## RESULT 6

US-09-448-894-113  
; Sequence 113, Application US/09448894  
; Patent No. 6312903  
; GENERAL INFORMATION:  
; APPLICANT: JANNES, GEERT  
; APPLICANT: ROSSAU, RUDI  
; APPLICANT: VAN HEUVERSWYN, HUGO  
; TITLE OF INVENTION: SIMULTANEOUS DETECTION, IDENTIFICATION  
; AND DIFFERENTIATION OF EUBACTERIAL TAXA USING A  
; HYBRIDIZATION ASSAY  
; NUMBER OF SEQUENCES: 216  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: NIXON & VANDERHUYE P.C.

STREET: 1100 NORTH GLEBE ROAD, 8TH FLOOR  
CITY: WASHINGTON  
STATE: D.C.  
COUNTRY: USA  
ZIP: 22201

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/448,894  
FILING DATE: 29-NOV-1999  
CLASSIFICATION: <Unknown>  
07-APR-1995  
24-JUN-1994

PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/765,332  
FILING DATE: <Unknown>  
APPLICATION NUMBER: EP 95870032.0  
FILING DATE: 07-APR-1995  
APPLICATION NUMBER: EP 94870106.5  
FILING DATE: 24-JUN-1994

ATTORNEY/AGENT INFORMATION:  
NAME: SADOFF, B.J.  
REGISTRATION NUMBER: 36,663  
REFERENCE/DOCKET NUMBER: 1487-14  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 703-816-4091  
TELEFAX: 703-816-4100

INFORMATION FOR SEQ ID NO: 113:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 504 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
SEQUENCE DESCRIPTION: SEQ ID NO: 113:

US-09-448-894-113

Query Match 43.8%; Score 205.2; DB 4; Length 504;  
Best Local Similarity 74.7%; Pred. No. 4.7e-61;  
Matches 378; Conservative 0; Mismatches 88; Indels 40; Gaps 8;

QY 1 ATCGACGACATCAGCTGCTCATAGTCCACACGAATGCTTGATCA-TTGAAGAG 59  
DB 1 ATCGAAGACCGGCTTCGTATAAGTCCACACGAATGCTTGATCACTTGGCGAAG 60

QY 60 ACGATTAGGTAGCAACCTT-----CGATTGGGTCTGTAGCTCAGTTGGTTAGAGCGCA 113  
DB 61 GCGATTGGTTAGACCCGAGAGTAACGATGGGTCTGTAGCTCAGTTGGTTAGAGCGCA 120

QY 114 CCCCTGATAAGGTGAGGTGCGGCAATCGAATCTCCAGACCCACCAATTTGCTGGGCG 173  
DB 121 CCCCTGATAAGGTGAGGTGCGGCAATCGAATCTCCAGACCCACCAATTTGCTGGGCG 179

QY 174 CATAGCTCAGCTGGGAGAGCGCTCGCTTGCACGAGGAGGTCAGATCCCGCT 233  
DB 180 CATAGCTCAGCTGGGAGAGCGCTCGCTTGCACGAGGAGGTCAGATCCCGCT 239

QY 234 TGGCTCCACC-----ACCCCGCTTGCCAGTTTGTCAAAGCTTAGAA 274  
DB 240 TGGCTCCACCATAACTAGTCGCGGAAAGCTCAGAATGAGTGTACAGGATGAGG 299

QY 275 ATGAATATTCGGTGCATATGATTTCTGAATCTT--ATCAATATCTCTTTTAAAT 332  
DB 300 TTGATTGCTGGTGAACATTTGATTTCTGGACTTTGGCCAGCACTGTTCTTTAAAT 359

QY 333 TTGGTATGATAGAAAGATAGACTGGACAGCACTTTCACTGGTGTGTTCAGCGTAA 392  
DB 360 TTGGTATGATAGAAAGATAG-CCGATGTGTGTTTCACTGGGAGCATGTGCGGTCAA 418

QY 393 GGTAAATTTGTGAGTAAT---TACAAGTTTTCGGCGAATGTTGTTCTTACAGTA----- 444  
DB 419 GGTAAATTTGCGTGTCTCTATGCAAAATTTTCGGCGAATGTCGTCTTACGTTATAGAC 478

QY 445 --TAACCAGATTGCTTGGGGTTATAT 468  
DB 479 AGTAACCAGATTGCTTGGGGTTATAT 504

RESULT 7  
US-08-765-332-114  
; Sequence 114, Application US/08765332  
; Patent No. 6025132  
; GENERAL INFORMATION:  
; APPLICANT: JANNES, GEERT  
; APPLICANT: ROSSAU, RUDI  
; APPLICANT: VAN HEUVERSWYN, HUGO  
; TITLE OF INVENTION: SIMULTANEOUS DETECTION, IDENTIFICATION  
; TITLE OF INVENTION: AND DIFFERENTIATION OF EUBACTERIAL TAXA USING A  
; TITLE OF INVENTION: HYBRIDIZATION ASSAY  
; NUMBER OF SEQUENCES: 216  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: NIXON & VANDERHYE P.C.  
; STREET: 1100 NORTH GLEBE ROAD, 8TH FLOOR  
; CITY: WASHINGTON  
; STATE: D.C.  
; COUNTRY: USA  
; ZIP: 22201

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/765,332  
FILING DATE: 23-DEC-1996  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: WO PCT/EP95/02452  
FILING DATE: 23-JUN-1995  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: EP 95870032.0  
FILING DATE: 07-APR-1995  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: EP 94870106.5  
FILING DATE: 24-JUN-1994  
ATTORNEY/AGENT INFORMATION:  
NAME: SADOFF, B.J.  
REGISTRATION NUMBER: 36,663  
REFERENCE/DOCKET NUMBER: 1487-14  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 703-816-4091  
TELEFAX: 703-816-4100  
INFORMATION FOR SEQ ID NO: 114:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 499 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
US-08-765-332-114

Query Match 42.4%; Score 198.4; DB 3; Length 499;  
Best Local Similarity 72.8%; Pred. No. 1e-58;  
Matches 367; Conservative 0; Mismatches 96; Indels 41; Gaps 7;

QY 1 ATCGACGACATCAGCTGCTCATAGTCCACACGAATGCTTGATTTGATTCAGAAAGA 60  
DB 1 ATCGAAGACTTCAGCTTCTTTCATAGTTCACACGAATGCTTGATTCAGTTCGGAAGA 60

QY 61 CGATTAGGTTAGCAACCTT-----CGATTGGTCTGTAGCTCAGTTGGTTAGAGCGCA 113  
Db 61 GCAGATTGGTTGAGACCCGAGAGTGACGATTTGGTCTGTAGCTCAGTTGGTTAGAGCGCA 120  
QY 114 CCCTGATAGAGGTGAGGTGGGAGTTCGATCTGCCAGACCCACCAATTTGC-----167  
Db 121 CCCTGATAGAGGTGAGGTGGGAGTTCGATCTGCCAGACCCACCAATTTGC-----180  
QY 168 -----TGGGCGCATAGCTCAGCTGGGAGAGCGCTGCTTGCACGCGAGGAGGT 215  
Db 181 GCAGATTGGTTGAGACCCGAGAGTGACGATTTGGTCTGTAGCTCAGTTGGTTAGAGCGCA 240  
QY 216 CAGCGTTTCGATCCCGCTTGGCTCCACACCCCGCTTGCAGATTTGTCAAAAGCTTAGAAA 275  
Db 241 CAGGAGTTCCATCCTCTGGCTCCACCA--TCAACTCAGCATCGCTGAAGCTCAGAAA 298  
QY 276 TGAATATTCG-CGTGCAATATGATTTCTGAACCTT--ATCAGAACTGTTCTTAAATAAT 332  
Db 299 TGAACATTTGATGTTCAATGTTGATTTCTGCTTTCGCCAGAACTGTTCTTAAATAAT 358  
QY 333 TTGGGTATGTGATAGAAAGATAGACTGCAGACGACTTTTCACTGTTGTGTTTCAAGGCTAA 392  
Db 359 TTGGGTATGTGATAGAAAGATAGACTGCAGACGACTTTTCACTGTTGTGTTTCAAGGCTAA 415  
QY 393 GGTAAATTTGATGATAGAAAGATAGACTGCAGACGACTTTTCACTGTTGTGTTTCAAGGCTAA 444  
Db 416 CAAATTTGCGAGTTCAAGCGCGAATTTTCGGCGAATGCTGCTTCAAGTTACGAATCTA 475  
QY 445 TAACAGATTGCTTGGGGTTATAT 468  
Db 476 TAACAGATTGCTTGGGGTTATAT 499

## RESULT 8

US-09-448-894-114  
; Sequence 114, Application US/09448894  
; Patent No. 6312903  
; GENERAL INFORMATION:  
; APPLICANT: JANNES, GEERT  
; VAN HEUVERSWYN, HUGO  
; ROSSAU, RUDI  
; TITLE OF INVENTION: SIMULTANEOUS DETECTION, IDENTIFICATION  
; AND DIFFERENTIATION OF EUBACTERIAL TAXA USING A  
; HYBRIDIZATION ASSAY  
; NUMBER OF SEQUENCES: 216  
; CORRESPONDENCE ADDRESS:  
; ADDRESS: NIXON & VANDERHVE P.C.  
; STREET: 1100 NORTH GLEBE ROAD, 8TH FLOOR  
; CITY: WASHINGTON  
; STATE: D.C.  
; COUNTRY: USA  
; ZIP: 22201  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patentin Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/448,894  
; FILING DATE: 29-Nov. 6312903-1999  
; CLASSIFICATION: <Unknown>  
; 07-APR-1995  
; 24-JUN-1994  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/765,332  
; FILING DATE: <Unknown>  
; APPLICATION NUMBER: EP 95870032.0  
; FILING DATE: 07-APR-1995  
; APPLICATION NUMBER: EP 94870106.5  
; FILING DATE: 24-JUN-1994  
; ATTORNEY/AGENT INFORMATION:  
; NAME: SADOFF, B.J.  
; REGISTRATION NUMBER: 36,663

REFERENCE/DOCKET NUMBER: 1487-14  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 703-816-4091  
TELEFAX: 703-816-4100  
INFORMATION FOR SEQ ID NO: 114:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 499 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
SEQUENCE DESCRIPTION: SEQ ID NO: 114:  
US-09-448-894-114

Query Match 42.4%; Score 198.4; DB 4; Length 499;  
Best Local Similarity 72.8%; Pred. No. 1e-58;  
Matches 367; Conservative 0; Mismatches 96; Indels 41; Gaps 7;  
QY 1 ATCGAGCATCAGCTGTCTCATAAGCTCCACACGAATTTGCTTGATTCATTGGAAGA 60  
Db 1 ATCGAGCATCAGCTGTCTCATAAGCTCCACACGAATTTGCTTGATTCATTGGAAGA 60  
QY 61 CGATTAGGTTAGCAACCTT-----CGATTGGTCTGTAGCTCAGTTGGTTAGAGCGCA 113  
Db 61 CGATTAGGTTAGCAACCTT-----CGATTGGTCTGTAGCTCAGTTGGTTAGAGCGCA 120  
QY 114 CCCCTGATAGAGGTGAGGTGGGAGTTCGAACTGCGCCAGACCCACCAATTTGC-----167  
Db 121 CCCCTGATAGAGGTGAGGTGGGAGTTCGAACTGCGCCAGACCCACCAATTTGC-----180  
QY 168 -----TGGGCGCATAGCTCAGCTGGGAGAGCGCTGCTTGCACGCGAGGAGGT 215  
Db 181 GCCAGTGTCAATGGGCGCATAGCTCAGCTGGGAGAGCGCTGCTTGCACGCGAGGAGGT 240  
QY 216 CAGCGTTTCGATCCCGCTTGGCTCCACACCCCGCTTGCAGATTTGTCAAAAGCTTAGAAA 275  
Db 241 CAGGAGTTCCATCCTCTGGCTCCACCA--TCAACTCAGCATCGCTGAAGCTCAGAAA 298  
QY 276 TGAATATTCG-CGTGCAATATGATTTCTGAACCTT--ATCAGAACTGTTCTTAAATAAT 332  
Db 299 TGAACATTTGATGTTCAATGTTGATTTCTGCTTTCGCCAGAACTGTTCTTAAATAAT 358  
QY 333 TTGGGTATGTGATAGAAAGATAGACTGCAGACGACTTTTCACTGTTGTGTTTCAAGGCTAA 392  
Db 359 TTGGGTATGTGATAGAAAGATAGACTGCAGACGACTTTTCACTGTTGTGTTTCAAGGCTAA 415  
QY 393 GGTAAATTTGATGATAGAAAGATAGACTGCAGACGACTTTTCACTGTTGTGTTTCAAGGCTAA 444  
Db 416 CAAATTTGCGAGTTCAAGCGCGAATTTTCGGCGAATGCTGCTTCAAGTTACGAATCTA 475  
QY 445 TAACAGATTGCTTGGGGTTATAT 468  
Db 476 TAACAGATTGCTTGGGGTTATAT 499

## RESULT 9

US-08-765-332-112  
; Sequence 112, Application US/08765332  
; Patent No. 6025132  
; GENERAL INFORMATION:  
; APPLICANT: JANNES, GEERT  
; VAN HEUVERSWYN, HUGO  
; ROSSAU, RUDI  
; TITLE OF INVENTION: SIMULTANEOUS DETECTION, IDENTIFICATION  
; AND DIFFERENTIATION OF EUBACTERIAL TAXA USING A  
; HYBRIDIZATION ASSAY  
; NUMBER OF SEQUENCES: 216  
; CORRESPONDENCE ADDRESS:  
; ADDRESS: NIXON & VANDERHVE P.C.  
; STREET: 1100 NORTH GLEBE ROAD, 8TH FLOOR  
; CITY: WASHINGTON



Db 61 AATGCTGTAAACGGACCCCGTGTATAGGCTGTAGCTAGTGGTTAGAGCGCACCCCTG 120  
QY 120 ATAAGGGTCAGGTCGGCAGTTCGAATCTGCCAGACCCACCAATTTGCT-----168  
Db 121 ATAAGGGTCAGGTCGGCAGTTCGAATCTGCCAGACCCACCAATTTGCTGGTTCGAGAAGA 180  
QY 169 -----GGGGCCATAGCTACAGCTGGGAGAGCGCCCTTCACGACAGGAGTTCAGCGGTTTC 224  
Db 181 ATACGGGGCCATAGCTACAGCTGGGAGAGCGCCCTTCACGACAGGAGTTCAGCGGTTTC 240  
QY 225 GATCCCGCTTGCTCCACACCC-----CGCTTCCAGTGTTCGAAGCTTAGAATG 277  
Db 241 GATCCCGCTTGCTCCACACCTCTCGTGTTCGCGTGTGTAAGAGAGTTCAGAAATG 300  
QY 278 A-----ATATTCGCGTCGAATATGATTTCTGAACCT-----TATCAGAA 317  
Db 301 ATGCCCTTCAGGTTGCTGTTGAGTGTGATTTCTGCTTTGACCGGTACGAAA 360  
QY 318 TCCTTCTTTAAATTTGGGATGTGATAGAAAGATAGACTGGACAGCACTTTCACTGGT 377  
Db 361 TCCTTCTTTAAATTTGGGATGTGATAGAAAGTACTGATTAATG--CTTTCACTGGC 418  
QY 378 GTGTGTTAGGCTAAGGTAATTTCTGAGT----AATTACAGTTTTCGGCGAATGTTG 433  
Db 419 AATTGATCTGGTCAAGTAAATTTAGTTCTCAGACGCAATTTTCGGCGAATGTCG 478  
QY 434 TCTTCAC-----AGTATAACACAGATGCTTGGGGTTATAT 468  
Db 479 TCTTCAGATTGAGACAGTAACAGATGCTTGGGGTTATAT 520

## RESULT 11

US-08-412-614-85  
; Sequence 85, Application US/08412614  
; Patent No. 5536638  
; GENERAL INFORMATION:  
; APPLICANT: Rossau, Rudi  
; TITLE OF INVENTION: Hybridization Probes Derived from the  
; TITLE OF INVENTION: Spacer Region Between the 16S and 23S rRNA Genes for the  
; TITLE OF INVENTION: Detection of No. 5536638-Viral Microorganisms  
; NUMBER OF SEQUENCES: 104  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Merchant & Gould  
; STREET: 3100 No. 5536638west Center  
; CITY: Minneapolis  
; STATE: MN  
; COUNTRY: USA  
; ZIP: 55402-4131

COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette 3.5 inch, 1.44 mb capacity  
COMPUTER: IBM PC compatible (Compaq Deskpro 286e)  
OPERATING SYSTEM: MS-DOS  
SOFTWARE: Wordperfect Version #5.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/412,614  
FILING DATE:  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/965,394  
FILING DATE: 17-DEC-1992  
APPLICATION NUMBER: PCT/EP91/00743  
FILING DATE: 18-APR-1991  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: GB/90901054.3  
FILING DATE: 18-APR-1990  
ATTORNEY/AGENT INFORMATION:  
NAME: Hillson, Randall A.  
REGISTRATION NUMBER: 31,838  
REFERENCE/DOCKET NUMBER: 8076,75-USWO  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 612-332-5300  
TELEFAX: 612-332-9081

## ; INFORMATION FOR SEQ ID NO: 85:

; SEQUENCE CHARACTERISTICS:  
; LENGTH: 603 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: DNA (genomic)  
; HYPOTHETICAL: NO  
; ANTI-SENSE: NO  
; ORIGINAL SOURCE:  
; ORGANISM: Neisserai gonorrhoeae  
; STRAIN: NCTC 8375  
; US-08-412-614-85

Query Match 23.3%; Score 109; DB 1; Length 603;

Best Local Similarity 62.5%; Pred. No. 8.1e-28;

Matches 187; Conservative 0; Mismatches 110; Indels 2; Gaps 1;

QY 85 GGCTCTGTAGCTCAGTTGGTTAGAGCGCACCCCTGTATAGGGTGGAGTTCGGCAGTTTCGAA 144  
Db 99 GGCTTTGTAGCTCAGCTGGTTAGAGCACACGCTTGATAAGCGTGAGGTTCGGAGGTTCAAG 158  
QY 145 TCTGCCCGACAGACCCACCAATTTGCTGGGGCCATAGCTCAGCTGGAGAGCGCTGCCCTTGC 204  
Db 159 TCTCCAGACCCACCA--GAACGGGGGCTAGCTAGTGGTAGAGCACTGCTTGC 216  
QY 205 ACCGAGGAGTACAGCGTTTCGATCCCGCTTGGCTCCACACCCCGCTTGCAGTTTGTCA 264  
Db 217 AAGCAGGGGGTTCATCGTTTCGATCCCGTTTGCCTCCACCAAACTTTTACAAATGAAAGCA 276  
QY 265 AAGCTTAGAATGAATATTCGCGTCGAATATTGATTTCTGAACTTTATCAGAATCGTTCT 324  
Db 277 AGTTTCTGTTTTCAGCAGCTTATTTTTCGGAAGTAGAATAAGCAGCATCGATCT 336  
QY 325 TTAATAATTTGGTGTATGTATAGAAAGATAGACTGGACAGCACTTTCACTGGTGTGTGT 383  
Db 337 TTAACAAATTTGGAAAGCCGGAATCAACAAACAAAGACAATGAGTTGTTGATTTTTT 395

## RESULT 12

US-08-412-614-86

; Sequence 86, Application US/08412614

; Patent No. 5536638

; GENERAL INFORMATION:

; APPLICANT: Rossau, Rudi

; TITLE OF INVENTION: Hybridization Probes Derived from the

; TITLE OF INVENTION: Spacer Region Between the 16S and 23S rRNA Genes for the

; TITLE OF INVENTION: Detection of No. 5536638-Viral Microorganisms

; NUMBER OF SEQUENCES: 104

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Merchant & Gould

; STREET: 3100 No. 5536638west Center

; CITY: Minneapolis

; STATE: MN

; COUNTRY: USA

; ZIP: 55402-4131

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Diskette 3.5 inch, 1.44 mb capacity

; COMPUTER: IBM PC compatible (Compaq Deskpro 286e)

; OPERATING SYSTEM: MS-DOS

; SOFTWARE: Wordperfect Version #5.1

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/412,614

; FILING DATE:

; CLASSIFICATION: 435

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 07/965,394

; FILING DATE: 17-DEC-1992

; APPLICATION NUMBER: PCT/EP91/00743

; FILING DATE: 18-APR-1991

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: GB/90901054.3



Rec'd 10/10



GenCore version 5.1.3  
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OM nucleic - nucleic search, using sw model

Run on: February 1, 2003, 03:05:22 ; Search time 26.0422 Seconds  
(without alignments)  
8073.649 Million cell updates/sec

Title: US-09-931-486-115

Perfect score: 468

Sequence: 1 ATCGACGACATCAGCTGTCT.....CAGATTGCTTGGGTATAT 468

Scoring table: IDENTITY\_NUC

Gapop 10.0 , Gapext 1.0

Searched: 396772 seqs, 224632407 residues

Total number of hits satisfying chosen parameters: 793544

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Published\_Applications\_NA.\*  
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2: /cgn2\_6/ptodata/1/pubpna/PCT\_NEW\_PUB.seq.\*  
3: /cgn2\_6/ptodata/1/pubpna/US06\_NEW\_PUB.seq.\*  
4: /cgn2\_6/ptodata/1/pubpna/US06\_PUBCOMB.seq.\*  
5: /cgn2\_6/ptodata/1/pubpna/US07\_NEW\_PUB.seq.\*  
6: /cgn2\_6/ptodata/1/pubpna/PCTUS\_PUBCOMB.seq.\*  
7: /cgn2\_6/ptodata/1/pubpna/US08\_NEW\_PUB.seq.\*  
8: /cgn2\_6/ptodata/1/pubpna/US08\_PUBCOMB.seq.\*  
9: /cgn2\_6/ptodata/1/pubpna/US09\_NEW\_PUB.seq.\*  
10: /cgn2\_6/ptodata/1/pubpna/US09\_PUBCOMB.seq.\*  
11: /cgn2\_6/ptodata/1/pubpna/US10\_NEW\_PUB.seq.\*  
12: /cgn2\_6/ptodata/1/pubpna/US10\_PUBCOMB.seq.\*  
13: /cgn2\_6/ptodata/1/pubpna/US60\_NEW\_PUB.seq.\*  
14: /cgn2\_6/ptodata/1/pubpna/US60\_PUBCOMB.seq.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description        |
|------------|-------|-------------|--------|-------|--------------------|
| 1          | 110.8 | 23.7        | 640681 | 10    | US-09-790-988-1    |
| 2          | 109   | 23.3        | 603    | 10    | US-09-863-086-85   |
| 3          | 109   | 23.3        | 603    | 10    | US-09-863-086-86   |
| 4          | 100.8 | 21.5        | 549    | 10    | US-09-863-086-92   |
| 5          | 99.4  | 21.2        | 498    | 10    | US-09-863-086-90   |
| 6          | 93    | 19.9        | 243    | 10    | US-09-815-242-1358 |
| 7          | 92.4  | 19.7        | 255    | 10    | US-09-815-242-1377 |
| 8          | 92.4  | 19.7        | 255    | 10    | US-09-815-242-1402 |
| 9          | 92.4  | 19.7        | 255    | 10    | US-09-815-242-1415 |
| 10         | 92.4  | 19.7        | 255    | 10    | US-09-815-242-1423 |
| 11         | 92.4  | 19.7        | 255    | 10    | US-09-815-242-1431 |
| 12         | 92.4  | 19.7        | 255    | 10    | US-09-815-242-1454 |
| 13         | 92.4  | 19.7        | 255    | 10    | US-09-815-242-1473 |
| 14         | 92.4  | 19.7        | 255    | 10    | US-09-815-242-1499 |
| 15         | 92.4  | 19.7        | 255    | 10    | US-09-815-242-1544 |
| 16         | 92.4  | 19.7        | 255    | 10    | US-09-815-242-1544 |
| 17         | 92.4  | 19.7        | 255    | 10    | US-09-815-242-1638 |
| 18         | 89    | 19.0        | 582    | 10    | US-09-863-086-87   |
| 19         | 89    | 19.0        | 590    | 10    | US-09-863-086-88   |

|    |      |      |         |    |                    |                   |
|----|------|------|---------|----|--------------------|-------------------|
| 20 | 87   | 18.6 | 654     | 10 | US-09-863-086-89   | Sequence 89, Appl |
| 21 | 86.4 | 18.5 | 3309400 | 9  | US-09-738-626-1    | Sequence 1, Appl  |
| c  | 23   | 82   | 9797    | 10 | US-09-070-927A-550 | Sequence 550, App |
| 22 | 74   | 17.5 | 290     | 10 | US-09-815-242-4692 | Sequence 4692, Ap |
| c  | 24   | 15.8 | 495     | 10 | US-09-815-242-2687 | Sequence 2687, Ap |
| c  | 25   | 74   | 495     | 10 | US-09-815-242-2891 | Sequence 2691, Ap |
| 26 | 72   | 15.4 | 2336    | 10 | US-09-842-552-102  | Sequence 102, App |
| 27 | 71.8 | 15.3 | 246     | 10 | US-09-863-086-95   | Sequence 95, Appl |
| 28 | 71.2 | 15.2 | 76      | 10 | US-09-974-300-4361 | Sequence 4361, Ap |
| 29 | 71.2 | 15.2 | 76      | 10 | US-09-974-300-4403 | Sequence 4403, Ap |
| 30 | 71.2 | 15.2 | 76      | 10 | US-09-974-300-4409 | Sequence 4409, Ap |
| 31 | 71.2 | 15.2 | 76      | 10 | US-09-974-300-4418 | Sequence 4418, Ap |
| 32 | 71.2 | 15.2 | 76      | 10 | US-09-974-300-8396 | Sequence 8396, Ap |
| 33 | 71.2 | 15.2 | 76      | 10 | US-09-974-300-8438 | Sequence 8438, Ap |
| 34 | 71.2 | 15.2 | 76      | 10 | US-09-974-300-8444 | Sequence 8444, Ap |
| 35 | 71.2 | 15.2 | 76      | 10 | US-09-974-300-8453 | Sequence 8453, Ap |
| 36 | 70.2 | 15.0 | 279     | 10 | US-09-863-086-96   | Sequence 96, Appl |
| 37 | 69.2 | 14.8 | 74      | 10 | US-09-974-300-4363 | Sequence 4363, Ap |
| 38 | 69.2 | 14.8 | 76      | 10 | US-09-974-300-8398 | Sequence 8398, Ap |
| c  | 39   | 68.2 | 1069    | 10 | US-09-070-927A-869 | Sequence 869, App |
| 40 | 65.8 | 14.1 | 836     | 9  | US-09-894-467-5    | Sequence 5, Appl  |
| 41 | 64.4 | 13.8 | 108     | 12 | US-10-046-722-9    | Sequence 9, Appl  |
| c  | 42   | 62   | 213     | 10 | US-09-815-242-1374 | Sequence 1374, Ap |
| c  | 43   | 62   | 213     | 10 | US-09-815-242-1375 | Sequence 1375, Ap |
| c  | 44   | 62   | 213     | 10 | US-09-815-242-1376 | Sequence 1376, Ap |
| c  | 45   | 62   | 213     | 10 | US-09-815-242-1412 | Sequence 1412, Ap |

## ALIGNMENTS

### RESULT 1

US-09-790-988-1  
; Sequence 1, Application US/09790988  
; Patent No. US20020127687A1  
; GENERAL INFORMATION:  
; APPLICANT: SHIGENOBU, SHUJI  
; APPLICANT: WATANABE, HIDEKI  
; APPLICANT: HATTORI, MASAHIRO  
; APPLICANT: SAKAKI, YOSHIYUKI  
; TITLE OF INVENTION: GENOME DNA OF BACTERIAL SYMBIONT OF APHIDS  
; FILE REFERENCE: 081356/0159  
; CURRENT APPLICATION NUMBER: US/09790,988  
; CURRENT FILING DATE: 2001-02-23  
; PRIOR APPLICATION NUMBER: JP2000-107160  
; PRIOR FILING DATE: 2000-04-07  
; NUMBER OF SEQ ID NOS: 7  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 1  
; LENGTH: 640681  
; TYPE: DNA  
; ORGANISM: Buchnera sp.  
US-09-790-988-1

|                       |        |                                                              |              |            |     |        |         |
|-----------------------|--------|--------------------------------------------------------------|--------------|------------|-----|--------|---------|
| Query Match           | 23.7%  | Score                                                        | 110.8;       | DB         | 10; | Length | 640681; |
| Best Local Similarity | 79.0%; | Pred.                                                        | No. 2.6e-24; | Mismatches | 32; | Indels | 7;      |
| Matches               | 147;   | Conservative                                                 | 0;           | Gaps       | 1;  |        |         |
| QY                    | 63     | ATTAGGTAGCAACCTTCGATTTGGTCTGTAGCTCAGTTGGTTAGAGCGCACCCCTGATA  | 122          |            |     |        |         |
| Db                    | 275618 | ATTATCTAATAAAAAAATTAGAAAGGCTTGTAGCTCAGATGTTAGAGCGCACCCCTGATA | 275677       |            |     |        |         |
| QY                    | 123    | AGGTTAGGTCGGCGATTCGATTCGCCAGACCCACC-----AATTTGCTGGGGCCA      | 175          |            |     |        |         |
| Db                    | 275678 | AGGTTAGGTCGGTCGTTCAATTCACCTCAGGCCTACCAATAAAAAATCATCTGGGGCTA  | 275737       |            |     |        |         |
| QY                    | 176    | TAGCTCAGTGGGAGAGCGCTTCCTTCAGCAGAGGTCAGCGTTTCGATCCCGCTTG      | 235          |            |     |        |         |
| Db                    | 275738 | TAGCTCAGTGGGAGAGCGCTTCCTTCAGCAGAGGTCAGCGTTTCATCCCGCTTA       | 275797       |            |     |        |         |
| QY                    | 236    | GCTCCA                                                       | 241          |            |     |        |         |
| Db                    | 275798 | GCTCCA                                                       | 275803       |            |     |        |         |

RESULT 2  
US-09-863-086-85  
; Sequence 85, Application US/09863086  
; Patent No. US20020048762A1  
; GENERAL INFORMATION:  
; APPLICANT: Rossau, Rudi  
; TITLE OF INVENTION: HYBRIDIZATION PROBES DERIVED FROM THE SPACER  
; REGION BETWEEN THE 16S A  
; NUMBER OF SEQUENCES: 104  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Merchant, Gould, Smith, Edell, Welter & Schmidt  
; STREET: 3100 No. US20020048762A1west Center, 90 S. 7th Street  
; CITY: Minneapolis  
; STATE: MN  
; COUNTRY: U.S.A.  
; ZIP: 55402  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: DOS  
; SOFTWARE: FastSeq Version 1.5  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/863,086  
; FILING DATE: 22-May-2001  
; CLASSIFICATION: <Unknown>  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 09/312,520  
; FILING DATE: <Unknown>  
; APPLICATION NUMBER: 08/412,614  
; FILING DATE: 29-MAR-1995  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Hillson, Randall A  
; REGISTRATION NUMBER: 31,838  
; REFERENCE/DOCKET NUMBER: 8076.75USC1  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 612/332-5300  
; TELEFAX: 612/332/9081  
; TELEX: <Unknown>  
; INFORMATION FOR SEQ ID NO: 85:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 603 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: Genomic DNA  
; HYPOTHETICAL: NO  
; ANTI-SENSE: NO  
; FRAGMENT TYPE: <Unknown>  
; ORIGINAL SOURCE:  
; SEQUENCE DESCRIPTION: SEQ ID NO: 85:  
US-09-863-086-85

Query Match 23.3%; Score 109; DB 10; Length 603;  
Best Local Similarity 62.5%; Pred. No. 1.8e-25;  
Matches 187; Conservative 0; Mismatches 110; Indels 2; Gaps 1;  
QY 85 GGGTCTGTAGCTCAGTTGGTTAGAGCGCACCCCTGATAGAGGTGAGGTGCGGAGTTTCGAA 144  
DB 99 GGGTTGTAGCTCAGCTGGTTAGAGCACACCGCTTGATAGCGGTGAGGTGCGGAGTTTCAG 158  
QY 145 TCTGCCAGACCCACCAATTTGCTGGGGCCATAGCTCAGCTGAGGAGAGCGGCTGCTTGC 204  
DB 159 TCCTCCAGAGGTCAGCGTTCGATCCCGCTTGGCTCCACCGCTTGGTGGTGGTGGTGGTGGT 216  
QY 205 ACCGAGAGGTGAGCGGTTCGATCCCGCTTGGCTCCACCGCTTGGTGGTGGTGGTGGTGGT 264  
DB 217 AAGCAGGGGTGATCGGTTCGATCCCGCTTGGCTCCACCGCTTGGTGGTGGTGGTGGTGGT 276  
QY 265 AAGCTTAGAATGAATATCGCGTCGAATATTTGATTCTCTGAACCTTTATCAGATTCGTTCT 324  
DB 277 AGTTTGTCTTTTAGCAGCTTATTTTGATTTCGGAAGTAGAATAACGACGATCGATCT 336

US-09-863-086-85  
Query Match 23.3%; Score 109; DB 10; Length 603;  
Best Local Similarity 62.5%; Pred. No. 1.8e-25;  
Matches 187; Conservative 0; Mismatches 110; Indels 2; Gaps 1;  
QY 85 GGGTCTGTAGCTCAGTTGGTTAGAGCGCACCCCTGATAGAGGTGAGGTGCGGAGTTTCGAA 144  
DB 99 GGGTTGTAGCTCAGCTGGTTAGAGCACACCGCTTGATAGCGGTGAGGTGCGGAGTTTCAG 158  
QY 145 TCTGCCAGACCCACCAATTTGCTGGGGCCATAGCTCAGCTGAGGAGAGCGGCTGCTTGC 204  
DB 159 TCCTCCAGAGGTCAGCGTTCGATCCCGCTTGGCTCCACCGCTTGGTGGTGGTGGTGGTGGT 216  
QY 205 ACCGAGAGGTGAGCGGTTCGATCCCGCTTGGCTCCACCGCTTGGTGGTGGTGGTGGTGGT 264  
DB 217 AAGCAGGGGTGATCGGTTCGATCCCGCTTGGCTCCACCGCTTGGTGGTGGTGGTGGTGGT 276  
QY 265 AAGCTTAGAATGAATATCGCGTCGAATATTTGATTCTCTGAACCTTTATCAGATTCGTTCT 324  
DB 277 AGTTTGTCTTTTAGCAGCTTATTTTGATTTCGGAAGTAGAATAACGACGATCGATCT 336





; PRIOR APPLICATION NUMBER: 60/191,078  
; PRIOR FILING DATE: 2000-03-21  
; PRIOR APPLICATION NUMBER: 60/206,848  
; PRIOR FILING DATE: 2000-05-23  
; PRIOR APPLICATION NUMBER: 60/207,727  
; PRIOR FILING DATE: 2000-05-26  
; PRIOR APPLICATION NUMBER: 60/242,578  
; PRIOR FILING DATE: 2000-10-23  
; PRIOR APPLICATION NUMBER: 60/253,625  
; PRIOR FILING DATE: 2000-11-27  
; PRIOR APPLICATION NUMBER: 60/257,931  
; PRIOR FILING DATE: 2000-12-22  
; PRIOR APPLICATION NUMBER: 60/269,308  
; PRIOR FILING DATE: 2001-02-16  
; NUMBER OF SEQ ID NOS: 14110  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 1402  
; LENGTH: 255  
; TYPE: DNA  
; ORGANISM: Staphylococcus aureus  
US-09-815-242-1402

Query Match 19.7%; Score 92.4; DB 10; Length 255;  
Best Local Similarity 66.5%; Pred. No. 2.7e-20;  
Matches 153; Conservative 0; Mismatches 66; Indels 11; Gaps 1;  
QY 10 ATCAGCTGTCTCATAGCTCCACAGCAATTCGCTTGCATTCATTGGAAGACGACGATTAGGT 69  
DB 230 AACATCTTCTTCAGAGATGCGGAATAACGTCACATATTGATTCAGTTTGAATGTTG 171  
QY 70 TAGCAACCTTCGATTCGCTGCTAGCTCAGTTGGTTAGAGCGACCCCTGATAAGGGTGA 129  
DB 170 TTCAATCAAAATTAATGGGCTATAGCTCAGCTGGTTAGAGCGACCCCTGATAAGGGTGA 111  
QY 130 GTCGCGAGTTCGAATCTGCCAGACCCACCAAT-----TTGCTGGGGCCATAG 178  
DB 110 GTCGCGTTCGATTCGCTCAGTCCACTTAGGCCACCAATTAATTAACCTATTGGGGGCTTAG 51  
QY 179 CTCAGCTGGGAGAGCGCTTCGCTTGCACGAGGAGTACGCGGTTTCGATC 228  
DB 50 CTCAGCTGGGAGAGCGCTTCGCTTGCACGAGGAGTACGCGGTTTCGATC 1

RESULT 9  
US-09-815-242-1415/c  
; Sequence 1415, Application US/09815242  
; Patent No. US20020061569A1  
; GENERAL INFORMATION:  
; APPLICANT: Haselbeck, Robert  
; APPLICANT: Ohlsen, Kari L.  
; APPLICANT: Zyskind, Judith W.  
; APPLICANT: Wall, Daniel  
; APPLICANT: Trawick, John D.  
; APPLICANT: Carr, Grant J.  
; APPLICANT: Yamamoto, Robert T.  
; APPLICANT: Xu, H. Howard  
; TITLE OF INVENTION: Identification of Essential Genes in  
; FILE REFERENCE: ELITRA.011A  
; CURRENT APPLICATION NUMBER: US/09/815,242  
; PRIOR FILING DATE: 2001-03-21  
; PRIOR APPLICATION NUMBER: 60/191,078  
; PRIOR FILING DATE: 2000-03-21  
; PRIOR APPLICATION NUMBER: 60/206,848  
; PRIOR FILING DATE: 2000-05-23  
; PRIOR APPLICATION NUMBER: 60/207,727  
; PRIOR FILING DATE: 2000-05-26  
; PRIOR APPLICATION NUMBER: 60/242,578  
; PRIOR FILING DATE: 2000-10-23  
; PRIOR APPLICATION NUMBER: 60/253,625  
; PRIOR FILING DATE: 2000-11-27  
; PRIOR APPLICATION NUMBER: 60/257,931  
; PRIOR FILING DATE: 2000-12-22

; PRIOR APPLICATION NUMBER: 60/269,308  
; PRIOR FILING DATE: 2001-02-16  
; NUMBER OF SEQ ID NOS: 14110  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 1415  
; LENGTH: 255  
; TYPE: DNA  
; ORGANISM: Staphylococcus aureus  
US-09-815-242-1415

Query Match 19.7%; Score 92.4; DB 10; Length 255;  
Best Local Similarity 66.5%; Pred. No. 2.7e-20;  
Matches 153; Conservative 0; Mismatches 66; Indels 11; Gaps 1;  
QY 10 ATCAGCTGTCTCATAGCTCCACAGCAATTCGCTTGCATTCATTGGAAGACGACGATTAGGT 69  
DB 230 AACATCTTCTTCAGAGATGCGGAATAACGTCACATATTGATTCAGTTTGAATGTTG 171  
QY 70 TAGCAACCTTCGATTCGCTGCTAGCTCAGTTGGTTAGAGCGACCCCTGATAAGGGTGA 129  
DB 170 TTCAATCAAAATTAATGGGCTATAGCTCAGCTGGTTAGAGCGACCCCTGATAAGGGTGA 111  
QY 130 GTCGCGAGTTCGAATCTGCCAGACCCACCAAT-----TTGCTGGGGCCATAG 178  
DB 110 GTCGCGTTCGATTCGCTCAGTCCACTTAGGCCACCAATTAATTAACCTATTGGGGGCTTAG 51  
QY 179 CTCAGCTGGGAGAGCGCTTCGCTTGCACGAGGAGTACGCGGTTTCGATC 228  
DB 50 CTCAGCTGGGAGAGCGCTTCGCTTGCACGAGGAGTACGCGGTTTCGATC 1

RESULT 10  
US-09-815-242-1423/c  
; Sequence 1423, Application US/09815242  
; Patent No. US20020061569A1  
; GENERAL INFORMATION:  
; APPLICANT: Haselbeck, Robert  
; APPLICANT: Ohlsen, Kari L.  
; APPLICANT: Zyskind, Judith W.  
; APPLICANT: Wall, Daniel  
; APPLICANT: Trawick, John D.  
; APPLICANT: Carr, Grant J.  
; APPLICANT: Yamamoto, Robert T.  
; APPLICANT: Xu, H. Howard  
; TITLE OF INVENTION: Identification of Essential Genes in  
; FILE REFERENCE: ELITRA.011A  
; CURRENT APPLICATION NUMBER: US/09/815,242  
; PRIOR FILING DATE: 2001-03-21  
; PRIOR APPLICATION NUMBER: 60/191,078  
; PRIOR FILING DATE: 2000-03-21  
; PRIOR APPLICATION NUMBER: 60/206,848  
; PRIOR FILING DATE: 2000-05-23  
; PRIOR APPLICATION NUMBER: 60/207,727  
; PRIOR FILING DATE: 2000-05-26  
; PRIOR APPLICATION NUMBER: 60/242,578  
; PRIOR FILING DATE: 2000-10-23  
; PRIOR APPLICATION NUMBER: 60/253,625  
; PRIOR FILING DATE: 2000-11-27  
; PRIOR APPLICATION NUMBER: 60/257,931  
; PRIOR FILING DATE: 2000-12-22  
; PRIOR APPLICATION NUMBER: 60/269,308  
; PRIOR FILING DATE: 2001-02-16  
; NUMBER OF SEQ ID NOS: 14110  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 1423  
; LENGTH: 255  
; TYPE: DNA  
; ORGANISM: Staphylococcus aureus  
US-09-815-242-1423  
Query Match 19.7%; Score 92.4; DB 10; Length 255;  
Best Local Similarity 66.5%; Pred. No. 2.7e-20;





APPLICANT: Haselbeck, Robert  
APPLICANT: Ohlsen, Kari L.  
APPLICANT: Zyskind, Judith W.  
APPLICANT: Wall, Daniel  
APPLICANT: Trawick, John D.  
APPLICANT: Carr, Grant J.  
APPLICANT: Yamamoto, Robert T.  
APPLICANT: Xu, H. Howard  
TITLE OF INVENTION: Identification of Essential Genes in  
FILE REFERENCE: ELITRA.011A  
CURRENT APPLICATION NUMBER: US/09/815,242  
CURRENT FILING DATE: 2001-03-21  
PRIOR APPLICATION NUMBER: 60/191,078  
PRIOR FILING DATE: 2000-03-21  
PRIOR APPLICATION NUMBER: 60/206,848  
PRIOR FILING DATE: 2000-05-23  
PRIOR APPLICATION NUMBER: 60/207,727  
PRIOR FILING DATE: 2000-10-23  
PRIOR APPLICATION NUMBER: 60/253,625  
PRIOR FILING DATE: 2000-11-27  
PRIOR APPLICATION NUMBER: 60/242,578  
PRIOR FILING DATE: 2000-05-26  
PRIOR APPLICATION NUMBER: 60/257,931  
PRIOR FILING DATE: 2000-12-22  
PRIOR APPLICATION NUMBER: 60/269,308  
PRIOR FILING DATE: 2001-02-16  
NUMBER OF SEQ ID NOS: 14110  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 1459  
LENGTH: 255  
TYPE: DNA  
ORGANISM: Staphylococcus aureus  
US-09-815-242-1459

Query Match 19.7%; Score 92.4; DB 10; Length 255;  
Best Local Similarity 66.5%; Pred. No. 2.7e-20;  
Matches 153; Conservative 0; Mismatches 66; Indels 11; Gaps 1;

QY 10 ATCAGCTCTCTCAATGCTCCACAGCAATTCCTGATTCATTTGAAGACGATAGGT 69  
DB 230 AACATCTCTTCAGAGATGCGGAATACGTGACATATTTGATTCAGTTTGAATGTTG 171

QY 70 TAGCAACCTTCGATGGTCTGTAGCTCAGTTGGTTAGAGCGCACCCCTGATAAGGGTGA 129  
DB 170 TTCATTCAAAATTAATGGGCTATAGCTCAGCTGGTTAGAGCGCACCCCTGATAAGGGTGA 111

QY 130 GGTGGGAGTTCGAATCTGCCAGACCCACCAAT-----TTGCTGGGGCCATAG 178  
DB 110 GGTGGGAGTTCGAATCTGCCAGACCCACCAAT-----TTGCTGGGGCCATAG 51

QY 179 CTCAGCTGGGAGAGCGCTGCTTGCACGAGGAGTTCAGCGGTTTCGATC 228  
DB 50 CTCAGCTGGGAGAGCGCTGCTTGCACGAGGAGTTCAGCGGTTTCGATC 1

RESULT 14  
US-09-815-242-1473/c  
Sequence 1473, Application US/09815242  
Patent No. US20020061569A1  
GENERAL INFORMATION:  
APPLICANT: Haselbeck, Robert  
APPLICANT: Ohlsen, Kari L.  
APPLICANT: Zyskind, Judith W.  
APPLICANT: Wall, Daniel  
APPLICANT: Trawick, John D.  
APPLICANT: Carr, Grant J.  
APPLICANT: Yamamoto, Robert T.  
APPLICANT: Xu, H. Howard  
TITLE OF INVENTION: Identification of Essential Genes in  
FILE REFERENCE: ELITRA.011A  
CURRENT APPLICATION NUMBER: US/09/815,242  
CURRENT FILING DATE: 2001-03-21  
PRIOR APPLICATION NUMBER: 60/191,078  
PRIOR FILING DATE: 2000-03-21  
PRIOR APPLICATION NUMBER: 60/206,848  
PRIOR FILING DATE: 2000-05-23  
PRIOR APPLICATION NUMBER: 60/207,727  
PRIOR FILING DATE: 2000-10-23  
PRIOR APPLICATION NUMBER: 60/242,578  
PRIOR FILING DATE: 2000-11-27  
PRIOR APPLICATION NUMBER: 60/253,625  
CURRENT APPLICATION NUMBER: US/09/815,242

CURRENT FILING DATE: 2001-03-21  
PRIOR APPLICATION NUMBER: 60/191,078  
PRIOR FILING DATE: 2000-03-21  
PRIOR APPLICATION NUMBER: 60/206,848  
PRIOR FILING DATE: 2000-05-23  
PRIOR APPLICATION NUMBER: 60/207,727  
PRIOR FILING DATE: 2000-05-26  
PRIOR APPLICATION NUMBER: 60/242,578  
PRIOR FILING DATE: 2000-10-23  
PRIOR APPLICATION NUMBER: 60/253,625  
PRIOR FILING DATE: 2000-11-27  
PRIOR APPLICATION NUMBER: 60/257,931  
PRIOR FILING DATE: 2000-12-22  
PRIOR APPLICATION NUMBER: 60/269,308  
PRIOR FILING DATE: 2001-02-16  
NUMBER OF SEQ ID NOS: 14110  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 1473  
LENGTH: 255  
TYPE: DNA  
ORGANISM: Staphylococcus aureus  
US-09-815-242-1473

Query Match 19.7%; Score 92.4; DB 10; Length 255;  
Best Local Similarity 66.5%; Pred. No. 2.7e-20;  
Matches 153; Conservative 0; Mismatches 66; Indels 11; Gaps 1;

QY 10 ATCAGCTCTCTCAATGCTCCACAGCAATTCCTGATTCATTTGAAGACGATAGGT 69  
DB 230 AACATCTCTTCAGAGATGCGGAATACGTGACATATTTGATTCAGTTTGAATGTTG 171

QY 70 TAGCAACCTTCGATGGTCTGTAGCTCAGTTGGTTAGAGCGCACCCCTGATAAGGGTGA 129  
DB 170 TTCATTCAAAATTAATGGGCTATAGCTCAGCTGGTTAGAGCGCACCCCTGATAAGGGTGA 111

QY 130 GGTGGGAGTTCGAATCTGCCAGACCCACCAAT-----TTGCTGGGGCCATAG 178  
DB 110 GGTGGGAGTTCGAATCTGCCAGACCCACCAAT-----TTGCTGGGGCCATAG 51

QY 179 CTCAGCTGGGAGAGCGCTGCTTGCACGAGGAGTTCAGCGGTTTCGATC 228  
DB 50 CTCAGCTGGGAGAGCGCTGCTTGCACGAGGAGTTCAGCGGTTTCGATC 1

RESULT 15  
US-09-815-242-1475/c  
Sequence 1475, Application US/09815242  
Patent No. US20020061569A1  
GENERAL INFORMATION:  
APPLICANT: Haselbeck, Robert  
APPLICANT: Ohlsen, Kari L.  
APPLICANT: Zyskind, Judith W.  
APPLICANT: Wall, Daniel  
APPLICANT: Trawick, John D.  
APPLICANT: Carr, Grant J.  
APPLICANT: Yamamoto, Robert T.  
APPLICANT: Xu, H. Howard  
TITLE OF INVENTION: Identification of Essential Genes in  
FILE REFERENCE: ELITRA.011A  
CURRENT APPLICATION NUMBER: US/09/815,242  
CURRENT FILING DATE: 2001-03-21  
PRIOR APPLICATION NUMBER: 60/191,078  
PRIOR FILING DATE: 2000-03-21  
PRIOR APPLICATION NUMBER: 60/206,848  
PRIOR FILING DATE: 2000-05-23  
PRIOR APPLICATION NUMBER: 60/207,727  
PRIOR FILING DATE: 2000-10-23  
PRIOR APPLICATION NUMBER: 60/242,578  
PRIOR FILING DATE: 2000-11-27  
PRIOR APPLICATION NUMBER: 60/253,625  
CURRENT APPLICATION NUMBER: 60/257,931

Search completed: February 1, 2003, 07:10:52  
Job time : 238.042 secs

GenCore version 5.1.3  
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OM nucleic - nucleic search, using sw model

Run on: February 1, 2003, 01:09:56 ; Search time 873.271 Seconds  
(without alignments)  
8679.427 Million cell updates/sec

Title: US-09-931-486-115

Perfect score: 468

Sequence: 1 ATCGACGACATCAGCTGTCT.....CAGATGCTTGGGTTATAT 468

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 16154066 seqs, 8097743376 residues

Total number of hits satisfying chosen parameters: 32308132

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

```

EST:*
1: em_estba:*
2: em_esthum:*
3: em_estin:*
4: em_estmu:*
5: em_estov:*
6: em_estpl:*
7: em_estro:*
8: em_hic:*
9: gb_est1:*
10: gb_est2:*
11: gb_hic:*
12: gb_est3:*
13: gb_est4:*
14: gb_est5:*
15: em_estfun:*
16: em_estom:*
17: gb_gss:*
18: em_gss_hum:*
19: em_gss_inv:*
20: em_gss_pin:*
21: em_gss_vrt:*
22: em_gss_fun:*
23: em_gss_mam:*
24: em_gss_mus:*
25: em_gss_other:*
26: em_gss_pro:*
27: em_gss_rod:*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

| Result No. | Score | Match | Length | DB | ID       | Description        |
|------------|-------|-------|--------|----|----------|--------------------|
| c 1        | 190.8 | 40.8  | 507    | 17 | BH200120 | BH200120 Sml-57J2. |
| c 2        | 187.6 | 40.1  | 629    | 17 | BH201541 | BH201541 Sml-57P13 |
| c 3        | 165.2 | 35.3  | 639    | 17 | AQ509640 | AQ509640 nbxb0096P |
| 4          | 117.2 | 25.0  | 319    | 10 | BE092111 | BE092111 IL2-BT073 |
| 5          | 80.4  | 17.2  | 497    | 13 | BI544108 | BI544108 S071 Grac |
| 6          | 80.4  | 17.2  | 548    | 13 | BI544155 | BI544155 S129 Grac |

|      |      |      |      |    |          |
|------|------|------|------|----|----------|
| 7    | 78.8 | 16.8 | 539  | 13 | BI544086 |
| c 8  | 77.8 | 16.6 | 593  | 17 | BH400944 |
| c 9  | 77.8 | 16.6 | 760  | 17 | BH393190 |
| c 10 | 69.2 | 14.8 | 6499 | 17 | BH771024 |
| c 11 | 68.4 | 14.6 | 191  | 17 | AZ578476 |
| c 12 | 66.6 | 14.2 | 904  | 17 | BH159957 |
| c 13 | 65.8 | 14.1 | 577  | 17 | BH815957 |
| c 14 | 59.6 | 12.7 | 287  | 17 | BH614410 |
| c 15 | 59.6 | 12.7 | 754  | 17 | BH405252 |
| c 16 | 58.6 | 12.5 | 619  | 9  | AA680996 |
| c 17 | 57.6 | 12.3 | 3268 | 17 | BH770998 |
| c 18 | 55   | 11.8 | 615  | 17 | CI16G5   |
| c 19 | 55   | 11.8 | 690  | 17 | CI19B2   |
| c 20 | 54.4 | 11.6 | 608  | 17 | BH375641 |
| c 21 | 54.4 | 11.6 | 696  | 17 | BH383241 |
| c 22 | 54.2 | 11.6 | 617  | 9  | AI526132 |
| c 23 | 54   | 11.5 | 712  | 17 | BH397037 |
| c 24 | 53.6 | 11.5 | 2149 | 17 | AQ012191 |
| c 25 | 53.2 | 11.4 | 713  | 13 | BJ096963 |
| c 26 | 52.8 | 11.3 | 579  | 17 | BH375975 |
| c 27 | 52.6 | 11.2 | 541  | 17 | BH387664 |
| c 28 | 51.8 | 11.1 | 679  | 13 | BI263958 |
| c 29 | 51.6 | 11.0 | 774  | 12 | BG354849 |
| c 30 | 51.4 | 11.0 | 715  | 17 | BH375497 |
| c 31 | 50.6 | 10.8 | 902  | 17 | CNS06M5P |
| c 32 | 50.2 | 10.7 | 551  | 10 | BE092053 |
| c 33 | 50   | 10.7 | 653  | 13 | BJ318992 |
| c 34 | 49   | 10.5 | 874  | 17 | CNS06GSM |
| c 35 | 48.4 | 10.3 | 432  | 13 | BI941477 |
| c 36 | 48.4 | 10.3 | 1258 | 17 | BH770957 |
| c 37 | 48.2 | 10.3 | 501  | 13 | BJ313245 |
| c 38 | 48   | 10.3 | 330  | 14 | BQ205940 |
| c 39 | 47.8 | 10.2 | 907  | 17 | CNS06N2C |
| c 40 | 47.4 | 10.1 | 1061 | 17 | CNS06MOV |
| c 41 | 47   | 10.0 | 612  | 17 | AQ989869 |
| c 42 | 46.6 | 10.0 | 372  | 10 | BE092243 |
| c 43 | 44.6 | 9.5  | 337  | 10 | AW238775 |
| c 44 | 44.6 | 9.5  | 381  | 10 | AW238039 |
| c 45 | 44.6 | 9.5  | 411  | 10 | AW238064 |

#### ALIGNMENTS

RESULT 1  
BH200120/c  
LOCUS  
DEFINITION  
Sml-57J2.TF Sml Schistosoma mansoni genomic clone Sml-57J2, DNA sequence.  
ACCESSION  
BH200120  
VERSION  
BH200120.1 GI:16370164  
KEYWORDS  
GSS:  
SOURCE  
Schistosoma mansoni.  
ORGANISM  
Schistosoma mansoni.  
REFERENCE  
AUTHORS  
Shetty,J., Simpson,A., Malek,J., Koo,H., LoVerde,P.T. and El-Sayed ,N.M.  
TITLE  
Use of end sequences from Schistosoma mansoni (Puerto Rico strain) Sml BAC library for gene discovery and map construction  
JOURNAL  
COMMENT  
Unpublished (2001)  
Other\_GSSs: Sml-57J2.TR  
Contact: Najib M. El-Sayed  
Department of Eukaryotic Genomics  
The Institute for Genomic Research  
9712 Medical Center Dr., Rockville, MD 20850, USA  
Tel: 301 838 0200  
Fax: 301 838 0208  
Email: nelsayed@tigr.org  
Seq primer: M13 For  
Class: BAC ends.

BI544086 S042 Grac  
BH400944 AG-ND-158  
BH393190 AG-ND-168  
BH771024 LMGtag74  
AZ578476 23H03 SHO  
BH159957 ENTP113TF  
BH815957 BACPP13-E  
BH614410 IC22AG2 S  
BH405252 AG-ND-127  
AA680996 SW3D9CA51  
BH770998 LMGtag72  
AJ227395 Clona int  
AJ228701 Clona int  
BH375641 AG-ND-133  
BH383241 AG-ND-137  
AI526132 pc3-2.B11  
BH397037 AG-ND-137  
AQ012191 430PIA043  
BJ096963 BJ096963  
BH375975 AG-ND-133  
BH387664 AG-ND-157  
BI263958 NF107H06P  
BG354849 MBTSM1A09  
BH375497 AG-ND-144  
AL405059 T7 end of  
BE092053 IL2-BT073  
BJ318992 BJ318992  
AL398108 T7 end of  
BI941477 dg07q11.Y  
BH770957 LMGtag68  
BJ313245 BJ313245  
BQ205940 UI-R-EP0-  
AL406234 T3 end of  
AL405749 T7 end of  
AQ989869 Rfc00532  
BE092243 IL2-BT073  
AW238775 xp08a08.x  
AW238039 xp13h02.x  
AW238064 xp16a02.x

|         |
|---------|
| TITLE   |
| JOURNAL |
| COMMENT |

FEATURES source

BASE COUNT  
ORIGIN

| Matches  |       |
|----------|-------|
| Qy       | 1 A   |
| Db       | 485 A |
| Qy       | 61 C  |
| Db       | 425 G |
| Qy       | 114 C |
| Db       | 365 C |
| Qy       | 168 - |
| Db       | 305 G |
| Qy       | 216 C |
| Db       | 245 C |
| Qy       | 276 T |
| Db       | 187 T |
| Qy       | 333 T |
| Db       | 127 T |
| Qy       | 393 C |
| Db       | 70 C  |
| RESULT 3 |       |

```

FEATURES             Location/Qualifiers
     1..507
     /organism="Schistosoma mansoni"
     /strain="Puerto Rico"
     /db_xref="taxon:6183"
     /clone="Sml-57J2"
     /clone_lib="Sml"
     /note="Vector: pBelOAC11; Site_1: Hin dIII; Constructed
in the laboratory of Dr. Denis Le Paslier at the Fondation
Jean Dausset, CEPH, Paris, France. Briefly, Schistosoma
mansoni agarose embedded DNA was partially digested with
Hin dIII. High molecular weight fragments were ligated in
pBelOAC11 digested with Hin dIII. The average insert size
is 100 kb. Total clone coverage: approx. 7.95 X the
haploid genome. (2000) Construction and characterization of
Le Paslier et al. (2000) Construction and characterization of
a Schistosoma mansoni bacterial artificial chromosome
library. Genomics 65: 87-94."
     136 a 129 c 117 g 125 t

```

|    | Query Match           | 40.8%;                                                             | Score 190.8;       | DB 17;     | Length 507; |
|----|-----------------------|--------------------------------------------------------------------|--------------------|------------|-------------|
|    | Best Local Similarity | 72.5%;                                                             | Pred. No. 1.4e-48; |            |             |
|    | Matches 342;          | Conservative 0;                                                    | Mismatches 97;     | Indels 33; | Gaps 6;     |
| QY | 1                     | ATCGAGCATCATCAGCTGCTCTCATAAAGTCGCCACACGAATTCGTGTGATTCATTTGAAAGAAGA | 60                 |            |             |
| Db | 485                   | ATCAAGACCTCASCCTCTTCATTAAGTTCACACACGAATTCGTGTGATTCACATTCGCGAATA    | 426                |            |             |
| QY | 61                    | CGATTAGGTTTAGCAACCTT-----CGATTGGGTCTGTAGCTTCAGTTGGTTAGAGCGCA       | 113                |            |             |
| Db | 425                   | CGCATTGGGTTTGAGACCCGAGAGTGACGATTGGGTCTGTAGCTTCAGTTGGTTAGAGCGCA     | 366                |            |             |
| QY | 114                   | CCCTTGATAAGGTTGAGGTCGGCAGTTCGAATCTGCCACAGACCCACCAATTTCG-----       | 167                |            |             |
| Db | 365                   | CCCTTGATAAGGTTGAGGTCGGCAGTTCGAATCTGCCACAGACCCACCAATTGTCTGGGATG     | 306                |            |             |
| QY | 168                   | -----TGGGGCCCATAGCTCAGCTTGGGAGAGCGCTGCCCTTGCACGAGGAGGT             | 215                |            |             |
| Db | 305                   | GCCAGTGTCAAAATGGGGCCATAGCTCAGCTGGGAGAGCGCTGCTTTGCACGAGGAGGT        | 246                |            |             |
| QY | 216                   | CAGGGTTTCGATCCGCTTGGCTGCCACACCCGCTGCCAGTTCGCCAGTTCGAAGCTTAGAAA     | 275                |            |             |
| Db | 245                   | CAGGAGTTCGATCCTCCTTGGCTCCACCA--TCAACTCAGGATCGCTGGAAGGTCAGAAA       | 188                |            |             |
| QY | 276                   | TGAATATTTCG-CGTCGGAATATTGATTTCTGAACCTTT--ATCAGAATCGTTCCTTTAAAAAT   | 332                |            |             |
| Db | 187                   | TGAACATTGGTAGTTCAATGTTGATTTCTGGCTTTGCGCCAGNACTGTTCTTTAAAAAT        | 128                |            |             |
| QY | 333                   | TTGGGTATGTGATAGAAGATAGACTGGACAGCACTTTCCTACTGGTGTGTGTTCAGGCTAA      | 392                |            |             |
| Db | 127                   | TTGGGTATGTGATAGA---AGTGACTAACACGGTGTTCCTACTGCACGCTTGTTAATCAAGG     | 71                 |            |             |
| QY | 393                   | GGTAAATTTGTGTAGTAATTACAGTTCCTTGGCGGAATGTTGTCTTCACAGTA              | 444                |            |             |
| Db | 70                    | CAAAATTTGGCAGTTCGAAGCGCGAAATTTTCGGCGGAATGTGTGTCTTCACAGTTA          | 19                 |            |             |

|            |            |                                                                     |             |                     |               |                 |
|------------|------------|---------------------------------------------------------------------|-------------|---------------------|---------------|-----------------|
| RESULT 2   | BH201541/c | BH201541                                                            | 629 bp      | DNA                 | linear        | GSS 24-OCT-2001 |
| LOCUS      |            | Sm1-57Pl3.TF                                                        | Sm1         | Schistosoma mansoni | genomic clone | Sm1-57Pl3, DNA  |
| DEFINITION |            |                                                                     |             |                     |               |                 |
|            |            |                                                                     |             |                     |               |                 |
| ACCESSION  |            | BH201541                                                            |             |                     |               |                 |
| VERSION    |            | BH201541.1                                                          | GI:16373041 |                     |               |                 |
| KEYWORDS   |            | GSS.                                                                |             |                     |               |                 |
| SOURCE     |            | Schistosoma mansoni.                                                |             |                     |               |                 |
| ORGANISM   |            | Schistosoma mansoni                                                 |             |                     |               |                 |
|            |            | Eukaryota; Metazoa; Platyhelminthes; Trematoda; Digenea;            |             |                     |               |                 |
|            |            | Strigoidida; Schistosomatidae; Schistosomatidae; Schistosoma.       |             |                     |               |                 |
| REFERENCE  |            | 1 (bases 1 to 629)                                                  |             |                     |               |                 |
| AUTHORS    |            | Shetty,J., Simpson,A., Malek,J., Koo,H., Loverde,P.T. and El-Sayed, |             |                     |               |                 |
|            |            | N.M.                                                                |             |                     |               |                 |

AQ509640/c

LOCUS nbxb0096p15f CUGI Rice BAC Library Oryza sativa genomic clone  
DEFINITION nbxb0096p15f, DNA sequence.  
ACCESSION AQ509640  
VERSION AQ509640.1 GI:4733723  
KEYWORDS GSS.

## ORGANISM

Oryza sativa  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
Ehrhartoideae; Oryzeae; Oryza.

## REFERENCE

1 (bases 1 to 639)  
Wing,R.A. and Dean,R.A.  
A BAC End Sequencing Framework to Sequence the Rice Genome  
Unpublished (1998)  
Contact: Wing RA

## JOURNAL

Clemson University Genomics Institute  
Clemson University  
100 Jordan Hall, Clemson, SC 29634, USA  
Tel: 864 656 7288  
Fax: 864 656 4293  
Email: rwing@clemson.edu

Seq primer: TAATACGACTCACTATAGGG  
Class: BAC ends

High quality sequence start: 86  
High quality sequence stop: 304.

Location/Qualifiers  
1..639

/organism="Oryza sativa"

/strain="Japonica"

/cultivar="Nipponbare"

/db\_xref="taxon:4530"

/clone="nbxb0096p15f"

/clone\_lib="CUGI Rice BAC Library"

/tissue\_type="leaf"

/lab\_host="E. coli DH10B"

/note="Vector: pBelobAC11; Site\_1: HindIII; Site\_2: HindIII; Rice is one of two most popular grains in the world. Half of the world population especially those inhabiting highly populated areas of the humid tropics and subtropics, rely on rice as their primary source of carbohydrate. Monocotyledonous rice is a diploid plant (2n=24) with a haploid genome equivalent of 431 Mbp (Arumuganathan and Earle, 1991). The relatively small genome of rice, three times larger than that of Arabidopsis, makes it suitable for genomic studies. In order to facilitate positional cloning, physical mapping and genome sequencing of rice, we have constructed a BAC library from Oryza sativa, Nipponbare variety. The library contains 36,864 clones with an average insert size of 128.5 Kb providing 10.9 haploid genome equivalents. The deep coverage allows the isolation a particular sequence with a probability of 99.9 %. Two high density filters, each containing 19,432 clones (doubly spotted), represent the whole library for colony screening."

## FEATURES

BASE COUNT 158 a 175 c 148 g 156 t  
ORIGIN

Query Match

Best Local Similarity 35.3%; Score 165.2; DB 17; Length 639;

Matches 271; Conservative 73.6%; Pred. No.1.8e-40; Mismatches 78; Indels 19; Gaps 4;

QY 80 CGATTGGGTCTAGTCTAGTTGGTTAGAGCGCACCCCTGATAAGGGTGAGGTCGGCACT 139

DB 580 CGATTGGGTCTAGTCTAGTTGGTTAGAGCGCACCCCTGATAAGGGTGAGGTCGGCACT 521

QY 140 TCGAATCTGCCAGACCCACCAATTTGCTGGGGCCATAGCTCAGCTGGGAGAGCGGCTGC 199

DB 520 TCGAATCTGCCAGACCCACCAATTTGCTGGGGCCATAGCTCAGCTGGGAGAGCGGCTGC 461

QY 200 CTTGCACGACGAGGCTCAGCGGTTGGTCCCGCTTTGGCTCCACCGCCGCTTGCAGT- 258

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Db 460 CTTGCACGACGAGGTCAGAGTTGCGATCCTCTTGGCTCCACCACTCCACCCCTGTGTC 401

QY 259 -----TTGTCAAAGCTTAGAAATGAATATTCGC--GTGGAATATTGATTTCT 303

Db 400 GATAACACGATTGCTTGAAGAGCTCAGAAGTGAGTGTTCGCTTGGCGAATCTTGACTTCT 341

QY 304 GAACATTT-ATCAGAATCGTTCTTTAAAAATTTGGGTATCTGATAGAAAGATAGACTGGAC 362

Db 340 GGTCTTTGATCAGAACTGTCTTTAAAAAATTTGGGAAAGTATAGAAAGTAGACATTTGA 281

QY 363 AGCACTTTCACTGGGTGTGTTTCAGCTAAGCTAAAATTTTGA--GTAATTTACAAGTTT 420

Db 280 CTGTTTTCACCTGGGAGTGCATGCTCAAGGTAAAATCTTGGAACTCAAGCGCAAGTTT 221

QY 421 TCGGCGAA 428

Db 220 TCGGCGAA 213

RESULT 4

BE092111

LOCUS IL2-BT0733-240400-073-G03 BT0733 Homo sapiens cDNA, mRNA sequence.

DEFINITION BE092111

ACCESSION BE092111

VERSION BE092111.1 GI:8482563

KEYWORDS EST.

SOURCE human.

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Carnivora; Hominoidea; Homo.

1 (bases 1 to 319)

Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R.,

Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F.,

Goldman,G.H., Carvalho,A.P., Matsukuma,A., Bala,G.S., Simpson,D.H.,

Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare

,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and

Simpson,A.J.J.

Shotgun sequencing of the human transcriptome with ORF expressed

sequence tags

JOURNAL Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)

MEDLINE 20202663

COMMENT Contact: Simpson A.J.J.

Laboratory of Cancer Genetics

Ludwig Institute for Cancer Research

Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,

Brazil

Tel: +55-11-2704922

Fax: +55-11-2707001

Email: asimpson@ludwig.org.br

This sequence was derived from the FAPESP/LICR Human Cancer Genome

Project. This entry can be seen in the following URL

(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=st3-IL2-BT0733-240

400-073-G03&t3=2000-04-24&t4=1)

Seq primer: puc 18 forward

High quality sequence stop: 298.

Location/Qualifiers

1..319

/organism="Homo sapiens"

/db\_xref="taxon:9606"

/clone\_lib="BT0733"

/dev\_stage="Adult"

/note="Organ: breast; Vector: puc18; Site\_1: SmaI; Site\_2:

SmaI; A mini-library was made by cloning products derived

from ORESTES PCR (U.S. Letters Patent application No. 196

,716 - Ludwig Institute for Cancer Research) profiles

into the puc 18 vector. Reverse transcription of tissue

mRNA and cDNA amplification were performed under low

stringency conditions."

BASE COUNT 73 a 62 c 91 g 93 t

ORIGIN

Query Match

Best Local Similarity 25.0%; Score 117.2; DB 10; Length 319;

Mismatches 70.9%; Pred. No.1.2e-25;

Matches 224; Conservative 0; Mismatches 38; Indels 54; Gaps 3;

QY 98 AGTTGTTAGAGCGACCCCTGATAAGGGTGGAGTGGCGAGTTGGAATCTGCCAGACCC 157  
 |||||  
 Db 1 AGTTGTTAGAGCGACCCCTGATAAGGGTGGAGTGGCGAGTTGGAATCTGCCAGACCC 60  
 |||||

QY 158 ACCAATTTGCT-----GGGSCCATAGCTCAGCTGGGAGAGCG 194  
 |||||  
 Db 61 ACCAATTTGCTGGGGGAAAGCCCTGTAGAATACGGGGCCATAGCTCAGCTGGGAGAGCG 120  
 |||||

QY 195 CTTGCCCTTGACGAGAGGTGACGGTTCGATCCCGCTTGGCTCCACCA-----244  
 |||||  
 Db 121 CTTGCCCTTGACGAGAGGTGACGGTTCGATCCCGCTTGGCTCCACCAATTTAGCTGT 180  
 |||||

QY 245 -----CCCCGCTGCCAGTTTGTCAAGCTTAGAATCAATATTC-----284  
 |||||

Db 181 GATGGTTGTTGGCTGTAGTCTCTCGGTTAGAGTTTGAAGATGAGCATTCATCATGCG 240  
 |||||

QY 285 -GCCTCGAATATTGATTTCTCAACTTATCAGAATCGTTCTTTAAAAATTTGGGTATGTG 343  
 |||||

Db 241 GATGGTGAATGTTGATTTCTAGTCTTTGATTAGATCGTTCTTTACAAATTTGGGTATGTG 300  
 |||||

QY 344 ATAGAAAGATAGACTG 359  
 |||||

Db 301 ATAGAAAGATAGACTG 316  
 |||||

RESULT 5  
 BI544108  
 LOCUS  
 DEFINITION S071 Gracilaria lemaneiformis gametophyte cDNA library Gracilaria lemaneiformis cDNA 5', mRNA sequence.

ACCESSION BI544108.1 GI:19033790

VERSION EST.

KEYWORDS Gracilaria lemaneiformis.

SOURCE Gracilaria lemaneiformis.

ORGANISM Eukaryota; Rhodophyta; Florideophyceae; Gracilariiales;

REFERENCE 1 (bases 1 to 497)

AUTHORS Sun, X., Yang, G.P., Mao, Y. X. and Zhang, X. C.

TITLE Analysis of expressed sequence tags of a marine red alga,

JOURNAL Gracilaria lemaneiformis

COMMENT Unpublished (2001)

Contact: Sun, X.; Zhang, X. C.

College of Marine Life Sciences

Ocean University of Qingdao

Yushan Road 5, Qingdao, 266003, Shandong, China

Tel: +86-0532-2032789

Fax: +86-0532-2032276

Email: xc Zhang@ouqd.edu.cn

PCR Primers

FORWARD: 5' -CGTGGTACCATGGTCTAGAGT-3'

BACKWARD: 5' -CTGATCTAGACCTGCAGGCTC-3'

Seq primer: 5' -CGTGGTACCATGGTCTAGAGT-3'

POLYA=No.

FEATURES Location/Qualifiers

1. 497

/organism="Gracilaria lemaneiformis"

/db\_xref="taxon:2778"

/clone\_lib="Gracilaria lemaneiformis gametophyte cDNA

library"

/tissue\_type="gametophyte thalli"

/note="Vector: pMD 18-T; Site 1: EcoR V with a T hang;

Wild type Gracilaria lemaneiformis were harvested from

Zhanshan Bay, Qingdao (China). After rinsed with boiled

seawater, younger thalli was cut and washed every 3-4

days until 1 month. Then thalli was cultivated in

Provasoli medium. Total RNA was isolated from thalli of

gametophyte algae, using UNIQ-10 Trizol Total RNA

Preparation Kit(Sangon Inc., Shanghai, China). The cDNA

was synthesized, amplified and cloned using cDNA

Synthesis Kit, cDNA PCR Library Kit and pMD 18-T vector

(Takara Biotechnology Co., Ltd., Dalian, China),  
 respectively."

BASE COUNT 151 a 77 c 103 g 166 t

ORIGIN

Query Match 17.2%; Score 80.4; DB 13; Length 497;

Best Local Similarity 73.4%; Pred. No. 6.3e-14;

Matches 116; Conservative 0; Mismatches 41; Indels 1; Gaps 1;

QY 85 GGGTCGTAGCTCAGTTGGTTAGAGCGCACCCCTGATAAGGGTGGAGTGGCGAGTTCGAA 144  
 |||||

Db 225 GGCTATTAGCTCAGTTGGTTAGAGCGCACCCCTGATAAGGGTGGAGTTCGCTGTTCAA 284  
 |||||

QY 145 TCTGCCAGACCCACCA-ATTTCGTGGGGCCATAGCTCAGTGGGAGAGCCCTGCCTTG 203  
 |||||

Db 285 TCCAGGATAGCCACCATGAATAAGGGGTATAGCTCAGCTGGTAGAGCGCTGCTTTTG 344  
 |||||

QY 204 CAGCAGGAGGTGAGCGTTTCGATCCCGCTTGGCTCCA 241  
 |||||

Db 345 CAAGGCAGATGTGAGCGGTTTCAATCCGCTTATCTCCA 382  
 |||||

RESULT 6

BI544155

LOCUS

DEFINITION S129 Gracilaria lemaneiformis gametophyte cDNA library Gracilaria lemaneiformis cDNA 5', mRNA sequence.

ACCESSION BI544155.1 GI:19033837

VERSION EST.

KEYWORDS Gracilaria lemaneiformis.

SOURCE Gracilaria lemaneiformis.

ORGANISM Eukaryota; Rhodophyta; Florideophyceae; Gracilariiales;

REFERENCE 1 (bases 1 to 548)

AUTHORS Sun, X., Yang, G.P., Mao, Y. X. and Zhang, X. C.

TITLE Analysis of expressed sequence tags of a marine red alga,

JOURNAL Gracilaria lemaneiformis

COMMENT Unpublished (2001)

Contact: Sun, X.; Zhang, X. C.

College of Marine Life Sciences

Ocean University of Qingdao

Yushan Road 5, Qingdao, 266003, Shandong, China

Tel: +86-0532-2032789

Fax: +86-0532-2032276

Email: xc Zhang@ouqd.edu.cn

PCR Primers

FORWARD: 5' -CGTGGTACCATGGTCTAGAGT-3'

BACKWARD: 5' -CTGATCTAGACCTGCAGGCTC-3'

Seq primer: 5' -CGTGGTACCATGGTCTAGAGT-3'

POLYA=Yes.

FEATURES Location/Qualifiers

1. 548

/organism="Gracilaria lemaneiformis"

/db\_xref="taxon:2778"

/clone\_lib="Gracilaria lemaneiformis gametophyte cDNA

library"

/tissue\_type="gametophyte thalli"

/note="Vector: pMD 18-T; Site 1: EcoR V with a T hang;

Wild type Gracilaria lemaneiformis were harvested from

Zhanshan Bay, Qingdao (China). After rinsed with boiled

seawater, younger thalli was cut and washed every 3-4

days until 1 month. Then thalli was cultivated in

Provasoli medium. Total RNA was isolated from thalli of

gametophyte algae, using UNIQ-10 Trizol Total RNA

Preparation Kit(Sangon Inc., Shanghai, China). The cDNA

was synthesized, amplified and cloned using cDNA

Synthesis Kit, cDNA PCR Library Kit and pMD 18-T vector

respectively."

BASE COUNT 183 a 92 c 107 g 166 t

ORIGIN

|                       |                                                                     |                                                                  |                                                                     |
|-----------------------|---------------------------------------------------------------------|------------------------------------------------------------------|---------------------------------------------------------------------|
| Db                    | 66                                                                  | GGGCTATTAGTCTAGTTGGTTAGAGCGCACCCCTGATAGGGTGAAGTCCCTGGTTCAA       | 125                                                                 |
| QY                    | 145                                                                 | TCTGCCAGACCCACCA-ATTTCGTGGGGCATAGCTCAGCTGGGAGAGCGCCTGCCTTG       | 203                                                                 |
| Db                    | 126                                                                 | TCCAGGTAGCCCAACCATGAATAAAGGGGTATAGCTCAGCTGTTAGAGTGCTGCTTTG       | 185                                                                 |
| QY                    | 204                                                                 | CACGACGAGGTACAGCGGTTTCGATCCCGCTTGGCTCCA                          | 241                                                                 |
| Db                    | 186                                                                 | CAAGCGAGATGTCAGCGGTTCAATCGCGCTTATCTCCA                           | 223                                                                 |
| RESULT 8              |                                                                     |                                                                  |                                                                     |
| BH400944/c            |                                                                     |                                                                  |                                                                     |
| LOCUS                 |                                                                     |                                                                  |                                                                     |
| DEFINITION            | BH400944                                                            | 593 bp                                                           | DNA linear GSS 11-DEC-2001                                          |
| ACCESSION             | BH400944                                                            |                                                                  | AG-ND-158022.TF ND-TAM Anopheles gambiae genomic clone AG-ND-158022 |
| VERSION               | BH400944.1                                                          | GI:17347147                                                      | , DNA sequence.                                                     |
| KEYWORDS              | GSS.                                                                |                                                                  |                                                                     |
| SOURCE                | African malaria mosquito.                                           |                                                                  |                                                                     |
| ORGANISM              | Anopheles gambiae                                                   |                                                                  |                                                                     |
|                       | Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;       |                                                                  |                                                                     |
|                       | Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea;           |                                                                  |                                                                     |
|                       | Anopheles.                                                          |                                                                  |                                                                     |
| REFERENCE             | 1 (bases 1 to 593)                                                  |                                                                  |                                                                     |
| AUTHORS               | Shetty,J., Malek,J., Koo,H., Collins,F., Gardner,M. and Loftus,B.J. |                                                                  |                                                                     |
| TITLE                 | Direct Submission of BAC-end sequences from Anopheles gambiae       |                                                                  |                                                                     |
| JOURNAL               | Unpublished (2001)                                                  |                                                                  |                                                                     |
| COMMENT               | Other GSSs: AG-ND-158022.TR                                         |                                                                  |                                                                     |
|                       | Contact: Brendan J Loftus                                           |                                                                  |                                                                     |
|                       | Department of Eukaryotic Genomics                                   |                                                                  |                                                                     |
|                       | The Institute for Genomic Research                                  |                                                                  |                                                                     |
|                       | 9712 Medical Center Dr., Rockville, MD 20850, USA                   |                                                                  |                                                                     |
|                       | Tel: 301 838 0208                                                   |                                                                  |                                                                     |
|                       | Fax: 301 838 3543                                                   |                                                                  |                                                                     |
|                       | Email: bjloftus@tigr.org                                            |                                                                  |                                                                     |
|                       | This clone is from an A. gambiae BAC library (ND-TAM) provided by   |                                                                  |                                                                     |
|                       | F.H. Collins and sequenced by The Institute for Genomic Research    |                                                                  |                                                                     |
|                       | (TIGR). The BAC library was generated from A. gambiae PEST strain   |                                                                  |                                                                     |
|                       | DNA. All DNA was extracted from newly hatched first instar larvae   |                                                                  |                                                                     |
|                       | to minimize the inclusion of DNA from microorganisms that inhabit   |                                                                  |                                                                     |
|                       | the gut. The DNA is derived from mixed sexes of larvae. The BAC     |                                                                  |                                                                     |
|                       | library was constructed at Texas A&M University BAC Center          |                                                                  |                                                                     |
|                       | University, College Station, Texas 77843-2123, USA using a HindIII  |                                                                  |                                                                     |
|                       | partial digest.                                                     |                                                                  |                                                                     |
|                       | Seq primer: M13 For                                                 |                                                                  |                                                                     |
|                       | Class: BAC ends.                                                    |                                                                  |                                                                     |
| FEATURES              |                                                                     |                                                                  |                                                                     |
| Source                | Location/Qualifiers                                                 |                                                                  |                                                                     |
|                       | 1..593                                                              |                                                                  |                                                                     |
|                       | /organism="Anopheles gambiae"                                       |                                                                  |                                                                     |
|                       | /strain="PEST"                                                      |                                                                  |                                                                     |
|                       | /db_xref="taxon:7165"                                               |                                                                  |                                                                     |
|                       | /clone="AG-ND-158022"                                               |                                                                  |                                                                     |
|                       | /clone_lib="ND-TAM"                                                 |                                                                  |                                                                     |
|                       | /note="Vector: pECBAC1; Site_1: HindIII"                            |                                                                  |                                                                     |
| BASE COUNT            | 119 a 157 c 118 g 199 t                                             |                                                                  |                                                                     |
| ORIGIN                |                                                                     |                                                                  |                                                                     |
| Query Match           | 16.6%;                                                              | Score 77.8;                                                      | DB 17; Length 593;                                                  |
| Best Local Similarity | 77.4%;                                                              | Pred: No. 4.7e-13;                                               |                                                                     |
| Matches 120;          | Conservative 0;                                                     | Mismatches 33;                                                   | Indels 3; Gaps 2;                                                   |
| QY                    | 91                                                                  | GTAGTCTAGTTGGTTAGAGCGCACCCCTGATAGGGTGAAGGTCAGCTGGCAGTTCCAATCTGCC | 150                                                                 |
| Ddb                   | 574                                                                 | GTAGTCTAGCTGTTAGAGCGCTACACTGATATGTAGAGGTGCGCAGTTTCGAGCCTGCC      | 515                                                                 |
| QY                    | 151                                                                 | CAGACCCACCAATT--TGC TTGGGGCCATAGCTCAGCTGG--GAGAGCGGCTGCCTTGCACG  | 207                                                                 |
| Ddb                   | 514                                                                 | CGAGACTACTTAATTGAAAAGGGGAATTAGCTCAGCTGGCTAGAGCGCTGCCTTGCACG      | 455                                                                 |
| QY                    | 208                                                                 | CAGGAGGTTCAGCGGTTTCGATCCCGCTTGGCTCCAC                            | 242                                                                 |

```

Db 454 CAGGAGTCAAGGTTGACTCCCTTATCTCCAC 420

RESULT 9
BH393190/c
LOCUS
DEFINITION AG-ND-168H12.TR ND-TAM Anopheles gambiae genomic clone AG-ND-168H12
, DNA sequence.
ACCESSION BH393190
VERSION BH393190.1 GI:17339331
KEYWORDS GSS.
SOURCE African malaria mosquito.
ORGANISM Anopheles gambiae
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea;
Anopheles.
REFERENCE 1 (bases 1 to 760)
AUTHORS Shetty,J., Malek,J., Koo,H., Collins,F., Gardner,M. and Loftus,B.J.
TITLE Direct Submission of BAC-end sequences from Anopheles gambiae
JOURNAL Unpublished (2001)
COMMENT Other_GSSs: AG-ND-168H12.TF
Contact: Brendan J Loftus
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 0208
Fax: 301 838 3543
Email: bjlftus@tigr.org
This clone is from an A. gambiae BAC library (ND-TAM) provided by
F.H. Collins and sequenced by The Institute for Genomic Research
(TIGR). The BAC library was generated from A. gambiae PEST strain
(DNA). All DNA was extracted from newly hatched first instar larvae
to minimize the inclusion of DNA from microorganisms that inhabit
the gut. The DNA is derived from mixed sexes of larvae. The BAC
library was constructed at Texas A&M University BAC Center
University, College Station, Texas 77843-2123, USA using a HindIII
partial digest.
Seq primer: M13 Rev
Class: BAC ends.
FEATURES
source
Location/Qualifiers
1..760
/organism="Anopheles gambiae"
/strain="PEST"
/db_xref="taxon:7165"
/clone_lib="AG-ND-168H12"
/notes="Vector: pECBAC1; Site_1: HindIII"
BASE COUNT 171 a 187 c 139 g 263 t
ORIGIN

Query Match 16.6%; Score 77.8; DB 17; Length 760;
Best Local Similarity 77.4%; Pred. No. 5.8e-13;
Matches 120; Conservative 0; Mismatches 32; Indels 3; Gaps 2;

QY 91 GTAGCTCAGTTGGTTAGACGCACCCCTGATAAGGTTGAGTTCGCGAGTTGCAATCTGCC 150
||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
Db 569 GTAGCTCAGCTGGTTAGACGCTACACTGATAATAGAGTTCGCGAGTTCGAGCTGCC 510
||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
QY 151 CAGACCCACCAATT--TGCTGGGCCATAGCTCAGCTGG-GAGAGCGCTGCTTGCAGC 207
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 509 CGAGACTACTAATTGAAAGGGGAATAGCTCAGCTGGTAGAGCGCTGCTTGCACG 450
||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
QY 208 CAGGAGTTCAGCGTTTCGATCCCGCTTGGCTCCAC 242
||||| ||||||| ||||||| || | | | | | | | | | | | | | | | | | | |
Db 449 CAGGAGTTCAGGTTTCGACTCCCTTATCTCCAC 415
||||| ||||||| ||||||| || | | | | | | | | | | | | | | | | | | |

RESULT 10
BH771024
LOCUS
DEFINITION LMGtag746 MG1363 Random Sequence Tag Library Lactococcus lactis
subsp. cremoris genomic, DNA sequence.
ACCESSION BH771024

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```

BH771024.1 GI:20373981
GSS.
Lactococcus lactis subsp. cremoris.
Lactococcus lactis subsp. cremoris
Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
Lactococcus.
REFERENCE 1 (bases 1 to 6499)
AUTHORS Bolotin,A., Ehrlich,S.D. and Sorokin,A.
TITLE Studies of genomes of dairy bacteria Lactococcus lactis
JOURNAL Sci. Aliments, (2002) In press
COMMENT Contact: Sorokin A
Genetique Microbienne
INRA
CRJ INRA, Domaine de Vilvert, 78352 Jouy en Josas cedex, France
Tel: 33 1 34 65 25 16
Fax: 33 1 34 65 25 21
Email: sorokine@jouy.inra.fr
best homologue in strain IL1403 is ywgA (78%)
Class: shotgun
High quality sequence start: 30
High quality sequence stop: 6471.
High quality Location/Qualifiers
1..6499
/organism="Lactococcus lactis subsp. cremoris"
/strain="MG1363"
/db_xref="taxon:1359"
/clone_lib="MG1363 Random Sequence Tag Library"
/notes="Vector: pSGMU2; Site_1: SmaI; Library of
chromosomal fragments of L.lactis strain MG1363 was
prepared by partial AluI digestion or by sonication."
BASE COUNT 1946 a 1228 c 1683 g 1642 t
ORIGIN

Query Match 14.8%; Score 69.2; DB 17; Length 6499;
Best Local Similarity 95.9%; Pred. No. 1.7e-09;
Matches 71; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 168 TGGGGCCATAGCTCAGCTGGGAGAGCGCCCTGCCTTCGACGAGTACGCGTTTCGAT 227
||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
Db 2164 TGGGGCCTTAGCTCAGCTGGGAGAGCGCCCTGCCTTCGACGAGTACGCGTTTCGAT 2223
||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||

QY 228 CCGCTTGGCTCCA 241
||||| |||||||
Db 2224 CCGCTAGGCTCCA 2237
||||| |||||||

RESULT 11
AZ578476/c
LOCUS
DEFINITION AZ578476
191 bp DNA linear GSS 08-DEC-2000
23h03 Shot-gun genomic library of Rhizobium strain ANU265 Rhizobium
sp. NGR234 genomic clone 23h03, DNA sequence.
ACCESSION AZ578476
VERSION AZ578476.1 GI:11605796
KEYWORDS GSS.
SOURCE Rhizobium sp. NGR234.
ORGANISM Rhizobium sp. NGR234
Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
Rhizobiaceae; Rhizobium.
REFERENCE 1 (bases 1 to 191)
AUTHORS Viprey,V., Rosenthal,A., Broughton,W.J. and Perret,X.
TITLE Genetic snapshots of the Rhizobium species NGR234 genome
JOURNAL Genome Biol. 1 (6), RESEARCH0014 (2000)
MEDLINE 2114532
COMMENT Contact: Virginie Viprey
Laboratoire de Biologie Molculaire des Plantes Supérieures
University of Geneva
1 Chemin de l'Imperatrice, Chambesy/Geneva 1292, Switzerland
Tel: +44(0)1603450000
Fax: +44(0)1603450045
Email: virginie.viprey@bbsrc.ac.uk
Class: shotgun.
Location/Qualifiers
1..191

```



/organism="Rhizobium sp. NGR234"  
/strain="ANU265"  
/db\_xref="taxon:394"  
/clone="23h03"  
/clone\_lib="Shot-gun genomic library of Rhizobium strain ANU265"  
/note="Vector: M13; derivative strain of NGR234 cured of pNGR234a"  
BASE COUNT 47 a 62 c 44 g 37 t 1 others  
ORIGIN  
Query Match 14.6%; Score 68.4; DB 17; Length 191;  
Best Local Similarity 78.6%; Pred. No. 1.7e-10;  
Matches 81; Conservative 0; Mismatches 22; Indels 0; Gaps 0;  
QY 151 CAGACCCACCAATTGCTGGGCGATAGCTCAGCTGAGAGCCCTGCTGCACGAG 210  
|||||  
Db 129 CAGATGATCAACAGGTTGGGCTGTAGCTCAGCTGGGAGACACNTGCTTTCGACG 70  
QY 211 GAGGTACGCGGTTCGATCCCGCTTGGCTCCACCCCGCTTG 253  
|||||  
Db 69 GGGGTACGCGGTTCGATCCCGCTCAGCTCCACCAATTGATG 27

RESULT 12  
BH159957/c  
LOCUS  
DEFINITION  
ENTSI13TF Entamoeba histolytica Sheared DNA linear GSS 24-SEP-2001  
genomic, DNA sequence.  
ACCESSION  
BH159957  
VERSION  
BH159957.1 GI:15733395  
KEYWORDS  
GSS.  
SOURCE  
Entamoeba histolytica.  
ORGANISM  
Entamoeba histolytica  
Eukaryota; Entamoebidae; Entamoeba.  
REFERENCE  
1 (bases 1 to 904)  
Loftus B., Wang, Z., Van Aken, S. and Fraser, C.  
Determination of clone end sequences from Entamoeba histolytica  
HMI:IMSS sheared DNA library (2001)  
Unpublished (2001)  
Contact: Brendan J Loftus  
Department of Eukaryotic Genomics  
The Institute for Genomic Research  
9712 Medical Center Dr., Rockville, MD 20850, USA  
Tel: 301 838 0208  
Fax: 301 838 3543  
Email: bjloftus@tigr.org  
Clones are derived from the Entamoeba histolytica HMI:IMSS sheared  
DNA library  
Seq primer: M13-Forward  
Class: Shotgun  
High quality sequence start: 34  
High quality sequence stop: 576.  
FEATURES  
source  
1..904  
Location/Qualifiers  
/organism="Entamoeba histolytica"  
/strain="HMI:IMSS"  
/db\_xref="taxon:5759"  
/clone\_lib="Entamoeba histolytica Sheared DNA"  
/note="Vector: PHOS1; Site 1: Bst I; Constructed at The  
Institute for Genomic Research (TIGR), Rockville, MD.  
Genomic DNA isolated from broth cultures of E. histolytica  
using a method described by Clark and Diamond (Clark,  
C.G., and Diamond, L.S. (1993) Entamoeba histolytica: a  
method for isolate identification. Exp. Parasitol.  
77:450.). The DNA was mechanically sheared to give a  
tight size distribution (~2 kb). The v + i method used for  
the library construction is described in detail in Smith,  
H.O. and Venter, J.C. (Making small insert libraries for  
whole genome shotgun sequencing projects. In Genome  
Sequencing: A Practical Approach, eds. M. Vaudin and B.  
Barell, Oxford University Press, 1999)."

BASE COUNT

304 a 166 c 96 g 338 t

## ORIGIN

Query Match 14.2%; Score 66.6; DB 17; Length 904;  
Best Local Similarity 63.9%; Pred. No. 2.2e-09;  
Matches 117; Conservative 0; Mismatches 64; Indels 2; Gaps 1;  
QY 62 GATTAGGTAGCAACCTTCGATTGGTCTGTAGCTCAGTTGAGCGCACCCCTCGAT 121  
|||||  
Db 882 GATTAGGTGGTTCGCCAGGTAATAGGATCTTAGCTCAGTGGTGAGACACCGGGTTCAT 823  
QY 122 AAGGTGAGGTGCGCAGTTCCAAATCTGCCAGACCCACCAATTTCTGGGGCCATGCTC 181  
|||||  
Db 822 ACCGGTAGGTCCCGGGTTGGATTCCCTGAAGGTCCCAATTT--TGGGGGTATAGTGC 765  
QY 182 AGCTGGGAGCGCTGCTGCTGCACGAGGAGTTCAGGCTTCCGATCCCGCTTGGCTCCA 241  
|||||  
Db 764 AGTGGGAAGAGCACTTGCTTGCAGGCGGGGTTCAGGAGTTTGATTCCTCTACTTCCA 705  
QY 242 CCA 244  
Db 704 CGA 702

## RESULT 13

BH819575  
LOCUS  
DEFINITION  
BACPP13-El4.y Pristionchus pacificus BAC ends Pristionchus  
pacificus genomic, DNA sequence.  
ACCESSION  
BH819575  
VERSION  
BH819575.1 GI:20993843  
KEYWORDS  
GSS.  
SOURCE  
Pristionchus pacificus.  
ORGANISM  
Pristionchus pacificus  
Eukaryota; Metazoa; Nematoda; Chromadorea; Diplogasterida;  
Neodiplogasteridae; Pristionchus.  
REFERENCE  
1 (bases 1 to 577)  
Srinivasan, J., Sinz, W., Lanz, C., Brand, A., Nandakumar, R., Raddatz  
G., Witte, H., Keller, H., Kipping, I., Pires da Silva, A., Jesse, T.,  
Millare, J., de Both, M., Schuster, S.C. and Sommer, R.J.  
A BAC-based genetic linkage map of the nematode Pristionchus  
pacificus  
Unpublished (2002)  
Contact: Sommer RJ  
Evolutionary Biology  
Max-Planck-Institute for Developmental Biology  
Spemannstr. 37-39, Tuebingen D-72076, Germany  
Tel: 00497071601371  
Fax: 00497071601498  
Email: ralf.sommer@tuebingen.mpg.de  
Class: BAC ends.

FEATURES  
source

1..577  
Location/Qualifiers  
/organism="Pristionchus pacificus"  
/strain="var. California"  
/db\_xref="taxon:54126"  
/clone\_lib="Pristionchus pacificus BAC ends"  
BASE COUNT 129 a 142 c 139 g 167 t  
ORIGIN

Query Match 14.1%; Score 65.8; DB 17; Length 577;  
Best Local Similarity 78.2%; Pred. No. 2.7e-09;  
Matches 79; Conservative 0; Mismatches 22; Indels 0; Gaps 0;  
QY 168 TGGGGCCATAGCTCAGCTGGGAGAGCGCTGCTTCACGACGAGGAGTTCAGCGGTTTCGAT 227  
Db 118 TGGGGCTATAGCTCAGCTGGGAGAGCGCTTGCATGCAAGAGTTCAGCGGTTTCGAT 177  
QY 228 CCGGCTTGCTCCACACCCCGCTTGCAGTTTGTCAAGC 268  
|||||  
Db 178 CCGGCTTAGCTCCACCAATTTCCACCCCTCGCTGCAGAAC 218  
RESULT 14

